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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:19:27 ; Search time 213.041 Seconds
(without alignments)
294.149 Million cell updates/sec

Title: US-08-325-278B-1_COPY_225_296

Perfect score: 370

Sequence: 1 KEKTPPEPKREVITKANLIY.....GRYTADLEDGGVTINIRFAG 72

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 5580241 seqs, 870357830 residues

Total number of hits satisfying chosen parameters: 5580241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents_AA_Main.*

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26: /cgn2_6/ptodata/1/paa/US100_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	370	100.0	72	23	US-09-808-212A-10
2	370	100.0	305	7	US-08-325-278-1

3	370	100.0	305	7	US-08-325-278A-1	Sequence 1, Appli
4	370	100.0	305	7	US-08-325-278B-1	Sequence 1, Appli
5	370	100.0	434	7	US-08-325-278-3	Sequence 3, Appli
6	370	100.0	434	7	US-08-325-278A-3	Sequence 3, Appli
7	370	100.0	434	7	US-08-325-278B-3	Sequence 3, Appli
8	370	100.0	457	25	US-09-980-469-12	Sequence 12, Appli
9	370	100.0	719	22	US-09-791-537-10210	Sequence 10210, A
10	370	100.0	719	22	US-09-791-537-96101	Sequence 96101, A
11	339	91.6	72	23	US-09-808-212A-8	Sequence 8, Appli
12	329	88.9	75	23	US-09-808-212A-18	Sequence 18, Appli
13	329	88.9	291	8	US-08-446-137A-4	Sequence 4, Appli
14	329	88.9	992	22	US-09-791-537-88366	Sequence 88366, A
15	329	88.9	1027	7	US-08-331-637-2	Sequence 2, Appli
16	329	88.9	1027	8	US-08-446-137A-2	Sequence 2, Appli
17	329	88.9	1027	15	US-09-187-295-2	Sequence 2, Appli
18	322	87.0	72	23	US-09-808-212A-6	Sequence 6, Appli
19	322	87.0	72	23	US-09-889-182A-4	Sequence 4, Appli
20	315.5	85.3	71	23	US-09-808-212A-14	Sequence 14, Appli
21	306	82.7	74	23	US-09-808-212A-16	Sequence 16, Appli
22	304	82.2	82	23	US-09-808-212A-2	Sequence 2, Appli
23	269	72.7	76	23	US-09-808-212A-4	Sequence 4, Appli
24	269	72.7	78	22	US-09-791-537-22553	Sequence 22553, A
25	254	68.6	182	19	US-09-509-031-2	Sequence 2, Appli
26	254	68.6	182	23	US-09-820-048A-2	Sequence 2, Appli
27	251.5	68.0	71	23	US-09-808-212A-12	Sequence 12, Appli
28	246	66.5	178	19	US-09-509-031-13	Sequence 13, Appli
29	246	66.5	178	23	US-09-820-048A-13	Sequence 13, Appli
30	246	66.5	198	19	US-09-509-031-8	Sequence 8, Appli
31	246	66.5	198	23	US-09-820-048A-8	Sequence 8, Appli
32	246	66.5	342	19	US-09-509-031-6	Sequence 6, Appli
33	246	66.5	342	23	US-09-820-048A-6	Sequence 6, Appli
34	246	66.5	482	19	US-09-509-031-16	Sequence 16, Appli
35	246	66.5	495	19	US-09-509-031-4	Sequence 4, Appli
36	246	66.5	495	23	US-09-820-048A-4	Sequence 4, Appli
37	73	19.7	1447	30	US-10-437-963-198658	Sequence 198658, A
38	71	19.2	166	31	US-60-452-680-16977	Sequence 16977, A
39	70	18.9	212	16	US-09-270-767-32555	Sequence 32555, A
40	70	18.9	212	16	US-09-270-767-47772	Sequence 47772, A
41	70	18.9	212	16	US-09-270-849B-185762	Sequence 185762, A
42	69.5	18.8	1032	1	PCT-US03-07858-1457	Sequence 1457, Ap
43	69.5	18.8	1032	1	PCT-US03-07858A-1457	Sequence 1457, Ap
44	69.5	18.8	1086	1	PCT-US03-07858-2239	Sequence 2239, Ap
45	69.5	18.8	1086	1	PCT-US03-07858A-2239	Sequence 2239, Ap

ALIGNMENTS

RESULT 1
US-09-808-212A-10
; Sequence 10, Application US/09808212A
; GENERAL INFORMATION:
; APPLICANT: Gore, Michael Graham
; APPLICANT: Beckingham, Jennifer Ann
; APPLICANT: Robertts, Sian Eleri
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN
; FILE REFERENCE: 100084.41405
; CURRENT APPLICATION NUMBER: US/09/808.212A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Peptostreptococcus sp.
US-09-808-212A-10

Query Match 100.0%; Score 370; DB 23; Length 72;
Best Local Similarity 100.0%; Pred. No. 5.5e-37;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEKTPPEPKREVITKANLIYADGKTQTAEKGFATATAYRYADLLAKENKYTDLE 60
1
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Db 1 KKTPEEPKEEVIKANLIYADGKTQTAEFGTFAETAEAYRYADLLAKENGKYTDLE 60
QY 61 DGGYTINIRFAG 72
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Db 61 DGGYTINIRFAG 72

RESULT 2
US-08-325-278-1
; Sequence 1, Application US/08325278
; GENERAL INFORMATION:
; APPLICANT: Bjorck, Lars
; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 26-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 450023.401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 305 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli LE392/pHDL, DSM 7054
;
US-08-325-278-1
Query Match 100.0%; Score 370; DB 7; Length 305;
Best Local Similarity 100.0%; Pred. No. 4.le-36;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKTPEEPKEEVIKANLIYADGKTQTAEFGTFAETAEAYRYADLLAKENGKYTDLE 60
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Db 225 KKTPEEPKEEVIKANLIYADGKTQTAEFGTFAETAEAYRYADLLAKENGKYTDLE 284
| | | | | | | | | |
QY 61 DGGYTINIRFAG 72
| | | | | | | | | |
Db 285 DGGYTINIRFAG 296

RESULT 3
US-08-325-278A-1
; Sequence 1, Application US/08325278A
; GENERAL INFORMATION:
; APPLICANT: Bjorck, Lars
; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed IP Law Group
; STREET: 701 Fifth Avenue Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 26-Oct-1994
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.

US-08-325-278B-1
; Sequence 1, Application US/08325278B
; GENERAL INFORMATION:
; APPLICANT: Bjorck, Lars
; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed IP Law Group
; STREET: 701 Fifth Avenue Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 26-Oct-1994
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.
```

REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 100084.402
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 305 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORGANISM: Escherichia coli LE392/pHDL, DSM 7054
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-08-325-278B-1

Query Match 100.0%; Score 370; DB 7; Length 305;
Best Local Similarity 100.0%; Pred. No. 4.1e-36;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKTPEPKKEVITKANLIYADGKTQTAEFGTFAEATAEAYRYADLLAKENGYTADLE 60
DB 225 KKTPEPKKEVITKANLIYADGKTQTAEFGTFAEATAEAYRYADLLAKENGYTADLE 284
QY 61 DGGYTINIRFAG 72
DB 285 DGGYTINIRFAG 296

RESULT 5
US-08-325-278-3
Sequence 3, Application US/08325278
GENERAL INFORMATION:
APPLICANT: Bjvick, Lars
APPLICANT: Sjobring, Ulf
TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,278
FILING DATE: 26-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McWaters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 450023.401
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORGANISM: Escherichia coli LE392/pHDLG, DSM 7055
US-08-325-278-3

Query Match 100.0%; Score 370; DB 7; Length 434;
Best Local Similarity 100.0%; Pred. No. 6.7e-36;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKTPEPKKEVITKANLIYADGKTQTAEFGTFAEATAEAYRYADLLAKENGYTADLE 60
DB 225 KKTPEPKKEVITKANLIYADGKTQTAEFGTFAEATAEAYRYADLLAKENGYTADLE 284
QY 61 DGGYTINIRFAG 72
DB 285 DGGYTINIRFAG 296

RESULT 6
US-08-325-278A-3
Sequence 3, Application US/08325278A
GENERAL INFORMATION:
APPLICANT: Bjvick, Lars
APPLICANT: Sjobring, Ulf
TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed IP Law Group
STREET: 701 Fifth Avenue Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,278A
FILING DATE: 26-Oct-1994
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 100084.402
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Escherichia coli LE392/pHDLG, DSM 7055
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-325-278A-3

Query Match 100.0%; Score 370; DB 7; Length 434;
Best Local Similarity 100.0%; Pred. No. 6.7e-36;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKTPEPKKEVITKANLIYADGKTQTAEFGTFAEATAEAYRYADLLAKENGYTADLE 60
DB 225 KKTPEPKKEVITKANLIYADGKTQTAEFGTFAEATAEAYRYADLLAKENGYTADLE 284
QY 61 DGGYTINIRFAG 72
DB 285 DGGYTINIRFAG 296

RESULT 7
US-08-325-278B-3

; Sequence 3, Application US/08325278B
; GENERAL INFORMATION:
; APPLICANT: Bjorck, Lars
; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed IP Law Group
; STREET: 701 Fifth Avenue Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,278B
; FILING DATE: 26-Oct-1994
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 100084.402
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 434 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli LE392/pHDLG, DSM 7055
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-325-278b-3

Query Match 100.0%; Score 370; DB 7; Length 434;
Best Local Similarity 100.0%; Pred. No. 6.7e-36;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKTPEEPKEEVTIRKANLIYADGKTQTAEFGKTFEAATAEAYRYADLLAKENGKYTDLE 60
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DB 225 KKTPEEPKEEVTIRKANLIYADGKTQTAEFGKTFEAATAEAYRYADLLAKENGKYTDLE 284
|||||

QY 61 DGGYTINIRFAG 72
|||||
DB 285 DGGYTINIRFAG 296
|||||

RESULT 8
US-09-980-469-12
; Sequence 12, Application US/09980469
; GENERAL INFORMATION:
; APPLICANT: ziv, Shani
; TITLE OF INVENTION: PROCESS OF EXPRESSING AND ISOLATING RECOMBINANT PROTEINS AND RECO
; TITLE OF INVENTION: PROTEIN PRODUCTS FROM PLANTS, PLANT DERIVED TISSUES OR CULTURED
; FILE REFERENCE: 01/22924
; CURRENT APPLICATION NUMBER: US/09/980,469
; CURRENT FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:

; OTHER INFORMATION: pUC19-cell-ProTL-cexNG-HDEL fusion encoded product
US-09-980-469-12

Query Match 100.0%; Score 370; DB 25; Length 467;
Best Local Similarity 100.0%; Pred. No. 7.4e-36;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKTPEEPKEEVTIRKANLIYADGKTQTAEFGKTFEAATAEAYRYADLLAKENGKYTDLE 60
|||||
DB 265 KKTPEEPKEEVTIRKANLIYADGKTQTAEFGKTFEAATAEAYRYADLLAKENGKYTDLE 324
|||||

QY 61 DGGYTINIRFAG 72
|||||
DB 325 DGGYTINIRFAG 336
|||||

RESULT 9
US-09-791-537-10210
; Sequence 10210, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10210
; LENGTH: 719
; TYPE: PRT
; ORGANISM: Peptostreptococcus magnus
US-09-791-537-10210

Query Match 100.0%; Score 370; DB 22; Length 719;
Best Local Similarity 100.0%; Pred. No. 1.4e-35;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKTPEEPKEEVTIRKANLIYADGKTQTAEFGKTFEAATAEAYRYADLLAKENGKYTDLE 60
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DB 318 KKTPEEPKEEVTIRKANLIYADGKTQTAEFGKTFEAATAEAYRYADLLAKENGKYTDLE 377
|||||

QY 61 DGGYTINIRFAG 72
|||||
DB 378 DGGYTINIRFAG 389
|||||

RESULT 10
US-09-791-537-96101
; Sequence 96101, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 96101
; LENGTH: 719
; TYPE: PRT
; ORGANISM: Peptostreptococcus magnus
US-09-791-537-96101

Query Match 100.0%; Score 370; DB 22; Length 719;
Best Local Similarity 100.0%; Pred. No. 1.4e-35;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KEKTPPEPKBEVTIKANLIYADGKTQTAEFGTFAEATAEAYRYADLLAKENGYTADLE 60
 Db 318 KEKTPPEPKBEVTIKANLIYADGKTQTAEFGTFAEATAEAYRYADLLAKENGYTADLE 377
 Qy 61 DGGYTINIRFAG 72
 Db 378 DGGYTINIRFAG 389

RESULT 11
 US-09-808-212A-8
 ; Sequence 8, Application US/09808212A
 ; GENERAL INFORMATION:
 ; APPLICANT: Gore, Michael Graham
 ; APPLICANT: Beckingham, Jennifer Ann
 ; APPLICANT: Roberts, Sian Eleri
 ; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN
 ; FILE REFERENCE: 100084.414US
 ; CURRENT APPLICATION NUMBER: US/09/808,212A
 ; CURRENT FILING DATE: 2001-03-13
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 8
 ; LENGTH: 72
 ; TYPE: PRT
 ; ORGANISM: Peptostreptococcus sp.
 US-09-808-212A-8

Query Match 91.6%; Score 339; DB 23; Length 72;
 Best Local Similarity 90.3%; Pred. No. 3.4e-33;
 Matches 65; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KEKTPPEPKBEVTIKANLIYADGKTQTAEFGTFAEATAEAYRYADLLAKENGYTADLE 60
 Db 1 KEKTPPEPKBEVTIKANLIYADGKTQTAEFGTFAEATAEAYRYADLLAKENGYTADVA 60
 Qy 61 DGGYTINIRFAG 72
 Db 61 DGGYTINIRFAG 72

RESULT 12
 US-09-808-212A-18
 ; Sequence 18, Application US/09808212A
 ; GENERAL INFORMATION:
 ; APPLICANT: Gore, Michael Graham
 ; APPLICANT: Beckingham, Jennifer Ann
 ; APPLICANT: Roberts, Sian Eleri
 ; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN
 ; FILE REFERENCE: 100084.414US
 ; CURRENT APPLICATION NUMBER: US/09/808,212A
 ; CURRENT FILING DATE: 2001-03-13
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 18
 ; LENGTH: 75
 ; TYPE: PRT
 ; ORGANISM: Peptostreptococcus sp.
 US-09-808-212A-18

Query Match 88.9%; Score 329; DB 23; Length 75;
 Best Local Similarity 90.0%; Pred. No. 6e-32;
 Matches 63; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 3 KTEPEPKBEVTIKANLIYADGKTQTAEFGTFAEATAEAYRYADLLAKENGYTADLEDG 62
 Db 5 ETPPEPKBEVTIKVNLIFADGKTQTAEFGTFAEATAEAYRYADLLAKVNGEYTDLEDG 64
 Qy 63 GYTINIRFAG 72
 Db 65 GYTINIRFAG 74

RESULT 13
 US-08-446-137A-4
 ; Sequence 4, Application US/08446137A
 ; GENERAL INFORMATION:
 ; APPLICANT:
 ; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEINS DERIVED
 ; FROM PROTEIN L AND THEIR USES
 ; NUMBER OF SEQUENCES: 4
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/446,137A
 ; FILING DATE: 22-05-1995
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MITCHARD, LEONARD C.
 ; REGISTRATION NUMBER: 29,009
 ; REFERENCE/DOCKET NUMBER: 1418-9
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 816-4000
 ; TELEFAX: (703) 816-4100
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 291 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-446-137A-4

Query Match 88.9%; Score 329; DB 8; Length 291;
 Best Local Similarity 90.0%; Pred. No. 4e-31;
 Matches 63; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 3 KTEPEPKBEVTIKANLIYADGKTQTAEFGTFAEATAEAYRYADLLAKENGYTADLEDG 62
 Db 221 ETPPEPKBEVTIKVNLIFADGKTQTAEFGTFAEATAEAYRYADLLAKVNGEYTDLEDG 280
 Qy 63 GYTINIRFAG 72
 Db 281 GYTINIRFAG 290

RESULT 14
 US-09-791-537-88366
 ; Sequence 88366, Application US/09791537
 ; GENERAL INFORMATION:
 ; APPLICANT: Bionomix, Inc.
 ; APPLICANT: Debe, Derek
 ; APPLICANT: Danzer, Joseph
 ; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
 ; TITLE OF INVENTION: METHODS OF USE THEREOF
 ; FILE REFERENCE: 261/210
 ; CURRENT APPLICATION NUMBER: US/09/791,537
 ; CURRENT FILING DATE: 2001-02-22
 ; NUMBER OF SEQ ID NOS: 153055
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 88366
 ; LENGTH: 992
 ; TYPE: PRT
 ; ORGANISM: Peptostreptococcus magnus
 US-09-791-537-88366

Query Match 88.9%; Score 329; DB 22; Length 992;
 Best Local Similarity 90.0%; Pred. No. 2.2e-30;
 Matches 63; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 3 KTEPEPKBEVTIKANLIYADGKTQTAEFGTFAEATAEAYRYADLLAKENGYTADLEDG 62
 Db 468 ETPPEPKBEVTIKVNLIFADGKTQTAEFGTFAEATAEAYRYADLLAKVNGEYTDLEDG 527

QY 63 GYTINIRFAG 72
| | | | | : | | |
Db 528 GYTINIKFAG 537

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RESULT 15
US-08-331-637-2
; Sequence 2, Application US/08331637
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROTEIN L AND PROCESS FOR ITS PREPARATION BY
; RECOMBINANT DNA TECHNOLOGY
; NUMBER OF SEQUENCES: 23
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,637
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-331-637-2

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Query Match 88.9%; Score 329; DB 7; Length 1027;
Best Local Similarity 90.0%; Pred. No. 2.3e-30;
Matches 63; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy	3	KTPEEPKEEVTIKANLIYADGKTQTAEFGTFEAATAEAYRYADLLAKENGKYTDLEDG	62
		:	
Db	503	ETPEEPKEEVTIKVNLFADGKTQTAEFGTFEAATAEAYRYADLLAKVNGEYTDLEDG	562

Qy 63 GYTINIRFAG 72
| | | | | : | | |
Db 563 GYTINIKFAG 572

Search completed: September 3, 2003, 11:40:09
Job time : 214.041 secs


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; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)E
; CURRENT APPLICATION NUMBER: US/10/613,520
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 10/389,566
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2578
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2239
; LENGTH: 1086
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-613-520-2239

Query Match      18.8%; Score 69.5; DB 6; Length 1086;
Best Local Similarity 25.6%; Pred. No. 2.5;
Matches 21; Conservative 15; Mismatches 29; Indels 17; Gaps 1;

QY 7 EPKEEVTIRANLIYADGKTQTAEFKGTAEAT-----AEAYRYADLLA 49
Db 497 EREDEDLGPAFVSAGQRAASSVGLFAGSSNNIYISTSQSFVNTLSELFQSA RLSA 556
QY 50 KENGKYTADLEDGGYTNIRFA 71
Db 557 SSLRYVYGLGLENGYTVTLQFA 578

RESULT 3
US-10-637-544-2
; Sequence 2, Application US/10637544
; GENERAL INFORMATION:
; APPLICANT: Chr. Hansen A/S
; TITLE OF INVENTION: Peptides with anti-hypertensive properties
; FILE REFERENCE: PI0320501
; CURRENT APPLICATION NUMBER: US/10/637,544
; CURRENT FILING DATE: 2003-08-11
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1849
; TYPE: PRT
; ORGANISM: Lactobacillus helveticus
US-10-637-544-2

Query Match      18.8%; Score 69.5; DB 6; Length 1849;
Best Local Similarity 35.1%; Pred. No. 4.8;
Matches 26; Conservative 9; Mismatches 28; Indels 11; Gaps 4;

QY 1 KEKTPPEPKEEVTIRANL---IYADGKTQ---TAEFKGTFAEATAEAYRYADLLAKENG 53
Db 1590 KENQSEDEKELAKENLOAKYDAGEKKLDKYTADSKDFNDALKKA---KDVLDKNA 1646
QY 54 KYTADLEDGGYTN 67
Db 1647 K-LADLQDAAKALD 1659

RESULT 4
US-10-613-520-1082
; Sequence 1082, Application US/10613520
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Laurie, Cathy C
; APPLICANT: Wu, Wei
; APPLICANT: Maolong, Lu
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)E
```

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; CURRENT APPLICATION NUMBER: US/10/613,520
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 10/389,566
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2578
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1082
; LENGTH: 2062
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-613-520-1082

Query Match      18.8%; Score 69.5; DB 6; Length 2062;
Best Local Similarity 25.6%; Pred. No. 5.6;
Matches 21; Conservative 15; Mismatches 29; Indels 17; Gaps 1;

QY 7 EPKEEVTIRANLIYADGKTQTAEFKGTAEAT-----AEAYRYADLLA 49
Db 1473 EREDEDLGPAFVSAGQRAASSVGLFAGSSNNIYISTSQSFVNTLSELFQSA RLSA 1532
QY 50 KENGKYTADLEDGGYTNIRFA 71
Db 1533 SSLRYVYGLGLENGYTVTLQFA 1554

RESULT 5
US-10-613-520-1944
; Sequence 1944, Application US/10613520
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Laurie, Cathy C
; APPLICANT: Wu, Wei
; APPLICANT: Maolong, Lu
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)E
; CURRENT APPLICATION NUMBER: US/10/613,520
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 10/389,566
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2578
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1944
; LENGTH: 858
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-613-520-1944

Query Match      18.5%; Score 68.5; DB 6; Length 858;
Best Local Similarity 35.7%; Pred. No. 2.4;
Matches 20; Conservative 9; Mismatches 22; Indels 5; Gaps 2;

QY 16 ANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTNIRFA 71
Db 305 SNNIYI--ATSLAQFINTM---DSELFQSA RLSSA SSSRYVYGLGLENGYTVTLQFA 355

RESULT 6
US-10-613-520-1237
; Sequence 1237, Application US/10613520
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
```

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; GENERAL INFORMATION:
; APPLICANT: Bauer et al.
; TITLE OF INVENTION: Protein Complexes and Methods for their Use
; FILE REFERENCE: 220615
; CURRENT APPLICATION NUMBER: US/10/326,956
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: EP 01 130 253.6
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 3282
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1315
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; US-10-326-956-1315

Query Match 18.1%; Score 67; DB 6; Length 283;
Best Local Similarity 25.7%; Pred No. 0.91;
Matches 18; Conservative 17; Mismatches 27; Indels 8; Gaps

QY 8 PKEVITKANLIYADGK--TQTAEPKGTGFAEATAEAYRYADLLA-----KENGKYTADL 529
      ||: ||: | | : : : || | | : | : : : : | | : | : | : |
Db 28 PQQAITSEASTTYPISRYISELLFKRQEAISLSAMAFLEQEMISQLHRTCKTAGDFETKL-87

QY 60 EDGGYITINIR 69
      | | : | | |
Db 88 SDYGHNIGIR 97

RESULT 9
US-10-613-520-1945
; Sequence 1945, Application US/10613520
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Laurie, Cathy C
; APPLICANT: Wu, Wei
; APPLICANT: Maolong, Lu
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)E
; CURRENT APPLICATION NUMBER: US/10/613,520
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 10/389,566
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2578
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1945
; LENGTH: 1029
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; US-10-613-520-1945

Query Match 18.0%; Score 66.5; DB 6; Length 1029;
Best Local Similarity 33.9%; Pred. No. 5.4;
Matches 19; Conservative 10; Mismatches 22; Indels 5; Gaps

QY 16 ANLIYADGKTQTAEPKGTGFAEATAEAYRYADLLAKENGKYTADLEDGGYITINIRFA 71
      : | | | : | : | : | : | : | : | : | : | : | : | : | : |
Db 473 SNNIYI--ATSQSFVNTL---DSELFQSFARLSASSVRYGGLGLENGGYVTVLQFA 523

RESULT 10
US-10-613-520-1238
; Sequence 1238, Application US/10613520
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Laurie, Cathy C
; APPLICANT: Wu, Wei

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; APPLICANT: Maolong, Lu
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)E
; CURRENT APPLICATION NUMBER: US/10/613,520
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 10/389,566
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2578
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1238
; LENGTH: 1032
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-613-520-1238

Query Match      18.0%; Score 66.5; DB 6; Length 1032;
Best Local Similarity 33.9%; Pred. No. 5.4;
Matches 19; Conservative 10; Mismatches 22; Indels 5; Gaps 2;

QY 16 ANLIYADGKTOTAEFKGTFAEATAEAYRYADLLAKENGYTADLEDGGYTIIRFA 71
Db 476 SNNIYL--ATSOQFNTL---DSSELFQASARSASSVRYGLGNGGYTVTLOFA 526

RESULT 11
PCT-US03-19070-2
; Sequence 2, Application PC/TUS0319070
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: INHIBITION OF T CELL ACTIVATION BY
; FILE REFERENCE: GNN-042PC
; CURRENT APPLICATION NUMBER: PCT/US03/19070
; CURRENT FILING DATE: 2003-06-17
; PRIOR APPLICATION NUMBER: US 60/389660
; PRIOR FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-19070-2

Query Match      17.6%; Score 65; DB 1; Length 334;
Best Local Similarity 30.4%; Pred. No. 2;
Matches 17; Conservative 11; Mismatches 18; Indels 10; Gaps 2;

QY 19 IYADGK----TOTAEFKGTFA-----EATAEAYRYADLLAKENGYTADLEDGGY 64
Db 78 VYADGKEVEDROSAPYRGRTSILRDGITAGKAAALRIHNVNTASDSGKYLICYFQDGF 133

RESULT 12
US-10-463-260-2
; Sequence 2, Application US/10463260
; GENERAL INFORMATION:
; APPLICANT: Wood, Clive R.
; APPLICANT: Carreno, Beatriz M.
; TITLE OF INVENTION: INHIBITION OF T CELL ACTIVATION BY
; FILE REFERENCE: GNN-042
; CURRENT APPLICATION NUMBER: US/10/463,260
; CURRENT FILING DATE: 2003-06-17
; PRIOR APPLICATION NUMBER: US 60/389660
; PRIOR FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 481
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-463-260-5

Query Match      17.6%; Score 65; DB 1; Length 481;
Best Local Similarity 30.4%; Pred. No. 3.1;
Matches 17; Conservative 11; Mismatches 18; Indels 10; Gaps 2;

QY 19 IYADGK----TOTAEFKGTFA-----EATAEAYRYADLLAKENGYTADLEDGGY 64
Db 78 VYADGKEVEDROSAPYRGRTSILRDGITAGKAAALRIHNVNTASDSGKYLICYFQDGF 133

RESULT 13
PCT-US03-19070-5
; Sequence 5, Application PC/TUS0319070
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: INHIBITION OF T CELL ACTIVATION BY
; FILE REFERENCE: GNN-042PC
; CURRENT APPLICATION NUMBER: PCT/US03/19070
; CURRENT FILING DATE: 2003-06-17
; PRIOR APPLICATION NUMBER: US 60/389660
; PRIOR FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 481
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-19070-5

Query Match      17.6%; Score 65; DB 1; Length 481;
Best Local Similarity 30.4%; Pred. No. 3.1;
Matches 17; Conservative 11; Mismatches 18; Indels 10; Gaps 2;

QY 19 IYADGK----TOTAEFKGTFA-----EATAEAYRYADLLAKENGYTADLEDGGY 64
Db 78 VYADGKEVEDROSAPYRGRTSILRDGITAGKAAALRIHNVNTASDSGKYLICYFQDGF 133

RESULT 14
US-10-463-260-5
; Sequence 5, Application US/10463260
; GENERAL INFORMATION:
; APPLICANT: Wood, Clive R.
; APPLICANT: Long, Andrew J.
; APPLICANT: Carreno, Beatriz M.
; TITLE OF INVENTION: INHIBITION OF T CELL ACTIVATION BY
; FILE REFERENCE: GNN-042
; CURRENT APPLICATION NUMBER: US/10/463,260
; CURRENT FILING DATE: 2003-06-17
; PRIOR APPLICATION NUMBER: US 60/389660
; PRIOR FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 481
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-463-260-5

Query Match      17.6%; Score 65; DB 6; Length 481;
Best Local Similarity 30.4%; Pred. No. 3.1;
Matches 17; Conservative 11; Mismatches 18; Indels 10; Gaps 2;

QY 19 IYADGK----TOTAEFKGTFA-----EATAEAYRYADLLAKENGYTADLEDGGY 64
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Db 78 VYADGREVEDQSAFYRGRTSILRDGITAGKAALRIHNVTASDSGKYLCTYFQDGF 133

RESULT 15

US-09-200-650E-7

; Sequence 7, Application US/09200650E

; GENERAL INFORMATION:

; APPLICANT: Patti, Joseph M.

; APPLICANT: Foster, Timothy J.

; APPLICANT: Hook, Magnus A.O.

; APPLICANT: Eihmann, Deirdre Ni

; APPLICANT: Perkins, Samuel L.

; TITLE OF INVENTION: Extracellular Matrix-Binding Proteins from Staphylococcus aureus

; FILE REFERENCE: P06283US2/BAS

; CURRENT APPLICATION NUMBER: US/09/200,650E

; CURRENT FILING DATE: 1998-11-25

; PRIOR APPLICATION NUMBER: 60/066,815

; PRIOR FILING DATE: 1997-11-26

; PRIOR APPLICATION NUMBER: 60/098,427

; PRIOR FILING DATE: 1998-08-31

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 7

; LENGTH: 1166

; TYPE: PRT

; ORGANISM: Staphylococcus aureus

US-09-200-650E-7

Query Match 16.88; Score 62; DB 5; Length 1166;

Best Local Similarity 31.9%; Pred. No. 23;

Matches 15; Conservative 8; Mismatches 20; Indels 4; Gaps 2;

QY 24 KTQTAEPKGTFAEATAEAYRYADLLAKENGKYTADLE-DGGYITINIR 69

Db 752 KDSGTGVIGTTTDDASGKYKFTDL---DNGNYTVEETPAGYTPVK 795

Search completed: September 3, 2003, 11:40:57

Job time : 11.1096 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:04:52 ; Search time 9.12329 Seconds
(without alignments)
371.130 Million cell updates/sec

Title: US-08-325-278B-1_COPY_225_296

Perfect score: 370

Sequence: 1 KKKTPPEPKEVTIRANLIY.....GKYTADLEGGYTNIRFAG 72

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	71.5	19.3	398	1	RPC4_HUMAN
2	70.5	19.1	398	1	RPC4_MOUSE
3	64.5	17.4	1179	1	DP3A_STRCO
4	64	17.3	2459	1	MAPB_RAT
5	64	17.3	2464	1	MAPB_MOUSE
6	63.5	17.2	367	1	GPR_OCEIH
7	63.5	17.2	550	1	THS_PYRAB
8	62	16.8	953	1	LKAL_PASHA
9	62	16.8	953	1	LKAB_PASHA
10	61.5	16.6	404	1	ASSY_VIBCH
11	61.5	16.6	439	1	GLNA_PYRAB
12	61	16.5	471	1	TNAE_ECO57
13	61	16.5	471	1	TNAE_ECOLI
14	60.5	16.4	238	1	RNPH_VIBCH
15	60.5	16.4	263	1	RCY3_ASTLO
16	60.5	16.4	451	1	Y996_METJA
17	60.5	16.4	556	1	SYR_LISIN
18	60.5	16.4	674	1	COAA_BACTJ
19	60.5	16.4	692	1	MYS_PODCA
20	60.5	16.4	787	1	OSTA_VIBCH
21	60	16.2	451	1	TBB4_PORPU
22	60	16.2	596	1	RGPI_DROME
23	59.5	16.1	245	1	RNPH_STRCO
24	59.5	16.1	257	1	FAEJ_ECOLI
25	59.5	16.1	390	1	IRKB_CAVPO
26	59.5	16.1	425	1	IRK6_MOUSE
27	59.5	16.1	425	1	IRK6_RAT
28	59.5	16.1	658	1	TRAG_AGR5
29	59	15.9	490	1	CPCJ_HUMAN
30	59	15.9	582	1	TNPA_BACFR
31	59	15.9	627	1	ABPX_YEAST
32	58.5	15.8	374	1	FCGL_HUMAN
33	58.5	15.8	423	1	IRK6_HUMAN

RESULT 1

ID	RPC4_HUMAN	STANDARD;	PRT;	398 AA.
AC	P05423; Q9BPV7; Q9BP21; Q9BXB3;			
DT	01-NOV-1988 (Rel. 09, Created)			
DT	15-SEP-2003 (Rel. 42, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	DNA-directed RNA polymerase III 47 kDa polypeptide (EC 2.7.7.6) (RNA polymerase C subunit 4) (RPC4) (RPC53) (BN51 protein).			
GN	BN51T OR BN51 OR POLR3D.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RA	Ittmann M., Greco A., Basilio C.,			
RT	"Isolation of the human gene that complements a temperature-sensitive cell cycle mutation in BHK cells."			
RL	Mol. Cell. Biol. 7:3386-3393(1987).			
RN	[1]			
RX	SEQUENCE FROM N.A.			
RX	MEDLINE=88065472; PubMed=3683386;			
RA	Hernandez N.,			
RT	"Characterization of human RNA polymerase III identifies orthologues for Saccharomyces cerevisiae RNA polymerase III subunits."			
RL	Mol. Cell. Biol. 22:8044-8055(2002).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lung, and Lymph;			
RX	MEDLINE=2278866; PubMed=12391170;			
RA	Hu P., Wu S., Sun Y., Yuan C.-C., Kobayashi R., Myers M.P.,			
RA	Hernandez N.,			
RT	"Characterization of human RNA polymerase III identifies orthologues for Saccharomyces cerevisiae RNA polymerase III subunits."			
RL	Mol. Cell. Biol. 22:8044-8055(2002).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lung, and Lymph;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marudina K., Farmer A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villaion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettelman M., Madao A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,			
RA	Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.,			
RT	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[4]			
RP	SEQUENCE OF 1-50 FROM N.A.			
RX	MEDLINE=21282972; PubMed=11279001;			

P49658 mesocricetu
P36049 saccharomyc
P23536 osmunda cin
P22346 lactococcus
Q94526 drosophila
P05519 bacillus th
Q8y7n6 listeria mo
Q58367 methanococ
Q8uhn3 agrobacteri
P48070 euglena gen
Q94740 schizosacch
P00878 euglena gra

ALIGNMENTS


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CC polymerase III complex (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-C FAMILY. DNAE
CC SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF108191; AAD16978.1; -
CC DR EMBL: AL096884; CAB51456.1; -
CC DR PIR: T35093; T35093.
CC DR InterPro: IPR004013; PHP_C.
CC DR InterPro: IPR003141; PHP_N.
CC DR InterPro: IPR004805; PolC_alpha.
CC DR InterPro: IPR004365; tRNA_anti.
CC DR Pfam: PF02811; PHP_C; 1.
CC DR Pfam: PF02231; PHP_N; 1.
CC DR Pfam: PF01336; tRNA_anti; 1.
CC DR SMART: SM00481; POLI1IAC; 1.
CC DR TIGRFAMs: TIGR00594; polc; 1.
CC KW Transferrase; DNA-directed DNA polymerase; DNA replication;
CC KW Complete proteome. 802 E-> K (IN MUTANT TS-38).
CC FT VARIANT 802 802 E-> K (IN MUTANT TS-38).
CC SQ SEQUENCE 1179 AA; 130795 MW; 7E4B58675B634CD3 CRC64;
Query Match 17.4%; Score 64.5; DB 1; Length 1179;
Best Local Similarity 31.5%; Pred. No. 40;
Matches 23; Conservative 9; Mismatches 34; Indels 7; Gaps 2;

QY 2 EKTPPEEKKEVT-----IKANLIYADGKTQTAEFGTFAETAEAYADLLAKENGKYT 56
Db 131 QKPRMDKETISOWSEGIVASTGCPSEGVETRLRLGHFDKALKAAADYQDIFGKD--RYF 188
QY 57 ADLEDGGYTNIR 69
Db 189 LELMDHGIEIHR 201

RESULT 4
MAPB_RAT
ID MAPB_RAT STANDARD; PRT: 2459 AA.
P15205; Q62958; Q9ER21; O9QW92;
01-APR-1990 (Rel. 14, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Microtubule-associated protein 1B (MAP 1B) (Neuraxin) [Contains: MAP1
DE light chain LC1].
DE MAP1B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE OF 1-142 FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Testis;
RX MEDLINE=96257242; PubMed=8666295;
FA Liu D., Fischer I.;
RT "Isolation and sequencing of the 5' end of the rat microtubule-
RT associated protein (MAP1B)-encoding cDNA.";
RL Gene 172:307-308(1996).
[2]
RC SEQUENCE OF 96-2459 FROM N.A., DOMAIN, AND INDUCTION.
RC STRAIN=Sprague-Dawley; TISSUE=Brain, and Glial tumor;
RX MEDLINE=92347374; PubMed=1639092;
FA Zauner W., Kratz J., Staunton J., Feick P., Wiche G.;
RT "Identification of two distinct microtubule binding domains on
RT recombinant rat MAP 1B.";
RL Eur. J. Cell Biol. 57:66-74(1992).

```

FT	DOMAIN	588	786	LYS-RICH (HIGHLY BASIC, CONTAINS MANY KKEE AND KKEI/V REPEATS).
FT	DOMAIN	2224	2312	LYS-RICH.
FT	CONFLICT	127	127	M -> V (IN REF. 1).
FT	CONFLICT	140	140	T -> S (IN REF. 1).
FT	CONFLICT	2112	2112	R -> K (IN REF. 3).
FT	CONFLICT	2169	2169	L -> I (IN REF. 3).
FT	SEQUENCE	2459 AA;	269497 MW;	2E3F6872DED8BA2 CRC64;
Query Match		17.38;	Score 64;	DB 1; Length 2459;
Best Local Similarity		30.48;	Pred. No. 1e+02;	
Matches	24;	Conservative	11;	Mismatches 26; Indels 18; Gaps 4;
QY	2 EKTPEEPKE	-----EVTIKANLIYADG-----	-----KTOTAFFKGFIAEATAEAYRYADL 47	
Db	1918 EKTTPEDGGYSCIEITEKTRTPEEGGYEISEKTRTPEVSGYTYEKTSTERSRLDD	1917		
QY	48 LAKENGYKTADLEDGGYTI 66			
Db	1978 IS--NG--YDDEDGGHTL 1992			
RESULT 5				
MAPB_MOUSE				
ID	MAPB_MOUSE	STANDARD;	PRT;	2464 AA.
AC	P14873;			
DT	01-APR-1990 (Rel. 14, Created)			
DT	01-APR-1990 (Rel. 14, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Microtubule-associated protein 1B (MAP 1B) (MAP1.2) (MAP1(X))			
DE	[Contains: MAP1 light chain LC1].			
GN	MAP1B OR MTAP1B OR MTAP5.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
NCBI_TaxID=10090;				
SEQUENCE FROM N.A., AND DOMAIN.				
RC	SPRAIN=Swiss Webster; TISSUE=Brain;			
RX	MEDLINE=50094539; PubMed=2480963;			
RX	Noble M., Lewis S.A., Cowan N.J.;			
RT	"The microtubule binding domain of microtubule-associated protein			
RT	MAP1B contains a repeated sequence motif unrelated to that of MAP2			
RT	and tau.";			
RL	J. Cell Biol. 109:3367-3376(1989).			
CC	-!- FUNCTION: THE FUNCTION OF BRAIN MAPS IS ESSENTIALLY UNKNOWN.			
CC	PHOSPHORYLATED MAP1B MAY PLAY A ROLE IN THE CYTOSKELETAL CHANGES			
CC	THAT ACCOMPANY NEURITE EXTENSION. POSSIBLY MAP1B BINDS TO AT LEAST			
CC	TWO TUBULIN SUBUNITS IN THE POLYMER, AND THIS BRIDGING OF SUBUNITS			
CC	MIGHT BE INVOLVED IN NUCLEATING MICROTUBULE POLYMERIZATION AND IN			
CC	STABILIZING MICROTUBULES.			
CC	-!- SUBUNIT: 3 DIFFERENT LIGHT CHAINS, LC1, LC2 AND LC3, CAN ASSOCIATE			
CC	WITH MAP1A AND MAP1B PROTEINS.			
CC	-!- DOMAIN: Has a highly basic region with many copies of the sequence			
CC	KKEE and KKEI/V, repeated but not at fixed intervals, which is			
CC	responsible for the binding of MAP1B to microtubules.			
CC	-!- PTM: LC1 IS COEXPRESSED WITH MAP1B. IT IS A POLYPEPTIDE GENERATED			
CC	FROM MAP1B BY PROTEOLYTIC PROCESSING. IT IS FREE TO ASSOCIATE WITH			
CC	BOTH MAP1A AND MAP1B. IT INTERACTS WITH THE AMINO-TERMINAL REGION			
CC	OF MAP1B.			
CC	-!- SIMILARITY: TO MAP1A.			
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CC	modified and this statement is not removed. Usage by and for commercial			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; X51396; CAA35761.1;			
DR	PIR; S07549; QRMSP1.			
DR	MGD; MGI:1306778; Mtap1b.			

PFam: PF03418; Peptidase_U3; 1.
TIGRfams: TIGR01441; GPR; 1.
KW Hydrolyase; Protease; Zymogen; Complete proteome.
FT PROPEP 1 13 BY SIMILARITY.
FT CHAIN 14 367 GERMINATION PROTEASE.
SQ SEQUENCE 367 AA; 40467 MW; 3F4985F73F2CE5C7 CRC64;

Query Match 17.2%; Score 63.5; DB 1; Length 367;
Best Local Similarity 28.0%; Pred. No. 14;
Matches 21; Conservative 14; Mismatches 27; Indels 13; Gaps 4;

QY 1 KETTPPEKPEVTKANLIYADGK---TQTAEKPG-TFAETAEAYR--YAD-----L 47
DB 3 EQQIPQVRYDLAIEAKDMYTESKPEETNDKEIKGVTFKRSYKDIKVSIVYDDEGEKL 62
QY 48 LAKENGKYTADLEDG 62
DB 63 LGKKPGSYVIYADG 77

RESULT 7
THS_PYRAB
ID THS_PYRAB STANDARD; PRT; 550 AA.
AC Q9V2Q7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Thermosome subunit (Chaperonin subunit).
GN THS OR THSA OR PYRAB00180 OR PAB2341.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=29292;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=GE5 / Orsay;
RX PubMed=12622808;
RA Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O.,
RA Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C.,
RA Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.;
RT "An integrated analysis of the genome of the hyperthermophilic
RT archaeon Pyrococcus abyssi".
RL Mol. Microbiol. 47:1495-1512(2003).
CC -1- FUNCTION: MOLECULAR CHAPERONE; BINDS UNFOLDED POLYPEPTIDES IN
CC VITRO, AND HAS A WEAK ATPASE ACTIVITY (BY SIMILARITY).
CC -1- SUBUNIT: FORMS AN OLIGOMERIC COMPLEX OF EIGHT-MEMBERED RINGS
CC (BY SIMILARITY).
CC -1- SIMILARITY: Belongs to the TCP-1 chaperonin family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AJ248283; CAB48941.1; -
CC PIR: F75186; F75186.
CC HSSP: P48424; IASS.
CC InterPro: IPR002194; Chaperonin_TCP-1.
CC InterPro: IPR001844; Chaperonin_Cpn60.
CC InterPro: IPR002423; Cpn60_TCP1.
CC Pfam: PF00118; cpn60_TCP1_1.
CC PRINTS: PR00298; CHAPERONIN60.
CC PRINTS: PR00304; TCOMPLEXTCP1.
CC PROSITE: PS00750; TCP1_1; 1.
CC PROSITE: PS00751; TCP1_2; 1.
CC PROSITE: PS00995; TCP1_3; 1.
CC Chaperone; ATP-binding; Complete proteome.
KW SEQUENCE 550 AA; 59717 MW; 523196D4BB2BAC53 CRC64;
SQ

Query Match 17.2%; Score 63.5; DB 1; Length 550;

```

Best Local Similarity 31.5%; Pred. No. 22;
Matches 23; Conservative 9; Mismatches 24; Indels 17; Gaps 3;

QY 1 KEKTPPEKKEVITKANLIYADGKTQTAEFGKFAEATAEAYRYADLLAKENGKYTDLE 60
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
Db 144 KEVKPDD--EVLKKAWTAITGK-----AAEEERYLAKLAVEAVKLVAEEK 189

QY 61 DGGYTI---NIRF 70
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
Db 190 DGRFKVDIDNIKF 202

RESULT 8
LKAL_PASHA
ID LKAL_PASHA STANDARD; PRT; 953 AA.
AC P16535;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leukotoxin from serotype A1.
GN LKTA.
OS Pasteurella haemolytica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Mannheimia.
OX NCBI_TaxID=75985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Serotype A1.
RX MEDLINE=87306837; PubMed=3040588;
RA Lo R.Y.C.; Strathdee C.A.; Shewen P.E.;
RT "Nucleotide sequence of the leukotoxin genes of Pasteurella
   haemolytica A1."
RL Infect. Immun. 55:1987-1996(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Serotype A1 / PH1101;
RX MEDLINE=89210283; PubMed=2707120;
RA Highlander S.K.; Chidambaram M.; Engler M.J.; Weinstock G.M.;
RT "DNA sequence of the Pasteurella haemolytica leukotoxin gene
   cluster."
RL DNA 8:15-28(1989).
RN [3]
RP SEQUENCE OF 884-953 FROM N.A.
RC STRAIN=Serotype A1 / PH1101;
RX MEDLINE=90236888; PubMed=2185213;
RA Highlander S.K.; Engler M.J.; Weinstock G.M.;
RT "Secretion and expression of the Pasteurella haemolytica Leukotoxin."
RL J. Bacteriol. 172:2343-2350(1990)
CC -!- FUNCTION: Bacterial hemolysins are exotoxins that attack blood
   cell membranes and cause cell rupture by mechanisms not clearly
   defined.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DOMAIN: The Gly-rich region is probably involved in binding
   calcium, which is required for target cell-binding or cytolytic
   activity.
CC -!- DOMAIN: The three transmembrane domains are believed to be
   involved in pore formation by the cytotoxin (By similarity).
CC -!- PTM: Palmitoylated by lktC. The toxin only becomes active when
   modified (By similarity).
CC -!- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
CC -----
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CC -----
CC EMBL; M20730; AAA25529.1; -
CC EMBL; M24197; AAA25543.1; -
CC PIR; B30169; B30169.
CC InterPro; IPR001343; Hemlysn_Ca_bind.

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DR InterPro; IPR003995; RTxA.
DR Pfam; PF00353; hemolysinCabin; 5.
DR Pfam; PF02382; RTX; 1.
DR PRINTS; PR00313; CABNDNGRPT.
DR PRINTS; PR01488; RTXTOXINA.
DR PROSITE; PS00330; HEMOLYSIN_CALCIIUM; 4.
KW Hemolysis; Toxin; Cytolysis; Repeat; Calcium; Transmembrane;
KW Lipoprotein; Palmitate.
FT TRANSMEM 229 249 POTENTIAL.
FT TRANSMEM 297 318 POTENTIAL.
FT TRANSMEM 366 390 POTENTIAL.
FT DOMAIN 734 784 6 X REPEATS, GLY-RICH (BY SIMILARITY).
FT REPEAT 734 739 1.
FT REPEAT 743 748 2.
FT REPEAT 752 757 3.
FT REPEAT 761 766 4.
FT REPEAT 770 775 5.
FT REPEAT 779 784 6.
FT CONFLICT 409 414 FEHVN -> LSTLQI (IN REF. 2).
FT CONFLICT 742 743 D -> Y (IN REF. 2).
SQ SEQUENCE 953 AA; 101996 MW; 7F93D113A118C05F CRC64;

Query Match 16.8%; Score 62; DB 1; Length 953;
Best Local Similarity 33.3%; Pred. No. 59;
Matches 20; Conservative 7; Mismatches 23; Indels 10; Gaps 1;

QY 9 KEEVTIKANLIYADGKTQTAEFGKFAEATAE-----AYRYADLLAKENGKYTD 58
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
Db 832 KEKVTIQNFREADFKEVPNYKATKDEKIEIIGQGERITSQVDDLIKNGKITQD 891

RESULT 9
LKAL_PASHA
ID LKAL_PASHA STANDARD; PRT; 953 AA.
AC P55118;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leukotoxin from serotype A1.
GN LKTA.
OS Pasteurella haemolytica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Mannheimia.
OX NCBI_TaxID=75985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Serotype A1;
RX MEDLINE=94041617; PubMed=8225575;
RA Burrows L.L.; Olah-Winfield E.; Lo R.Y.C.;
RT "Molecular analysis of the leukotoxin determinants from Pasteurella
   haemolytica serotypes 1 to 16."
RL Infect. Immun. 61:5001-5007(1993).
CC -!- FUNCTION: Bacterial hemolysins are exotoxins that attack blood
   cell membranes and cause cell rupture by mechanisms not clearly
   defined.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DOMAIN: The Gly-rich region is probably involved in binding
   calcium, which is required for target cell-binding or cytolytic
   activity.
CC -!- DOMAIN: The three transmembrane domains are believed to be
   involved in pore formation by the cytotoxin (BY SIMILARITY).
CC -!- PTM: Palmitoylated by lktC. The toxin only becomes active when
   modified (By similarity).
CC -!- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
CC -----
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   or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M20730; AAA25529.1; -
CC EMBL; M24197; AAA25543.1; -
CC PIR; B30169; B30169.
CC InterPro; IPR001343; Hemlysn_Ca_bind.

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DR EMBL; U01215; AAB35689.1; -.
DR InterPro; IPR001343; Hemlysn_Ca_bind.
DR InterPro; IPR003995; RtxA.
DR Pfam; PF00353; hemolysinCabin; 5.
DR Pfam; PF02382; RTX; 1.
DR PRINTS; PR00313; CABNDNGRPT.
DR PRINTS; PR01488; RYTXOXINA.
DR PROSITE; PS00330; HEMOLYSIN_CALCIIUM; 4.
KW Hemolysins; Toxin; Cytolysis; Repeat; Calcium; Transmembrane;
KW Lipoprotein; Palmitate.
DR TRANSMEM 230 250
FT FT TRANSMEM 297 317 POTENTIAL.
FT FT TRANSMEM 381 401 POTENTIAL.
FT FT DOMAIN 734 784 6 X REPEATS, GLY-RICH.
FT FT REPEAT 734 739 1.
FT FT REPEAT 743 748 2.
FT FT REPEAT 752 757 3.
FT FT REPEAT 761 766 4.
FT FT REPEAT 770 775 5.
FT FT REPEAT 779 784 6.
SQ SEQUENCE 953 AA; 102206 MW; 927FF56CFC884F12 CRC64;

Query Match 16.8%; Score 62; DB 1; Length 953;
Best Local Similarity 33.3%; Pred. No. 59;
Matches 20; Conservative 7; Mismatches 23; Indels 10; Gaps 1;

QY 9 KEEVTIKANLIYADGKTQTAEFRGTFAEATAE-----AYRYADLLAKENGKYTAD 58
||:||||: || : :| | | | | : : : ||:| || | |
DB 832 KEKVTIQDWREADFAKEVRYNRKATKDEKTEEIIQNGERITSKQVDDLLAKNGKITQD 891

RESULT 10
ASSY_VIECH
ID ASSY_VIECH STANDARD; PRT; 404 AA.
AC Q9KNT8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2003 (Rel. 42, Last annotation update)
DE Argininosuccinate synthase (EC 6.3.4.5) (Citrulline--aspartate
ligase).
GN ARGG OR VC2642.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
ON NCBI_TaxID=666;
OX [1]
SEQUENCE FROM N.A.
STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; Pubmed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Dragoi I., Sellers P.,
RA Emolava M.D., Vamathevan J., Bass S., Qin H., Ragoi I.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RA "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae."
RL Nature 406:477-483(2000).
CC -I- CATALYTIC ACTIVITY: ATP + L-citrulline + L-aspartate = AMP +
CC diphosphate + L-argininosuccinate.
CC -I- PATHWAY: Arginine biosynthesis; seventh step.
CC -I- SUBUNIT: Homotetramer (By similarity).
CC -I- SIMILARITY: Belongs to the argininosuccinate synthase family.
CC Subfamily 1.
-----
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```

DR HAMAP; MF_00544; ; 1.
DR InterPro; IPR001597; Beta_elim_lyase.
DR Pfam; PF01212; Beta_elim_lyase; 1.
DR PROSITE; PD005927; Beta_elim_lyase; 1.
DR PRODOM; PS00853; BETA_ELIM_LYASE; 1.
KW Tryptophan catabolism; Lyase; Pyridoxal phosphate; Complete proteome.
FT BINDING 270 270
FT SEQUENCE 471 AA; 52789 MW; 49DD2D41BD9D0034 CRC64;

Query Match 16.5%; Score 61; DB 1; Length 471;
Best Local Similarity 41.5%; Pred. No. 35;
Matches 17; Conservative 7; Indels 15; Gaps 2;

QY 24 KQTAEFKG-TFAETAAYRYADLLAKENGKKTADLEGG 63
| : | | | : | : | | | | | : | : | : | |
Db 239 KOREAEYKDWITTEQITRETYKYADMLAM-SAKDKAMVPMGG 278

RESULT 13
TNRA_ECOLI STANDARD; PRT; 471 AA.
ID TNAA_ECOLI STANDARD; PRT; 471 AA.
AC P00913; P78123;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tryptophanase (EC 4.1.99.1) (L-tryptophan indole-lyase) (TNase).
GN TNAA OR IND OR B3708 OR SF3754.
OS Escherichia coli, and
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562, 623;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=K12;
RX MEDLINE=82007678; PubMed=6268608;
RA Deeley M.C., Yanofsky C.;
RT "Nucleotide sequence of the structural gene for tryptophanase of
RT Escherichia coli K-12";
RT J. Bacteriol. 147:787-796(1981).
RN [2]
RP SEQUENCE FROM N.A., AND IMPORTANCE OF CYS-298.
RC SPECIES=E.coli; STRAIN=B/1t7-A;
RX MEDLINE=89323226; PubMed=2502187;
RA Tokushige M., Tsujimoto N., Oda T., Honda T., Yumoto N., Ito S.,
RA Yamamoto M., Kim E.H., Hiragi Y.;
RT "Role of cysteine residues in tryptophanase for monovalent cation-
RT induced activation";
RT Biochimie 71:711-720(1989).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=K12 / MGI655;
RX MEDLINE=93315143; PubMed=7686882;
RA Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.;
RT "DNA sequence and analysis of 136 kilobases of the Escherichia coli
RT genome: organizational symmetry around the origin of replication.";
RT Genomics 16:551-561(1993).
RN [4]
RP SEQUENCE OF TRYPTIC PEPTIDES.
RC SPECIES=E.coli; STRAIN=K12;
RX MEDLINE=72134434; PubMed=4551944;
RA Kagamiyama H., Matsuura H., Snell E.E.;
RT "The chemical structure of tryptophanase from Escherichia coli. 3.
RT Isolation and amino acid sequence of the tryptic peptides.";
RT J. Biol. Chem. 247:1576-1586(1972).
RN [5]
RP SEQUENCE OF 1-21 FROM N.A.
RC SPECIES=E.coli; STRAIN=K12;
RX MEDLINE=86033634; PubMed=3902796;
RA Stewart V., Yanofsky C.;
RT "Evidence for transcription antitermination control of tryptophanase
RT operon expression in Escherichia coli K-12";
RT J. Bacteriol. 164:731-740(1985).
RN [6]


```

[6]
RP SEQUENCE OF 463-471 FROM N.A.
RC SPECIES=E.coli;
RX MEDLINE=91216998; PubMed=2022620;
RA Sarsero J.P., Wooley P.J., Gollnick P.D., Yanofsky C., Pittard A.J.;
RT "A new family of integral membrane proteins involved in transport of
RL aromatic amino acids in Escherichia coli.";
RJ J. Bacteriol. 173:3231-3234(1991).
[7]
RP SEQUENCE OF 1-12.
RC SPECIES=E.coli; STRAIN=K12 / EMG2;
RX MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded
RL in the genome of Escherichia coli K-12.";
RJ Electrophoresis 18:1259-1313(1997).
[8]
RP SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
RX MEDLINE=2272406; PubMed=12384590;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RJ Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RJ Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RJ Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RL through comparison with genomes of Escherichia coli K12 and O157.";
RJ Nucleic Acids Res. 30:4432-4441(2002).
[9]
RP MUTAGENESIS OF CYS-294 AND CYS-298.
RC SPECIES=E.coli;
RX MEDLINE=89278130; PubMed=2659590;
RA Phillips R.S., Gollnick P.D.;
RT "Evidence that cysteine 298 is in the active site of tryptophan
RL indole-lyase.";
RJ J. Biol. Chem. 264:10627-10632(1989).
CC -1- CATALYTIC ACTIVITY: L-tryptophan + H(2)O = indole + pyruvate +
CC NH(3).
CC -1- COFACTOR: Pyridoxal phosphate.
CC -1- PATHWAY: Tryptophan catabolism.
CC -1- SUBUNIT: Homotetramer.
CC -1- SIMILARITY: BELONGS TO THE BETA-ELIMINATING LYASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; K00032; AAA24676.1; -.
DR EMBL; X15974; CAA34096.1; -.
DR EMBL; M11990; AAA24679.1; -.
DR EMBL; M59914; -. NOT_ANNOTATED_CDS.
DR EMBL; L10328; AAA62059.1; ALT_INIT.
DR EMBL; AE000448; AAC76731.1; ALT_INIT.
DR EMBL; AE015382; AAM45197.1; ALT_INIT.
DR PIR; B65173; WZEC.
DR HSP; P28796; 1AX4.
DR ECO2DBASE; G046.5; 6TH EDITION.
DR Ecogen; EG11005; tnaA.
DR HAMAP; MF_00544; -. 1.
DR InterPro; IPR001597; Beta_elim_lyase.
DR Pfam; PF01212; Beta_elim_lyase; 1.
DR ProDom; PD005927; Beta_elim_lyase; 1.
DR PROSITE; PS00853; BETA_ELIM_LYASE; 1.
RW Tryptophan catabolism; Lyase; Pyridoxal phosphate; Complete proteome.
FT BINDING 270 270 PYRIDOXAL PHOSPHATE.
FT MUTAGEN 294 294 C->S: IDENTICAL TO WILD-TYPE.
FT MUTAGEN 298 298 C->S: ALTERED ACTIVITY.
FT CONFLICT 137 140 DTQ -> TTQG (IN REF. 1).
FT CONFLICT 379 380 QA -> TG (IN REF. 1 AND 2).
SQ SEQUENCE 471 AA; 52773 MW; 5AFC1F41BD9D0034 CRC64;
Query Match 16.5%; Score 61; DB 1; Length 471;
Best Local Similarity 41.5%; Pred. No. 35;
Matches 17; Conservative 7; Mismatches 15; Indels 2; Gaps 2;
QY 24 KTQTAEFGK-TFAETAAYRYADLLAKENGKYTADLEDGG 63
| : ||| | : | | | | | : | : | : |
DB 239 KOREAEYKDWITIEQITRETYKYADMLAM-SAKKDAMVPMGG 278
RESULT 14
RNPH_VIBCH STANDARD; PRT; 238 AA.
ID AC Q9KVD6;
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RJ Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RJ Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RJ Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RJ Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RL cholerae.";
RL Nature 406:477-483(2000).
CC -1- FUNCTION: Phosphorylatic exoribonuclease that removes nucleotide
CC residues following the -CCA terminus of tRNA and adds nucleotides
CC to the ends of RNA molecules by using nucleoside diphosphates as
CC substrates (By similarity).
CC -1- CATALYTIC ACTIVITY: {tRNA}(NH1) + phosphate -> {tRNA}(N) + a
CC nucleoside diphosphate.
CC -1- SIMILARITY: BELONGS TO THE RNASE PH FAMILY.
CC -----
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CC -----
DR EMBL; AE004111; AAF93386.1; ALT_INIT.
DR TIGR; VC0210; -. 1.
DR HAMAP; MF_00564; -. 1.
DR InterPro; IPR001247; 3_ExoRNase.
DR InterPro; IPR002381; RNase_PH.
DR Pfam; PF01138; RNase_PH; 1.
DR Pfam; PF03725; RNase_PH_C; 1.
DR PROSITE; PS01277; RIBONUCLEASE_PH; 1.
RW Transferase; Nucleotidyltransferase; trna processing;
KW Complete proteome.
SQ SEQUENCE 238 AA; 25631 MW; C07828FBBC900E0D CRC64;
Query Match 16.4%; Score 60.5; DB 1; Length 238;
Best Local Similarity 38.5%; Pred. No. 19;
Matches 15; Conservative 8; Mismatches 13; Indels 3; Gaps 1;
QY 12 VTIKANLIYADGKTQTAEFGKTFATAYRYADLLAK 50
| : : ||| | | | : | : | : |

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Db      112 ITVDCDVIQADGGTRTASITGA---SVALADAFALHIAK 147

RESULT 15.
YCY3_ASTLO
ID YCY3_ASTLO STANDARD; PRT; 263 AA.
AC P58147;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 32.5 kDa protein in rpl14-rpl12 intergenic region
DE (ORF263).
OS Astasia longa (Euglenophyceae alga).
OG Chloroplast.
OC Eukaryota; Euglenozoa; Euglenida; Euglenales; Euglena.
OX NCBI_TaxID=3037;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CCAP 1204-17a;
RX MEDLINE=21080522; PubMed=11212895;
RA Gockel G., Hachtel W.;
RT "Complete gene map of the plastid genome of the nonphotosynthetic
RT euglenoid flagellate Astasia longa.";
RL Protist 151:347-351(2000).
CC -1- SIMILARITY: BELONGS TO THE A.LONGA ORF167/ORF288 FAMILY.
-----
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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-----
CC EMBL; AJ294725; CAC24603.1;
DR InterPro; IPR006851; DUF613.
DR Pfam; PF04764; DUF613; 2.
KW Hypothetical protein; Chloroplast.
SQ SEQUENCE 263 AA; 32473 MW; 3508B02DB49CB4E6 CRC64;

Query Match 16.4%; Score 60.5; DB 1; Length 263;
Best Local Similarity 31.9%; Pred. No. 21;
Matches 23; Conservative 9; Mismatches 27; Indels 13; Gaps 3;

QY 1 KEKTPPEPKPEVTIKANLIYADGKTQTAEFGKTFEAETAEAYRYADLLAKENGYTADLE 60
Db 173 KDKYLEEPTELEYIVLDLF-----LLGPLEKEYSENYKIIYLINERNKRY-KDMY 221
QY 61 DGG--YTINIRF 70
Db 222 DMGEIYGINIRF 233
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Search completed: September 3, 2003, 11:20:07
Job time : 10.1233 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:04:17 ; Search time 51.0137 Seconds
(without alignments)
236.470 Million cell updates/sec

Title: US-08-325-278b-1_COPY_5_80

Perfect score: 389

Sequence: 1 KEETPETDSEEVTKA.....GEYTDVADKGYTLNIKFA 76

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	389	100.0	76	21	AAV82537
2	389	100.0	305	14	AAV82537
3	389	100.0	434	14	AAV82537
4	384	98.7	467	22	AAV82537
5	326	83.8	182	18	AAV82537
6	326	83.8	182	20	AAV82537
7	323	83.0	178	18	AAV82537
8	323	83.0	178	20	AAV82537
9	323	83.0	198	18	AAV82537

10	323	83.0	198	20	AAV82537
11	323	83.0	342	18	AAV82537
12	323	83.0	342	20	AAV82537
13	323	83.0	482	20	AAV82537
14	323	83.0	495	18	AAV82537
15	323	83.0	495	20	AAV82537
16	314	80.7	72	21	AAV82537
17	314	80.7	367	21	AAV82537
18	299	76.9	72	21	AAV82537
19	298.5	76.7	1027	14	AAV82537
20	298.5	76.7	1027	14	AAV82537
21	298	76.6	71	21	AAV82537
22	298	76.6	291	14	AAV82537
23	284.5	73.1	75	21	AAV82537
24	270.5	69.5	74	21	AAV82537
25	269	69.2	72	21	AAV82537
26	262.5	67.5	82	21	AAV82537
27	262	67.4	71	21	AAV82537
28	255.5	65.7	82	21	AAV82537
29	255.5	65.7	82	21	AAV82537
30	253.5	65.2	82	21	AAV82537
31	249.5	64.1	82	21	AAV82537
32	71.5	18.4	841	22	AAU34283
33	71.5	18.4	841	22	AAU34283
34	71.5	18.4	930	20	AAU34283
35	71.5	18.4	947	24	ABJ18940
36	69	17.7	123	19	AAW65763
37	69	17.7	1377	22	ABW65439
38	67	17.2	571	12	AAU10376
39	67	17.2	574	23	ABE29074
40	67	17.2	588	22	AAU49638
41	66	17.0	447	22	AAU49638
42	66	17.0	450	22	AAU49638
43	65	16.7	419	23	ABP38596
44	64.5	16.6	280	21	AAU39253
45	64.5	16.6	282	21	AAU39253

ALIGNMENTS

RESULT 1
AAV82537
ID AAV82537 standard; Protein; 76 AA.
XX AC
XX AAV82537;
XX
XX
XX 20-JUL-2000 (first entry)
XX
XX Peptostreptococcus strain 312 protein L domain B1 protein sequence.
XX
XX Immunoglobulin light chain binding protein; PPL; protein L;
XX Peptostreptococcus; human immunoglobulin kappa chain;
XX immunofluorescence chromatography.
XX
XX Peptostreptococcus sp.
XX
XX WO200015803-A1.
XX
XX 23-MAR-2000.
XX
XX 14-SEP-1999; 99WO-GB03048.
XX
XX 14-SEP-1998; 98GB-0019998.
XX 26-APR-1999; 99GB-0009578.
XX
XX (ACTI-) ACTINOVA LTD.
XX
XX Gore MG, Beckingham JA, Roberts SE;
XX WPI; 2000-271441/23.
XX N-PSDB; AAA08426.

PT New modified immunoglobulin light chain binding protein, useful in
PT immunoaffinity chromatography, has a dissociation constant of 400 nM or
XX more at pH8 with respect to human immunoglobulin kappa-chain -
XX
PS Disclosure; Page 40-41; 56pp; English.
XX
CC The present invention describes an immunoglobulin (Ig) light chain
CC binding protein (PI) which has been modified by one or more amino acid
CC substitutions such that the dissociation constant (Kd) of the protein
CC with respect to human Ig kappa-chain is 400 nM or more at pH8. PI is
CC useful in immunoaffinity chromatography. The present sequence is a
CC Peptostreptococcus protein L Ig light chain binding domain, which is
CC given in the disclosure of the present invention.
XX
XX Sequence 76 AA;
XX
XX Query Match 100.0%; Score 389; DB 21; Length 76;
XX Best Local Similarity 100.0%; Pred. No. 1.7e-37;
XX Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 KEETPETPTDSEEEVTIKANLIFANGSTQTAEFGTSEAYAYADTLKNGEY 60
Db 1 KEETPETPTDSEEEVTIKANLIFANGSTQTAEFGTSEAYAYADTLKNGEY 60
XX
QY 61 VDVADKGYTLNKFAG 76
Db 61 VDVADKGYTLNKFAG 76
XX
XX RESULT 2
XX AAR42993
XX ID AAR42993 standard; Protein; 305 AA.
XX AC AAR42993;
XX
XX 25-MAR-2003 (updated)
XX 16-MAY-1994 (first entry)
XX
XX Immunoglobulin light chain binding protein (Protein L).
XX
XX Immunoglobulin; light chain; binding; identification; purification;
XX separation.
XX
XX E. coli LE392/pHDL, DSM 7054.
XX
XX Key Location/Qualifiers
XX Domain 5..305
XX /label= B1 immunoglobulin light chain binding
XX domain.
XX Domain 81..305
XX /label= B2 immunoglobulin light chain binding
XX domain.
XX Domain 153..305
XX /label= B3 immunoglobulin light chain binding
XX domain.
XX Domain 225..305
XX /label= B4 immunoglobulin light chain binding
XX domain.
XX Domain 297..305
XX /label= B5 immunoglobulin light chain binding
XX domain.
XX
XX W09322342-A1.
XX
XX 11-NOV-1993.
XX
XX 28-APR-1993; 93WO-SE00375.
XX
XX 28-APR-1992; 92SE-0001331.
XX
XX (HIGH-) HIGHTECH RECEPTOR AB.
XX
XX Bjoerck L, Sjoebing U;
PI

XX
DR WPI; 1993-368722/46.
DR N-PSDB; AAQ50452.
XX
PT New protein L binding light chains of all immunoglobulin classes
PT - for binding purifying and identifying immunoglobulin, also
XX related DNA, vectors and host cells
XX
XX Claim 1; Page 36; 71pp; English.
XX
CC The protein (Protein L) is capable of binding to immunoglobulin G
CC light chains. It is useful for binding, separating (purifying) and
CC identifying immunoglobulin and for removing immunoglobulin molecules
CC from serum. Hybrid proteins of the L protein can bind all human
CC immunoglobulin classes and many immunoglobulins from other species.
CC They are highly soluble and retain their binding activity at high
CC temperatures over a pH range of 3-10. They can be immobilised
CC without loss of activity.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 305 AA;
XX
XX Query Match 100.0%; Score 389; DB 14; Length 305;
XX Best Local Similarity 100.0%; Pred. No. 1.1e-36;
XX Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 KEETPETPTDSEEEVTIKANLIFANGSTQTAEFGTSEAYAYADTLKNGEY 60
Db 5 KEETPETPTDSEEEVTIKANLIFANGSTQTAEFGTSEAYAYADTLKNGEY 64
XX
QY 61 VDVADKGYTLNKFAG 76
Db 65 VDVADKGYTLNKFAG 80
XX
XX RESULT 3
XX AAR42994
XX ID AAR42994 standard; Protein; 434 AA.
XX AC AAR42994;
XX
XX 25-MAR-2003 (updated)
XX 16-MAY-1994 (first entry)
XX
XX Sequence encoding immunoglobulin light chain binding protein.
XX
XX Immunoglobulin; light chain; binding; identification; purification;
XX separation; ss.
XX
XX E. coli L392/pHDLG, DSM 7055.
XX
XX Key Location/Qualifiers
XX Domain 5..305
XX /label= B1 immunoglobulin light chain binding
XX domain.
XX Domain 81..305
XX /label= B2 immunoglobulin light chain binding
XX domain.
XX Domain 153..305
XX /label= B3 immunoglobulin light chain binding
XX domain.
XX Domain 225..305
XX /label= B4 immunoglobulin light chain binding
XX domain.
XX Domain 297..305
XX /label= B5 immunoglobulin light chain binding
XX domain.
XX Domain 309..434
XX /label= C1 immunoglobulin heavy chain binding
XX domain.
XX Domain 364..434
XX /label= D intermediate immunoglobulin heavy
XX chain binding domain.
XX

FT Domain 379..434
 FT /label= C2 immunoglobulin heavy chain binding
 FT domain.
 XX WO9322342-A1.
 XX 11-NOV-1993.
 XX 28-APR-1993; 93WO-SE00375.
 XX 28-APR-1992; 92SE-0001331.
 XX (HIGH-) HIGTECH RECEPTOR AB.
 XX Bjoerck L, Sjoerbring U;
 XX WPI: 1993-368722/46.
 XX P-PSDB; AAR42994.
 XX New protein L binding light chains of all immunoglobulin classes
 PT - for binding purifying and identifying immunoglobulin, also
 PT related DNA, vectors and host cells
 XX Claim 6; Page 39-40; 71pp; English.
 XX Protein L (AAR42993) is capable of binding to immunoglobulin G light
 CC chains. It is useful for binding, separating (purifying) and
 CC identifying immunoglobulin and for removing immunoglobulin molecules
 CC from serum. This is the coding sequence of one hybrid protein of
 CC the L protein. The hybrid proteins can bind all human
 CC immunoglobulin classes and many immunoglobulins from other species.
 CC They are highly soluble and retain their binding activity at high
 CC temperatures over a pH range of 3-10. They can be immobilised
 CC without loss of activity.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 434 AA;

Query Match 100.0%; Score 389; DB 14; Length 434;
 Best Local Similarity 100.0%; Pred. No. 1.8e-36;
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KETPTPTDSEEVYTIKANLIFANGSTQTAEFGKTFEKATSEAYAYADTLKKNGEYT 60
 DB 5 KETPTPTDSEEVYTIKANLIFANGSTQTAEFGKTFEKATSEAYAYADTLKKNGEYT 64
 QY 61 DVVADKGYTLNIFAG 76
 DB 65 DVVADKGYTLNIFAG 80

RESULT 4
 AAB31372
 ID AAB31372 standard; Protein; 467 AA.
 XX AAB31372;
 XX 20-APR-2001 (first entry)
 XX Amino acid sequence of protein L/CBD cex/ER retaining peptide fusion.
 DE Protein production; food processing; protein antibiotic; feed enzyme;
 XX protein L: CBD cex protein; cell signal peptide.
 KW Synthetic.
 XX WO20007174-A1.
 XX 21-DEC-2000.
 XX 07-JUN-2000; 2000WO-IL00330.
 XX 10-JUN-1999; 99US-0329234.

XX (CBDT-) CBD TECHNOLOGIES LTD.
 PA (VISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
 XX Shani Z, Shoseyov O;
 XX WPI: 2001-112219/12.
 DR N-PSDB; AAF24730.
 XX Expressing and isolating recombinant protein in a plant, useful for
 PT producing large quantities of recombinant proteins, by expressing a
 PT fusion protein including a cellulose binding peptide fused to a
 PT recombinant protein
 XX Example; Fig 2a; 87pp; English.
 XX The specification describes a method for expressing and isolating a
 CC recombinant protein in a plant. The method comprising expressing a
 CC fusion protein including the recombinant protein and a cellulose
 CC binding peptide fused to it, where the fusion protein is
 CC compartmentalised and sequestered within plant cells, plant derived
 CC tissue or cultured plant cells. The method is useful for obtaining large
 CC quantities of the recombinant proteins and protein products in a simple
 CC and cost-effective manner. Recombinant proteins may be used commercially,
 CC such as in the food processing industry, e.g. glucamylases and glucose
 CC isomerases are used for converting starch to high fructose corn syrup,
 CC proteinases for the hydrolysis of high molecular weight proteins and in
 CC manufacturing leather or alcoholic beverages, pectinesterases for
 CC pectin hydrolysis in food industry, lipases for cleaving ester linkage
 CC in triglycerides, and for effluent treatment. The recombinant proteins
 CC may further be used to produce protein antibiotics, which can be used
 CC in healing processes, and to produce animal feed enzymes. The present
 CC sequence represents a fusion protein of the invention, and comprises a
 CC fusion of a cell signal peptide, protein L, CBD cex, and an endoplasmic
 CC reticulum retaining peptide.
 XX Sequence 467 AA;

Query Match 98.7%; Score 384; DB 22; Length 467;
 Best Local Similarity 98.7%; Pred. No. 7.4e-36;
 Matches 75; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KETPTPTDSEEVYTIKANLIFANGSTQTAEFGKTFEKATSEAYAYADTLKKNGEYT 60
 DB 44 KETPTPTDSEEVYTIKANLIFANGSTQTAEFGKTFEKATSEAYAYADTLKKNGEYT 103
 QY 61 DVVADKGYTLNIFAG 76
 DB 104 DVVADKGYTLNIFAG 119

RESULT 5
 AAW32479
 ID AAW32479 standard; Protein; 182 AA.
 XX AAW32479;
 XX 27-MAR-1998 (first entry)
 XX Growth factor LHL (catalytic antibody precursor).
 DE Catalytic antibody; growth factor; B-cell mitogenesis; LHL;
 XX L protein; hen egg lysozyme.
 KW Chimeric - Peptostreptococcus magnus.
 OS Chimeric - Gallus sp.
 XX WO9735887-A1.
 XX 02-OCT-1997.
 XX 26-MAR-1997; 97WO-AU00194.
 XX

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PR 27-FEB-1997; 97AU-0005375.
PR 26-MAR-1996; 96AU-0008951.
XX
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI Koentgen F, Suess GM, Tarlinton DM, Treutlein HR;
XX
XX WPI; 1997-489572/45.
DR N-PSDB; AAT91582.
XX
XX New catalytic antibody precursors - comprising a B-cell surface
PT molecule binding portion which can induce B-cell mitogenesis
XX
XX Claim 11; Page 56-57; 109pp; English.
XX
XX This polypeptide comprises growth factor LHL, where L is the
CC immunoglobulin binding entity from Peptostreptococcus magnus and H
CC is residues 42-62 of hen egg lysozyme. It was expressed in
CC Escherichia coli using a DNA construct (see AAT91586) generated by PCR.
CC Production of catalytic antibodies to a specific antigen comprises
CC administering to an animal a growth factor comprising an antigen
CC capable of interacting with a B cell bound catalytic antibody. The
CC antigen is fused to a B cell surface molecule binding protein for
CC the antigen to be cleaved and for the remainder of the molecule to
CC induce B cell mitogenesis (claimed). LHL crosslinks with surface
CC immunoglobulin on B cells. This induces B cell activation and blast
CC formation. Internalisation and processing of LHL leads to the
CC presentation of the H peptide on MHC II. T cell recognition of MHC
CC II with the H peptide signals the activated B cell to proliferate
CC and undergo antibody class switching and secretion. LHL has been
CC modified to contain a FLAG epitope and strep-tag (see AAW32481),
CC to contain a variable kappa light chain (see AAW32482) and to be
CC flanked by tumour necrosis factor (see AAW32480). The catalytic
CC antibodies generated by the process have diagnostic and therapeutic
CC applications.
XX
SQ Sequence 182 AA;

Query Match 83.8%; Score 326; DB 18; Length 182;
Best Local Similarity 97.0%; Pred. No. 1.le-29;
Matches 64; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 DSEEVTTKANLIFANGSTQTAERFGTPEKATSEAYAYADTLKDKNGEYTVADVADKGYTL 70
DB 25 DNTVEVTKANLIFANGSTQTAERFGTPEKATSEAYAYADTLKDKNGEYTVADVADKGYTL 84
QY 71 NIKFAG 76
DB 85 NIKFAG 90

RESULT 6
AAW06907
ID AAY06907 standard; Protein; 182 AA.
AC AAY06907;
XX
XX 01-JUL-1999 (first entry)
XX
XX LHL growth factor amino acid sequence.
XX
XX Growth factor precursor; B-cell surface; T cell surface; CAB; hepatitis;
XX catalytic antibody; immunoglobulin; tumour necrosis factor; influenza;
XX rheumatoid arthritis; toxic shock syndrome; viral docking receptor;
XX human immune virus; tumour-specific antigen; amyloid plaque; myeloma;
XX Alzheimer's disease; IGE; allergy; asthma; drug detoxification;
XX autoimmune; inflammatory disease; gene therapy; protein L; P. magnus;
XX hen egg lysozyme; HEL; LHL.
XX
XX Peptostreptococcus magnus.
OS Gallus sp.
XX
XX WO9915563-A1.
PN

```

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XX 01-APR-1999.
XX
XX 18-SEP-1998; 98WO-AU00783.
XX
XX 19-SEP-1997; 97AU-0009306.
XX
XX (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
XX Koentgen F, Suess GM, Tarlinton DM, Treutlein HR;
XX
XX WPI; 1999-244394/20.
DR N-PSDB; AAX34590.
XX
XX Growth factor precursor cleaved by antigen-specific catalytic
PT antibody
XX
XX Example 1; Page 62; 101pp; English.
XX
XX The invention relates to a growth factor precursor that comprises B-cell
CC surface binding part, T cell surface binding part, antigen cleavable
CC by a catalytic antibody (CAB); and a peptide comprising heavy and light
CC chains of immunoglobulin. When the antigen is cleaved the B cell surface
CC part can interact with its target. The growth factor precursors are used
CC to select B cells that produce Ag-specific CAB, and to generate CAB from
CC such cells (by inducing mitogenesis, caused by the growth factor released
CC by specific cleavage). The Ag-specific CAB can be directed against, e.g.
CC tumour necrosis factor (treatment of rheumatoid arthritis or toxic shock
CC syndrome); viral docking receptors (treatment of human immune virus,
CC hepatitis and influenza infections); tumour-specific antigens; amyloid
CC plaque (treatment of Alzheimer's disease or myeloma) or IGE (treatment of
CC allergies such as asthma). CAB may also be used for drug detoxification,
CC to treat autoimmune or inflammatory diseases and to eliminate
CC environmental or industrial pollutants, such as plastics and petroleum.
CC Particularly the growth factor precursors are produced by delivering the
CC corresponding nucleic acid in a viral or other gene therapy vector. The
CC present sequence represents the amino acid sequence of the LHL growth
CC factor. L is a B cell surface molecule binding portion from protein L of
CC P. magnus; H is a T cell surface molecule binding portion from hen egg
CC lysozyme (HEL). LHL is a growth factor comprising H flanked by two L
CC molecules.
XX
SQ Sequence 182 AA;

Query Match 83.8%; Score 326; DB 20; Length 182;
Best Local Similarity 97.0%; Pred. No. 1.le-29;
Matches 64; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 DSEEVTTKANLIFANGSTQTAERFGTPEKATSEAYAYADTLKDKNGEYTVADVADKGYTL 70
DB 25 DNTVEVTKANLIFANGSTQTAERFGTPEKATSEAYAYADTLKDKNGEYTVADVADKGYTL 84
QY 71 NIKFAG 76
DB 85 NIKFAG 90

RESULT 7
AAW32486
ID AAW32486 standard; Protein; 178 AA.
XX
XX AAW32486;
XX
XX 27-MAR-1998 (first entry)
XX
XX Growth factor LHL-omp (catalytic antibody precursor).
XX
XX Catalytic antibody; growth factor; B-cell mitogenesis; LHL-omp;
XX L protein; hen egg lysozyme; HEL.
XX
XX Chimeric - Peptostreptococcus magnus.
OS Chimeric - Gallus sp.
XX
XX Chimeric - Synthetic.
OS

```

XX Key Location/Qualifiers
 FH Peptide 2..9
 FT /note= "FLAG epitope"
 FT Peptide 170..178
 FT /note= "strept-tag"
 XX W09735887-AL.
 XX 02-OCT-1997.
 XX 26-MAR-1997; 97WO-AU00194.
 XX 27-FEB-1997; 97AU-0005375.
 XX 26-MAR-1996; 96AU-0008951.
 XX (AMRA-) AMRAD OPERATIONS PTY LTD.
 XX Koentgen F, Suess GM, Tarlinton DM, Treutlein HR;
 PI WPI; 1997-489572/45.
 DR N-PSDB; AAT91591.
 XX New catalytic antibody precursors - comprising a B-cell surface
 PT molecule binding portion which can induce B-cell mitogenesis
 XX
 XX Example 27; Page 76; 109pp; English.
 XX This polypeptide comprises growth factor LHL-omp, where L is the
 CC immunoglobulin binding entity from Peptostreptococcus magnus and H
 CC is residues 42-62 of hen egg lysozyme. It was generated from
 CC LHL.seq (see AAW32481) such that the E. coli ompA signal sequence
 CC (generated by purifying LHL.seq from whole bacterial host cells) was
 CC eliminated. The N-terminal omp peptide found in LHL (see AAW32479),
 CC LHL.seq (see AAW32481) and TLHL (see AAW32482) induces multimerisation
 CC as demonstrated by a potentiation of biological activity as
 CC compared to recombinant LHL-omp. Production of catalytic antibodies
 CC to a specific antigen comprises administering to an animal a growth
 CC factor comprising an antigen capable of interacting with a B cell
 CC bound catalytic antibody. The antigen is fused to a B cell surface
 CC molecule binding portion for the antigen to be cleaved and for the
 CC remainder of the molecule to induce B cell mitogenesis (claimed).
 CC The observation that omp induces multimerisation allows the design
 CC of simpler molecules with the same desired biological function as
 CC LHL, TLHL and CATAB (see AAW32480). The catalytic antibodies
 CC generated by the process can have diagnostic and therapeutic
 CC applications.
 XX Sequence 178 AA;
 SQ Query Match 83.0%; Score 323; DB 18; Length 178;
 Best Local Similarity 98.5%; Pred. No. 2.3e-29;
 Matches 64; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 12 SEEEVIKANLIFANGSTQTAEPKGFKEKATSEAYAYADTLKKDNGEYTVDVADKGYTLN 71
 DB 102 SAEETIKANLIFANGSTQTAEPKGFKEKATSEAYAYADTLKKDNGEYTVDVADKGYTLN 161
 QY 72 IKFAG 76
 DB 162 IKFAG 166
 RESULT 8
 AAY06913
 ID AAY06913 standard; Protein; 178 AA.
 XX AAY06913;
 AC
 XX 01-JUL-1999 (first entry)
 DT
 XX Amino acid sequence of a form of LHL growth factor (LHL.omp).
 DE
 XX

KW Growth factor precursor; B-cell surface; T cell surface; CAB; hepatitis;
 KW catalytic antibody; immunoglobulin; tumour necrosis factor; influenza;
 KW rheumatoid arthritis; toxic shock syndrome; viral docking receptor;
 KW human immune virus; tumour-specific antigen; amyloid plaque; myeloma;
 KW Alzheimer's disease; IGE; allergy; asthma; drug detoxification;
 KW autoimmune; inflammatory disease; gene therapy; protein L; P. magnus;
 KW hen egg lysozyme; HEL; LHL.
 XX Peptostreptococcus magnus.
 OS Gallus sp.
 XX W09915563-AL.
 XX 01-APR-1999.
 XX 18-SEP-1998; 98WO-AU00783.
 XX 19-SEP-1997; 97AU-0009306.
 XX (AMRA-) AMRAD OPERATIONS PTY LTD.
 XX Koentgen F, Suess GM, Tarlinton DM, Treutlein HR;
 PI WPI; 1999-244394/20.
 DR N-PSDB; AAX34595.
 XX Growth factor precursor cleaved by antigen-specific catalytic
 PT antibody
 PT Examples; Page 74; 101pp; English.
 PS The invention relates to a growth factor precursor that comprises B-cell
 XX surface binding part, T cell surface binding part, antigen cleavable
 CC by a catalytic antibody (CAB); and a peptide comprising heavy and light
 CC chains of immunoglobulin. When the antigen is cleaved the B cell surface
 CC part can interact with its target. The growth factor precursors are used
 CC to select B cells that produce Ag-specific CAB, and to generate CAB from
 CC such cells (by inducing mitogenesis, caused by the growth factor released
 CC by specific cleavage). The Ag-specific CAB can be directed against, e.g.
 CC tumour necrosis factor (treatment of rheumatoid arthritis or toxic shock
 CC syndrome); viral docking receptors (treatment of human immune virus,
 CC hepatitis and influenza infections); tumour-specific antigens; amyloid
 CC plaque (treatment of Alzheimer's disease or myeloma) or IGE (treatment of
 CC allergies such as asthma). CAB may also be used for drug detoxification,
 CC to treat autoimmune or inflammatory diseases and to eliminate
 CC environmental or industrial pollutants, such as plastics and petroleum.
 CC Particularly the growth factor precursors are produced by delivering the
 CC corresponding nucleic acid in a viral or other gene therapy vector. The
 CC present sequence represents the amino acid sequence of the LHL growth
 CC factor carrying an ompA signal peptide (LHL.omp). L is a B cell surface
 CC molecule binding portion from protein L of P. magnus; H is a T cell
 CC surface molecule binding portion from hen egg lysozyme (HEL). LHL is a
 CC growth factor comprising H flanked by two L molecules.
 XX Sequence 178 AA;
 SQ Query Match 83.0%; Score 323; DB 20; Length 178;
 Best Local Similarity 98.5%; Pred. No. 2.3e-29;
 Matches 64; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 12 SEEEVIKANLIFANGSTQTAEPKGFKEKATSEAYAYADTLKKDNGEYTVDVADKGYTLN 71
 DB 102 SAEETIKANLIFANGSTQTAEPKGFKEKATSEAYAYADTLKKDNGEYTVDVADKGYTLN 161
 QY 72 IKFAG 76
 DB 162 IKFAG 166
 RESULT 9
 AAW32481
 ID AAW32481 standard; Protein; 198 AA.
 XX

AC		AAW32481;	
XX	27-MAR-1998	(first entry)	
XX	Growth factor LHL.seq	catalytic antibody precursor).	
DE	Catalytic antibody; growth factor; B-cell mitogenesis; LHL.seq;	L protein; hen egg lysozyme; HEL.	
KW	Chimeric - Peptostreptococcus magnus.		
XW	Chimeric - Gallus sp.		
XX	Chimeric - Synthetic.		
OS			
OS			
OS			
XX			
FH	Key	Location/Qualifiers	
FT	Peptide	22..29	
FT	/note= "FLAG epitope"		
PT	Peptide	190..198	
FT	/note= "strept-tag"		
XX			
PV	WO9735887-A1.		
PN			
XX			
PD	02-OCT-1997.		
XX			
PF	26-MAR-1997;	97WO-AU00194.	
PR	27-FEB-1997;	97AU-0005375.	
PR	26-MAR-1996;	96AU-0008951.	
XX	(AMRA-) AMRAD OPERATIONS PTY LTD.		
PA			
XX	Koentgen F, Suess GM, Tarlinton DM, Treutlein HR;		
PI	WPI; 1997-489572/45.		
DR	N-PSDB; AAT91588.		
DR	New catalytic antibody precursors - comprising a B-cell surface molecule binding portion which can induce B-cell mitogenesis		
PT	Example 3; Page 70-71; 109pp; English.		
PT	This polypeptide comprises growth factor LHL.seq, where L is the immunoglobulin binding entity from Peptostreptococcus magnus and H is residues 42-62 of hen egg lysozyme. It is a modified form of LHL (see AAW32479) having an N-terminal FLAG epitope (see AAW32484) and a C-terminal strep-tag (see AAW32485) that facilitates purification.		
CC	Production of catalytic antibodies to a specific antigen comprises administering to an animal a growth factor comprising an antigen capable of interacting with a B cell bound catalytic antibody. The antigen is fused to a B cell surface molecule binding protein for the antigen to be cleaved and for the remainder of the molecule to induce B cell mitogenesis (claimed). LHL.seq has the same biological activity as LHL, which crosslinks with surface immunoglobulin on B cells. This induces B cell activation and blast formation. Internalisation and processing of LHL leads to the presentation of the H peptide on MHC II." cell recognition of MHC II with the H peptide signals the activated B cell to proliferate and undergo antibody class switching and secretion. The catalytic antibodies generated by the process can have diagnostic and therapeutic applications.		
CC	SQ Sequence	198 AA;	
Query Match	83.0%; Score 323; DB 18; Length 198;		
Best Local Similarity	98.5%; Pred. No. 2.7e-29;		
Matches	64; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
OY	12 SEEVETKANLIFANGSTQTAEFGTPEKATSAYAYADTLKKDNGEYTDVDVKGYTLN 71 I		
Dd	122 SAEVTIKANLIFANGSTQTAEFGTPEKATSAYAYADTLKKDNGEYTDVDVKGYTLN 181 I		
Oy	72 IKFAG 76		
d _b	182 IKFAG 186 		


```
Query Match      83.0% ; Score 323 ; DB 18; Length 342;
Best Local Similarity 96.5%; Pred. No. 5.6e-29;
Matches 64; Conservative 0; Mismatches 1; Indels 0; Gaps 0
```

QF	72	IKFAG 70
		11111
Db	234	IKFAG 238

RESULT 12
AAY06909
ID AAY06909 standard: Protein: 342 AA.

AA
AC
XX
XX
DT
XX

XX Growth factor precursor; B-cell surface; T cell surface; CAB; hepatitis;
 DE catalytic antibody; immunoglobulin; tumour necrosis factor; influenza;
 TLHL amino acid sequence.

KW
rheumatoid arthritis; toxic shock syndrome; viral docking receptor;
KW
human immune virus: tumour-specific antigen: amyloid plaque myeloma:

KW Alzheimer's disease; IGE; allergy; asthma; drug detoxification;
KW autoimmune: inflammatory disease: gene therapy: protein L: P. magnus;

KW hen egg lysosyme; HEL; LHL; TLHL.
XX

OS Peptostreptococcus magnus.
OS Gallus sp.

XX PN WO9915563-A1.

FD
VI-APK-1999.
XX

XX
TO DEF 1960
5000 OMW 5000

FX 1991, 9150 0009300, XX

FA (AMRA -) AIRMAD OPERATIONS F11 LTD.
XX

XX
XX

W-8; 1503 247034/20.
N-PSDB; AAX34592.

DR
XX
XX
PT
PT
XX
XX
PS
XX
XX

Growth factor precursor cleaved by antigen-specific catalytic antibody

Example 11; Page 67-69; 101pp; English.

The invention relates to a growth factor precursor that comprises B-cell surface binding part, T cell surface binding part, antigen cleavable by a catalytic antibody (CAB); and a peptide comprising heavy and light chains of immunoglobulin. When the antigen is cleaved the B cell surface part can interact with its target. The growth factor precursors are used to select B cells that produce Ag-specific CAB, and to generate CAB from such cells (by inducing mitogenesis, caused by the growth factor released by specific cleavage). The Ag-specific CAB can be directed against, e.g., tumour necrosis factor (treatment of rheumatoid arthritis or toxic shock syndrome); viral docking receptors (treatment of human immune virus, hepatitis and influenza infections); tumour-specific antigens; amyloid plaque (treatment of Alzheimer's disease or myeloma) or IGE (treatment of allergies such as asthma). CAB may also be used for drug detoxification, to treat autoimmune or inflammatory diseases and to eliminate environmental or industrial pollutants, such as plastics and petroleum. Particularly the growth factor precursors are produced by delivering the

CC corresponding nucleic acid in a viral gene therapy vector. The LHL is a CC present sequence represents the amino acid sequence of TLHL. The LHL is a

CC to treat autoimmune or inflammatory diseases and to eliminate
CC environmental or industrial pollutants, such as plastics and petroleum.
CC Particularly the growth factor precursors are produced by delivering the
CC corresponding nucleic acid in a viral or other gene therapy vector. The
CC present sequence represents the amino acid sequence of the ccMTLgI growth
CC factor. L is a B cell surface molecule binding portion from protein L of
CC P. magnus; LcL is two L molecules linked via glycine-serine peptide.
CC ccMTLgI is a growth factor comprising IgL linked to variable heavy and
CC light chain domains from antibody McPC603 via TEV (tobacco etch virus)
CC sensitive peptide.

XX
SO Sequence 482 AA;

Query Match 83.0%; Score 323; DB 20; Length 482;
Best Local Similarity 98.5%; Pred. No. 8.9e-29;
Matches 64; Conservative 0; Mismatches 1; Indels 0; Gaps 0

QY 12 SEEEVTIKANLIFANGSTQTAEFGKTFEKATSEAYAYADTLTKDNGEYTVDAVKGYTLN 71
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 321 SAEVETIKANLIFANGSTQTAEFGKTFEKATSEAYAYADTLTKDNGEYTVDAVKGYTLN 380

QY 72 IKFAG 76
| | | | |
Db 381 IKFAG 385

RESULT 14
AAW32480
ID AAW32480 standard; Protein; 495 AA.
XX
AC AAW32480;
XX
DT 27-MAR-1998 (first entry)
XX
DE Growth factor CATAB-TEV (catalytic antibody precursor).
XX
KW Catalytic antibody; growth factor; B-cell mitogenesis; LHL;
KW L protein; hen egg lysozyme; kappa light chain.
XX
OS Chimeric - Peptostreptococcus magnus.
OS OS Chimeric - Gallus sp.
OS OS Chimeric - Homo sapiens.
XX
PN WQ9735887-A1.
XX
PD 02-OCT-1997.
XX
PF 26-MAR-1997; 97WO-AU00194.
XX
PR 27-FEB-1997; 97AU-0005375.
PR 26-MAR-1996; 96AU-0008951.
XX
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI Koentgen F, Suess GM, Tarlinton DM, Treutlein HR;
XX
DR WPI: 1997-489572/45.
DR N-PSDB; AAT91587.
XX
PT New catalytic antibody precursors - comprising a B-cell surface
PT molecule binding portion which can induce B-cell mitogenesis
XX
PS Claim 12; Page 61-63; 109pp; English.
XX
CC This polypeptide comprises CATAB-TEV, a synthetic growth factor
CC composed of: (a) TLHL (see AAW91589), where L is the immunoglobulin
CC binding entity of Peptostreptococcus magnus, H is residues 42-62 of
CC hen egg lysozyme, and T represents the variable kappa light chain
CC (see AAW32483) from human myeloma protein LEN; and (b) an additional,
CC C-terminal kappa protein, the elements of CATAB-TEV being joined by
CC linkers containing recognition sites for tobacco etch virus (TEV)
CC protease. .CATAB-TEV was designed so that the kappa portions of the
CC protein are removed by TEV protease to release 'T' and 'LHL'

CC moieties. Production of catalytic antibodies to a specific antigen
 CC comprises administering to an animal a growth factor comprising an
 CC antigen capable of interacting with a B cell bound catalytic
 CC antibody. The antigen is fused to a B cell surface molecule
 CC binding protein for the antigen to be cleaved and for the remainder
 CC of the molecule to induce B cell mitogenesis (claimed). LHL (see
 CC AA032479) crosslinks with surface immunoglobulin on B cells. This
 CC induces B cell activation and blast formation. Internalisation
 CC and processing of LHL leads to the presentation of the H peptide on
 CC MHC II. T cell recognition of MHC II with the H peptide signals the
 CC activated B cell to proliferate and undergo antibody class switching
 CC and secretion. The catalytic antibodies generated by the process
 CC can have diagnostic and therapeutic applications.
 XX
 SQ Sequence 495 AA;
 Query Match 83.0%; Score 323; DB 18; Length 495;
 Best Local Similarity 98.5%; Pred. No. 9.2e-29;
 Matches 64; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 12 SEEVTKANLIFANGSTQTAEFKGTPEKATSEAYAYADTLKDNGETVDVADKGYTLN 71
 I|||||
 Db 174 SAEVTKANLIFANGSTQTAEFKGTPEKATSEAYAYADTLKDNGETVDVADKGYTLN 233
 Qy 72 IKFAG 76
 I|||||
 Db 234 IKFAG 238
 RESULT 15
 ID AAY06908 standard; Protein: 495 AA.
 XX
 AC AAY06908;
 DT 01-JUL-1999 (first entry)
 XX
 DE CATAB-TEV aminoacid sequence.
 XX
 KW Growth factor precursor; B-cell surface; T cell surface; CAB; hepatitis;
 KW catalytic antibody; immunoglobulin; tumour necrosis factor; influenza;
 KW rheumatoid arthritis; toxic shock syndrome; viral docking receptor;
 KW human immune virus; tumour-specific antigen; amyloid plaque; myeloma;
 KW Alzheimer's disease; IGE; allergy; asthma; drug detoxification;
 KW autoimmune; inflammatory disease; gene therapy; protein L; P. magnus;
 KW hen egg lysosyme; HEL; LHL; CATAB-TEV; tobacco etch virus; TLHL.
 XX
 OS Peptostreptococcus magnus.
 OS Gallus sp.
 XX
 PN W09915563-A1.
 XX
 PD 01-APR-1999.
 XX
 PF 18-SEP-1998; 98WO-AU00783.
 XX
 PR 19-SEP-1997; 97AU-0009306.
 XX
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 XX
 PI Koentgen F, Suess GM, Tarlington DM, Treutlein HR;
 XX
 DR WPI; 1999-244394/20.
 DR N-PSDB; AAX34591.
 XX
 PT Growth factor precursor cleaved by antigen-specific catalytic
 PT antibody
 XX
 PS Example 15; Page 64-66; 101pp; English.
 XX
 CC The invention relates to a growth factor precursor that comprises B-cell
 CC surface binding part, T cell surface binding part, antigen cleavable
 CC by a catalytic antibody (CAB); and a peptide comprising heavy and light

CC chains of immunoglobulin. When the antigen is cleaved the B cell surface
 CC part can interact with its target. The growth factor precursors are used
 CC to select B cells that produce Ag-specific CAB, and to generate CAB from
 CC such cells (by inducing mitogenesis, caused by the growth factor released
 CC by specific cleavage). The Ag-specific CAB can be directed against, e.g.
 CC tumour necrosis factor (treatment of rheumatoid arthritis or toxic shock
 CC syndrome); viral docking receptors (treatment of human immune virus,
 CC hepatitis and influenza infections); tumour-specific antigens; amyloid
 CC plaque (treatment of Alzheimer's disease or myeloma) or IGE (treatment of
 CC allergies such as asthma). CAB may also be used for drug detoxification,
 CC to treat autoimmune or inflammatory diseases and to eliminate
 CC environmental or industrial pollutants, such as plastics and petroleum.
 CC Particularly the growth factor precursors are produced by delivering the
 CC corresponding nucleic acid in a viral or other gene therapy vector. The
 CC present sequence represents the amino acid sequence of CATAB-TEV which
 CC is assembled from TLHL and kappa by PCR. The LHL is a growth factor
 CC comprising H flanked by two L molecules where L is a B cell surface
 CC molecule binding portion from protein L of P. magnus; H is a T cell
 CC surface molecule binding portion from hen egg lysosyme (HEL). TLHL is
 CC LHL linked to kappa chain via TEV (tobacco etch virus) sensitive
 CC peptide and g attached to N terminus region.
 XX
 SQ Sequence 495 AA;

Query Match 83.0%; Score 323; DB 20; Length 495;
 Best Local Similarity 98.5%; Pred. No. 9.2e-29;
 Matches 64; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 SEEVTKANLIFANGSTQTAEFKGTPEKATSEAYAYADTLKDNGETVDVADKGYTLN 71
 I|||||
 Db 174 SAEVTKANLIFANGSTQTAEFKGTPEKATSEAYAYADTLKDNGETVDVADKGYTLN 233
 Qy 72 IKFAG 76
 I|||||
 Db 234 IKFAG 238

Search completed: September 3, 2003, 11:19:17
 Job time : 52.0137 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:16:02 ; Search time 16.6575 Seconds
(without alignments)
193.043 Million cell updates/sec

Title: US-08-325-278b-1_COPY_5_80

Perfect score: 389

Sequence: 1 KEETPTPTDSEEVTKA.....GEYTVADKGYTLNIKFG 76

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfilesl.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	389	100.0	305	2	US-08-795-475-1
2	389	100.0	434	2	US-08-795-475-3
3	326	83.8	182	3	US-08-828-741B-2
4	326	83.8	182	4	US-09-160-567-2
5	326	83.8	182	4	US-09-710-299-2
6	323	83.0	178	3	US-08-828-741B-13
7	323	83.0	178	4	US-09-160-567-13
8	323	83.0	178	4	US-09-710-299-13
9	323	83.0	198	3	US-08-828-741B-8
10	323	83.0	198	4	US-09-160-567-8
11	323	83.0	198	4	US-09-710-299-8
12	323	83.0	342	3	US-08-828-741B-6
13	323	83.0	342	4	US-09-160-567-6
14	323	83.0	342	4	US-09-710-299-6
15	323	83.0	495	3	US-08-828-741B-4
16	323	83.0	495	4	US-09-160-567-4
17	323	83.0	495	4	US-09-710-299-4
18	298.5	76.7	1027	3	US-08-446-137B-2
19	298	76.6	71	3	US-08-446-137B-5
20	298	76.6	291	3	US-08-446-137B-4
21	284.5	73.1	75	3	US-08-446-137B-8
22	270.5	69.5	74	3	US-08-446-137B-7
23	262	67.4	71	3	US-08-446-137B-6
24	123	17.7	123	3	US-08-795-444-3
25	65	16.7	419	4	US-09-134-001C-3441
26	64.5	16.6	300	4	US-09-254-465A-10
27	63.5	16.3	8991	4	US-08-714-741-32

28	62.5	16.1	138	6	5218098-1	Patent No. 5218099
29	62.5	16.1	182	4	US-08-858-207A-434	Sequence 434, App
30	61.5	15.8	235	4	US-09-134-001C-4150	Sequence 4150, Ap
31	61	15.7	821	4	US-09-252-991A-21013	Sequence 21013, A
32	61	15.7	1094	4	US-09-268-347-32	Sequence 32, Appl
33	61	15.7	1167	2	US-08-589-756-2	Sequence 2, Appl
34	61	15.7	1167	3	US-09-206-800-2	Sequence 2, Appl
35	61	15.7	1167	4	US-09-206-898-2	Sequence 2, Appl
36	61	15.7	1181	4	US-09-206-898-23	Sequence 23, Appl
37	60	15.4	312	3	US-08-961-083-12	Sequence 12, Appl
38	60	15.4	312	4	US-09-536-784-12	Sequence 12, Appl
39	60	15.4	515	4	US-09-107-532A-5603	Sequence 5603, Ap
40	60	15.4	558	4	US-09-071-035-268	Sequence 268, App
41	60	15.4	1024	4	US-09-562-737-90	Sequence 90, Appl
42	60	15.4	1638	4	US-09-071-035-258	Sequence 258, App
43	60	15.4	1638	4	US-09-071-035-262	Sequence 262, App
44	60	15.4	1638	4	US-09-071-035-266	Sequence 266, App
45	60	15.4	3079	5	PCT-US94-00198-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-795-475-1
; Sequence 1, Application US/08795475
; Patent No. 5965390
; GENERAL INFORMATION:
; APPLICANT: Bjvreck, Lars
; APPLICANT: Sjöbring, Ulf
; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,475
; FILING DATE: 11-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 100084.402D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 305 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli LE392/pHDL, DSM 7054
US-08-795-475-1

Query Match 100.0%; Score 389; DB 2; Length 305;
Best Local Similarity 100.0%; Pred. No. 5.3e-41;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KEETPTPTDSEEVTKANLIFANGSTOAEKGTFFKATSEAYAYADTLKDCGEY 60
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Db 5 KEETPETDSEEVTKANLIFANGSTQTAFFKGTPEKATSEAYAYADTLKKNGEYT 64
QY 61 VDVAADKGYTLNKFAG 76
   |||||
Db 65 VDVAADKGYTLNKFAG 80
   |||||

RESULT 2
US-08-795-475-3
; Sequence 3, Application US/08795475
; Patent No. 5965390
; GENERAL INFORMATION:
; APPLICANT: Bjvrck, Lars
; APPLICANT: SJVdring, Ulf
; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,475
; FILING DATE: 11-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 100084.402D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 434 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli LE392/pHDLG, DSM 7055
; US-08-795-475-3

Query Match 100.0%; Score 389; DB 2; Length 434;
Best Local Similarity 100.0%; Pred. No. 8.7e-41;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEETPETDSEEVTKANLIFANGSTQTAFFKGTPEKATSEAYAYADTLKKNGEYT 60
Db 5 KEETPETDSEEVTKANLIFANGSTQTAFFKGTPEKATSEAYAYADTLKKNGEYT 64
QY 61 VDVAADKGYTLNKFAG 76
   |||||
Db 65 VDVAADKGYTLNKFAG 80
   |||||

RESULT 3
US-08-828-741B-2
; Sequence 2, Application US/08828741B
; Patent No. 6043069
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.
```

```
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
; TITLE OF INVENTION: PRODUCING SAME
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,741B
; FILING DATE: 26-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10591
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 182 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-828-741B-2

Query Match 83.8%; Score 326; DB 3; Length 182;
Best Local Similarity 97.0%; Pred. No. 2.3e-33;
Matches 64; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 DSEEVTKANLIFANGSTQTAFFKGTPEKATSEAYAYADTLKKNGEYTVVDADKGYTL 70
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Db 25 DNTEVTKANLIFANGSTQTAFFKGTPEKATSEAYAYADTLKKNGEYTVVDADKGYTL 84
   |||||
QY 71 NIKFAG 76
   |||||
Db 85 NIKFAG 90
   |||||

RESULT 4
US-09-160-567-2
; Sequence 2, Application US/09160567
; Patent No. 6326179
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
; TITLE OF INVENTION: PRODUCING SAME
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/09/160,567
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,741
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10591
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 182 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-160-567-2

Query Match      83.8%; Score 326; DB 4; Length 182;
Best Local Similarity 97.0%; Pred. No. 2.3e-33;
Matches 64; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 DSEEVTKANLIFANGSTQTAFFKGTFFKATSEAYAYADTLKKDNGEYTVDVADKGYTL 70
Db 25 DNTTEVTIRANLIFANGSTQTAFFKGTFFKATSEAYAYADTLKKDNGEYTVDVADKGYTL 84
QY 71 NIKFAG 76
Db 85 NIKFAG 90

RESULT 5
US-09-710-299-2
; Sequence 2, Application US/09710299
; Patent No. 6521741
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; Applicant: Sues, Gabriele M.
; Applicant: Tarlington, David M.
; Applicant: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
; PRODUCING SAME
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/710,299
; FILING DATE: 09-NO. 6521741-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,741
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10591
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
```

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; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 182 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-710-299-2

Query Match      83.8%; Score 326; DB 4; Length 182;
Best Local Similarity 97.0%; Pred. No. 2.3e-33;
Matches 64; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 DSEEVTKANLIFANGSTQTAFFKGTFFKATSEAYAYADTLKKDNGEYTVDVADKGYTL 70
Db 25 DNTTEVTIRANLIFANGSTQTAFFKGTFFKATSEAYAYADTLKKDNGEYTVDVADKGYTL 84
QY 71 NIKFAG 76
Db 85 NIKFAG 90

RESULT 6
US-08-828-741B-13
; Sequence 13, Application US/08828741B
; Patent No. 6043069
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; Applicant: Sues, Gabriele M.
; Applicant: Tarlington, David M.
; Applicant: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
; PRODUCING SAME
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,741B
; FILING DATE: 26-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10591
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-828-741B-13

Query Match      83.0%; Score 323; DB 3; Length 178;
Best Local Similarity 98.5%; Pred. No. 5.2e-33;
Matches 64; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 SEEVTKANLIFANGSTQTAFFKGTFFKATSEAYAYADTLKKDNGEYTVDVADKGYTL 71
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Db 102 SAEVTIKANLIFANGSTQTAETFKGTSEAYAYADTLKKDNGEYTVDVADKGYTLN 161
QY 72 IKFAG 76
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Db 162 IKFAG 166

RESULT 7
US-09-160-567-13
; Sequence 13, Application US/09160567
; Patent No. 6326179
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlington, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
; TITLE OF INVENTION: PRODUCING SAME
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/160,567
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,741
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10591
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-160-567-13

Query Match 83.0%; Score 323; DB 4; Length 178;
Best Local Similarity 98.5%; Pred. No. 5.2e-33;
Matches 64; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 SAEVTIKANLIFANGSTQTAETFKGTSEAYAYADTLKKDNGEYTVDVADKGYTLN 71
    | |||||
Db 102 SAEVTIKANLIFANGSTQTAETFKGTSEAYAYADTLKKDNGEYTVDVADKGYTLN 161

QY 72 IKFAG 76
    |||||
Db 162 IKFAG 166

RESULT 8
US-09-710-299-13
; Sequence 13, Application US/09710299
; Patent No. 6521741
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
```

```
; Suess, Gabriele M.
; Tarlington, David M.
; Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
; TITLE OF INVENTION: PRODUCING SAME
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/710,299
; FILING DATE: 09-No. 6521741-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,741
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10591
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-710-299-13

Query Match 83.0%; Score 323; DB 4; Length 178;
Best Local Similarity 98.5%; Pred. No. 5.2e-33;
Matches 64; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 SAEVTIKANLIFANGSTQTAETFKGTSEAYAYADTLKKDNGEYTVDVADKGYTLN 71
    | |||||
Db 102 SAEVTIKANLIFANGSTQTAETFKGTSEAYAYADTLKKDNGEYTVDVADKGYTLN 161

QY 72 IKFAG 76
    |||||
Db 162 IKFAG 166

RESULT 9
US-08-828-741B-8
; Sequence 8, Application US/08828741B
; Patent No. 6043069
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlington, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
; TITLE OF INVENTION: PRODUCING SAME
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States of America
```


US-09-710-299-8

```

: Sequence 6, Application US/09160567
: Patent No. 6326179
: GENERAL INFORMATION:
:
: APPLICANT: Koentgen, Frank
: APPLICANT: Suess, Gabriele M.
: APPLICANT: Tarlinton, David M.
: APPLICANT: Treutlein, Herbert R.
: TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
: TITLE OF INVENTION: PRODUCING SAME
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
: STREET: 400 Garden City Plaza

```

CITY: Garden City
 STATE: New York
 COUNTRY: United States of America
 ZIP: 11530
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/160,567
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/828,741
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Digiglio, Frank S.
 REGISTRATION NUMBER: 31,346
 REFERENCE/DOCKET NUMBER: 10591
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (516) 742-4343
 TELEFAX: (516) 742-4366
 TELEEX: 230 901 SANS UR
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 342 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-160-567-6

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RESULT 14
US-09-710-299-6
; Sequence 6, Application US/09710299
; Patent No. 6531741
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; Suess, Gabriele M.
; Tarlinton, David M.
; Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
; PRODUCING SAME
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
;

```

ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza

;
; CITY: Garden City
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/710,299
; FILING DATE: 09-No. 6521741-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,741
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10591
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 342 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-710-299-6

Query Match 83.0%; Score 323; DB 4; Length 342;
Best Local Similarity 98.5%; Pred. No. 1.3e-32;
Matches 64; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 174 SAEVITKANLIIFANGSTQTAETKGTPEKATSEAYAYADTLKKDNGEYTVDVADKGYTLN 233
QY 72 IKFAG 76
Db 234 IKFAG 238

RESULT 15
US-08-828-741B-4
; Sequence 4, Application US/08828741B
; Patent No. 6043069
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlington, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
; TITLE OF INVENTION: PRODUCING SAME
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,741B
; FILING DATE: 26-MAR-1997

;
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10591
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 495 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-828-741B-4
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Best Local Similarity 98.5%; Pred. No. 2.2e-32;
Matches 64; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 12 SEEEVTIKANLIIFANGSTQTAETKGTPEKATSEAYAYADTLKKDNGEYTVDVADKGYTLN 71
Db 174 SAEVITKANLIIFANGSTQTAETKGTPEKATSEAYAYADTLKKDNGEYTVDVADKGYTLN 233
QY 72 IKFAG 76
Db 234 IKFAG 238
Search completed: September 3, 2003, 11:25:35
Job time : 17.6575 secs

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	Score	Match	Length		
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2	389	100.0	305	8	Sequence 1, Appli
3	389	100.0	434	8	Sequence 3, Appli
4	326	83.8	182	12	Sequence 2, Appli
5	323	83.0	178	12	Sequence 13, Appli
6	323	83.0	198	12	Sequence 8, Appli
7	323	83.0	342	12	Sequence 6, Appli
8	323	83.0	482	12	Sequence 16, Appli
9	323	83.0	495	12	Sequence 4, Appli
10	324	80.7	72	10	Sequence 6, Appli
11	299	76.9	72	10	Sequence 8, Appli
12	298	76.6	71	10	Sequence 12, Appli
13	284.5	73.1	75	10	Sequence 18, Appli
14	270.5	69.5	74	10	Sequence 10, Appli
15	269	69.2	72	10	Sequence 16, Appli

APPLICANT: Bjvrck, Lars
APPLICANT: Sjvbring, Ulf
TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,278
FILING DATE: 26-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 450023.401
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 305 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Escherichia coli LE392/pHDL, DSM 7054
US-08-325-278-1

Query Match 100.0%; Score 389; DB 8; Length 305;
Best Local Similarity 100.0%; Pred. No. 1.6e-36;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEETPETDSEEEVTKANLIFANGSTQTAFFKGTFFKATSEAYAYADTLKNGEY 60
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Db 5 KEETPETDSEEEVTKANLIFANGSTQTAFFKGTFFKATSEAYAYADTLKNGEY 64
|||||

QY 61 VDVADKGYTLNKFAG 76
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Db 65 VDVADKGYTLNKFAG 80
|||||

RESULT 3
US-08-325-278-3
Sequence 3, Application US/08325278
Publication No. US20030027283A1
GENERAL INFORMATION:
APPLICANT: Bjvrck, Lars
APPLICANT: Sjvbring, Ulf
TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,278
FILING DATE: 26-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 450023.401
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Escherichia coli LE392/pHDL, DSM 7055
US-08-325-278-3

Query Match 100.0%; Score 389; DB 8; Length 434;
Best Local Similarity 100.0%; Pred. No. 2.5e-36;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 5 KEETPETDSEEEVTKANLIFANGSTQTAFFKGTFFKATSEAYAYADTLKNGEY 64
|||||

QY 61 VDVADKGYTLNKFAG 76
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Db 65 VDVADKGYTLNKFAG 80
|||||

RESULT 4
US-10-345-618-2
Sequence 2, Application US/10345618
Publication No. US2003014848A1
GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
APPLICANT: Sues, Gabriele M.
APPLICANT: Tarlington, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF PRODUCING SAME
FILE REFERENCE: 13474
CURRENT APPLICATION NUMBER: US/10/345,618
CURRENT FILING DATE: 2003-01-16
PRIOR APPLICATION NUMBER: US/09/509,031
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 182
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:LHL protein
OTHER INFORMATION: sequence
US-10-345-618-2

Query Match 83.8%; Score 326; DB 12; Length 182;
Best Local Similarity 97.0%; Pred. No. 1.3e-29;
Matches 64; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db 25 DNTEEVTKANLIFANGSTQTAFFKGTFFKATSEAYAYADTLKNGEYTVADKGYTL 84
|:|||||

QY 71 NIKFAG 76
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Db 85 NIKFAG 90
|||||

Db 122 SAEVTKANLIFANGSTQAEFGKTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLN 181

QY 72 IKFAG 76
182 IKFAG 186

RESULT 7
US-10-345-618-6
; Sequence 6, Application US/10345618
; Publication No. US20030148484A1
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING SAME
; FILE REFERENCE: 13474
; CURRENT APPLICATION NUMBER: US/10/345,618
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US/09/509,031
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:TLHL protein
; OTHER INFORMATION: sequence
US-10-345-618-6

Query Match 83.0%; Score 323; DB 12; Length 342;
Best Local Similarity 98.5%; Pred. No. 6.5e-29;
Matches 64; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 SEEVTKANLIFANGSTQAEFGKTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLN 71
174 SAEVTKANLIFANGSTQAEFGKTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLN 233

QY 72 IKFAG 76
234 IKFAG 238

RESULT 8
US-10-345-618-16
; Sequence 16, Application US/10345618
; Publication No. US20030148484A1
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING SAME
; FILE REFERENCE: 13474
; CURRENT APPLICATION NUMBER: US/10/345,618
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US/09/509,031
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 16
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:cmTlgL protein
; OTHER INFORMATION: sequence
US-10-345-618-16

Query Match 83.0%; Score 323; DB 12; Length 482;

RESULT 5
US-10-345-618-13
; Sequence 13, Application US/10345618
; Publication No. US20030148484A1
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING SAME
; FILE REFERENCE: 13474
; CURRENT APPLICATION NUMBER: US/10/345,618
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US/09/509,031
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 13
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:LHL-omp
; OTHER INFORMATION: protein sequence
US-10-345-618-13

Query Match 83.0%; Score 323; DB 12; Length 178;
Best Local Similarity 98.5%; Pred. No. 2.8e-29;
Matches 64; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 SEEVTKANLIFANGSTQAEFGKTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLN 71
102 SAEVTKANLIFANGSTQAEFGKTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLN 161

QY 72 IKFAG 76
162 IKFAG 166

RESULT 6
US-10-345-618-8
; Sequence 8, Application US/10345618
; Publication No. US20030148484A1
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING SAME
; FILE REFERENCE: 13474
; CURRENT APPLICATION NUMBER: US/10/345,618
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US/09/509,031
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:LHL.seq
; OTHER INFORMATION: protein sequence
US-10-345-618-8

Query Match 83.0%; Score 323; DB 12; Length 198;
Best Local Similarity 98.5%; Pred. No. 3.2e-29;
Matches 64; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 SEEVTKANLIFANGSTQAEFGKTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLN 71
174 SAEVTKANLIFANGSTQAEFGKTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLN 233

Query Match	80.7%;	Score 314;	DB 10;	Length 72;
Best Local Similarity	81.6%;	Pred. No. 9.3e-29;		

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Best Local Similarity	85.99;	Pred. No. 6.le-27;		
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QY	66	KGYTLNLIKFAK	76	

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:19:27 ; Search time 224.877 Seconds
(without alignments)
294.149 Million cell updates/sec

Title: US-08-325-278B-1_COPY_5_80

Perfect score: 389

Sequence: 1 KEETPETPDSSEEVTIKAKLIFANGSTOTAFKGTFFKATSEAYAYDTLKDNCEYT 60

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Searched: 5580241 seqs, 870357830 residues

Total number of hits satisfying chosen parameters: 5580241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

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- 2: /cgn2_6/ptodata/1/paa/US06_COMB.pep.*
- 3: /cgn2_6/ptodata/1/paa/US07_COMB.pep.*
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- 31: /cgn2_6/ptodata/1/paa/US105_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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					Sequence 22553, A

3	389	100.0	305	7	US-08-325-278-1	Sequence 1, Appli
4	389	100.0	305	7	US-08-325-278B-1	Sequence 1, Appli
5	389	100.0	305	7	US-08-325-278B-1	Sequence 1, Appli
6	389	100.0	434	7	US-08-325-278-3	Sequence 3, Appli
7	389	100.0	434	7	US-08-325-278A-3	Sequence 3, Appli
8	389	100.0	434	7	US-08-325-278B-3	Sequence 3, Appli
9	389	100.0	719	22	US-09-791-537-10210	Sequence 10210, A
10	389	100.0	719	22	US-09-791-537-96101	Sequence 96101, A
11	384	98.7	467	25	US-09-800-469-12	Sequence 12, Appli
12	326	83.8	182	19	US-09-509-031-2	Sequence 2, Appli
13	326	83.8	182	23	US-09-820-048A-2	Sequence 2, Appli
14	323	83.0	178	19	US-09-509-031-13	Sequence 13, Appli
15	323	83.0	178	23	US-09-820-048A-13	Sequence 13, Appli
16	323	83.0	198	19	US-09-509-031-8	Sequence 8, Appli
17	323	83.0	198	23	US-09-820-048A-8	Sequence 8, Appli
18	323	83.0	342	19	US-09-509-031-6	Sequence 6, Appli
19	323	83.0	342	23	US-09-820-048A-6	Sequence 6, Appli
20	323	83.0	482	19	US-09-509-031-16	Sequence 16, Appli
21	323	83.0	495	19	US-09-509-031-4	Sequence 4, Appli
22	323	83.0	495	23	US-09-820-048A-4	Sequence 4, Appli
23	314	80.7	72	23	US-09-808-212A-6	Sequence 6, Appli
24	314	80.7	367	23	US-09-889-182A-4	Sequence 4, Appli
25	299	76.9	72	23	US-09-808-212A-8	Sequence 8, Appli
26	298.5	76.7	992	22	US-09-791-537-88366	Sequence 88366, A
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28	298.5	76.7	1027	8	US-08-446-137A-2	Sequence 2, Appli
29	298.5	76.7	1027	15	US-09-187-295-2	Sequence 2, Appli
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31	298	76.6	71	8	US-08-446-137A-4	Sequence 4, Appli
32	284.5	73.1	75	23	US-09-808-212A-18	Sequence 18, Appli
33	270.5	69.5	74	23	US-09-808-212A-16	Sequence 16, Appli
34	269	69.2	72	23	US-09-808-212A-10	Sequence 10, Appli
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36	262	67.4	71	23	US-09-808-212A-2	Sequence 2, Appli
37	74	19.0	269	19	US-09-540-209B-7625	Sequence 14, Appli
38	74	19.0	529	22	US-09-791-537-131077	Sequence 7625, Ap
39	73	18.8	634	22	US-09-791-537-126395	Sequence 131077,
40	72	18.5	243	21	US-09-708-427-12618	Sequence 126395,
41	72	18.5	487	21	US-09-708-427-12617	Sequence 12618, A
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43	71.5	18.4	841	1	PCT-US02-03987-5779	Sequence 28306, A
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						Sequence 5779, Ap

ALIGNMENTS

RESULT 1
US-09-808-212A-4
; Sequence 4, Application US/09808212A
; GENERAL INFORMATION:
; APPLICANT: Gore, Michael Graham
; APPLICANT: Beckingham, Jennifer Ann
; APPLICANT: Robertus, Iman Eleri
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN
; FILE REFERENCE: 100084.414US
; CURRENT APPLICATION NUMBER: US/09/808,212A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Peptostreptococcus sp.
US-09-808-212A-4

Query Match 100.0%; Score 389; DB 23; Length 76;
Best Local Similarity 100.0%; Pred. No. 3.6e-37;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEETPETPDSSEEVTIKAKLIFANGSTOTAFKGTFFKATSEAYAYDTLKDNCEYT 60
|||||

[illegible]

```

RESULT 5
US-08-325-278B-1
; Sequence 1, Application US/08325278B
; GENERAL INFORMATION:
; APPLICANT: Bjorck, Lars
; Sjobring, Ulf
; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed IP Law Group
; STREET: 701 Fifth Avenue Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,278B
; FILING DATE: 26-Oct-1994
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCRET NUMBER: 100084.402
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 305 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli LE392/pHDL, DSM 7054
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-08-325-278B-1

```

```

RESULT 6
US-08-325-278-3
; Sequence 3, Application US/08325278
;
; GENERAL INFORMATION:
;
; APPLICANT: Bjvick, Lars
; APPLICANT: Sjvbring, Ulf
; TITLE OF INVENTION: Protein L and Hybrid Proteins Thereof
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
;

```

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: ADDRESSEE: SEED and BERRY LLP
: STREET: 6300 Columbia Center, 701 Fifth Avenue
: City: Seattle
: STATE: Washington
: COUNTRY: USA
: ZIP: 98104-7092
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/325,278
: FILING DATE: 26-OCT-1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: McMasters, David D.
: REGISTRATION NUMBER: 33,963
: REFERENCE/DOCKET NUMBER: 450023.401
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206) 622-4900
: TELEFAX: (206) 682-6031
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 434 amino acids
: TYPE: amino acid
: STRANDEDNESS: unknown
: TOPOLOGY: unknown
: MOLECULE TYPE: protein
: HYPOTHETICAL: NO
: ORIGINAL SOURCE:
: ORGANISM: Escherichia coli LE392/PHDLG, DSM 7055
:
: US-08-325-278-3
:
: Query Match 100.0%; Score 389; DB 7; Length 434;
: Best Local Similarity 100.0%; Pred. No. 3.9e-36;
: Matches 76; Conservative 0; Mismatches 0; Indels 0
:
: QY 1 KEETPETPDSEEVTTKANLIFANGSTQTAEFKGTFEKATSEAYAYADTL
: Db 5 KEETPETPDSEEVTTKANLIFANGSTQTAEFKGTFEKATSEAYAYADTL
:
: QY 61 VDVAADGYTLNKFAG 76
: Db 65 VDVAADGYTLNKFAG 80
:
: RESULT 7
: US-08-325-278A-3
: Sequence 3, Application US/08325278A
: GENERAL INFORMATION:
: APPLICANT: Bjorck, Lars
: Sjöbring, Ulf
: TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
: NUMBER OF SEQUENCES: 15
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Seed IP Law Group
: STREET: 701 Fifth Avenue Suite 6300
: City: Seattle
: STATE: Washington
: COUNTRY: USA
: ZIP: 98104-7092
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/325,278A
: FILING DATE: 26-Oct-1994
: CLASSIFICATION: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Potter, Jane E. R.

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US-08-325-278B-3

Query Match          100.0%; Score 389; DB 7; Length 434;
Best Local Similarity 100.0%; Pred. No. 3.9e-36;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEETPETPDSSEEVTIKANLIFANGSTQTAEFKGTFFEKATSEAYAYADTLKKDNGEYT 60
    |||||||
Db 5 KEETPETPDSSEEVTIKANLIFANGSTQTAEFKGTFFEKATSEAYAYADTLKKDNGEYT 64
    |||||||

QY 61 VDVAADKGYTLNIRFAG 76
    |||||||
Db 65 VDVAADKGYTLNIRFAG 80
    |||||||

RESULT 9
US-09-791-537-10210
: Sequence 10210, Application US/09791537
: GENERAL INFORMATION:
: APPLICANT: Bionomix, Inc.
: APPLICANT: Danzer, Joseph
: TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
: TITLE OF INVENTION: METHODS OF USE THEREOF
: FILE REFERENCE: 261/210
: CURRENT APPLICATION NUMBER: US/09/791,537
: CURRENT FILING DATE: 2001-02-22
: NUMBER OF SEQ ID NOS: 153055
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 10210
: LENGTH: 719
: TYPE: PRT
: ORGANISM: Peptostreptococcus magnus
US-09-791-537-10210

Query Match          100.0%; Score 389; DB 22; Length 719;
Best Local Similarity 100.0%; Pred. No. 7.7e-36;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEETPETPDSSEEVTIKANLIFANGSTQTAEFKGTFFEKATSEAYAYADTLKKDNGEYT 60
    |||||||
Db 98 KEETPETPDSSEEVTIKANLIFANGSTQTAEFKGTFFEKATSEAYAYADTLKKDNGEYT 157
    |||||||

QY 61 VDVAADKGYTLNIRFAG 76
    |||||||
Db 158 VDVAADKGYTLNIRFAG 173
    |||||||

RESULT 10
US-09-791-537-96101
: Sequence 96101, Application US/09791537
: GENERAL INFORMATION:
: APPLICANT: Bionomix, Inc.
: APPLICANT: Debe, Derek
: APPLICANT: Danzer, Joseph
: TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
: TITLE OF INVENTION: METHODS OF USE THEREOF
: FILE REFERENCE: 261/210
: CURRENT APPLICATION NUMBER: US/09/791,537
: CURRENT FILING DATE: 2001-02-22
: NUMBER OF SEQ ID NOS: 153055
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 96101
: LENGTH: 719
: TYPE: PRT
: ORGANISM: Peptostreptococcus magnus
US-09-791-537-96101

Query Match          100.0%; Score 389; DB 22; Length 719;
Best Local Similarity 100.0%; Pred. No. 7.7e-36;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEETPETPDSSEEVTIKANLIFANGSTQTAEFKGTFFEKATSEAYAYADTLKKDNGEYT 60

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Db 98 KEETPETDSEEVTKANLIFANGSTQTAFFKGTSEAYAYADTLKDKNGEYTL 157
QY 61 VDVADKGYTLNFKFAG 76
Db 158 VDVADKGYTLNFKFAG 173

RESULT 11
US-09-980-469-12
; Sequence 12, Application US/09980469
; GENERAL INFORMATION:
; APPLICANT: Shoseyov, Oded
; APPLICANT: Ziv, Shani
; TITLE OF INVENTION: PROCESS OF EXPRESSING AND ISOLATING RECOMBINANT PROTEINS AND RECO
; TITLE OF INVENTION: PROTEIN PRODUCTS FROM PLANTS, PLANT DERIVED TISSUES OR CULTURED
; FILE REFERENCE: 01/22924
; CURRENT APPLICATION NUMBER: US/09/980,469
; CURRENT FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: puc19-cell-Protl-cexng-HDEL fusion encoded product
US-09-980-469-12

Query Match 98.7%; Score 384; DB 25; Length 467;
Best Local Similarity 98.7%; Pred. No. 1.6e-35;
Matches 75; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KEETPETDSEEVTKANLIFANGSTQTAFFKGTSEAYAYADTLKDKNGEYTL 60
Db 44 KEETPETDSEEVTKANLIFANGSTQTAFFKGTSEAYAYADTLKDKNGEYTL 103

QY 61 VDVADKGYTLNFKFAG 76
Db 104 VDVADKGYTLNFKFAG 119

RESULT 12
US-09-509-031-2
; Sequence 2, Application US/09509031
; GENERAL INFORMATION:
; APPLICANT: Koenigen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF PRODUCING SAME
; FILE REFERENCE: 13474
; CURRENT APPLICATION NUMBER: US/09/509,031
; CURRENT FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:LHL protein
; OTHER INFORMATION: sequence
US-09-509-031-2

Query Match 83.8%; Score 326; DB 19; Length 182;
Best Local Similarity 97.0%; Pred. No. 2.6e-29;
Matches 64; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 11 DSEEEVTKANLIFANGSTQTAFFKGTSEAYAYADTLKDKNGEYTVADVADKGYTL 70
Db 25 DNTTEEVTKANLIFANGSTQTAFFKGTSEAYAYADTLKDKNGEYTVADVADKGYTL 84

QY 71 NIKFAG 76
Db 85 NIKFAG 90

RESULT 13
US-09-820-048A-2
; Sequence 2, Application US/09820048A
; GENERAL INFORMATION:
; APPLICANT: Koenigen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
; PRODUCING SAME
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/820,048A
; FILING DATE: 28-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,741
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10591
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 182 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-820-048A-2

Query Match 83.8%; Score 326; DB 23; Length 182;
Best Local Similarity 97.0%; Pred. No. 2.6e-29;
Matches 64; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 DSEEEVTKANLIFANGSTQTAFFKGTSEAYAYADTLKDKNGEYTVADVADKGYTL 70
Db 25 DNTTEEVTKANLIFANGSTQTAFFKGTSEAYAYADTLKDKNGEYTVADVADKGYTL 84

QY 71 NIKFAG 76
Db 85 NIKFAG 90

RESULT 14
US-09-509-031-13
; Sequence 13, Application US/09509031
; GENERAL INFORMATION:
; APPLICANT: Koenigen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.

[illegible]

COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
SOFTWARE: <Unknown>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/617,320
FILING DATE: 10-Jul-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
APPLICATION NUMBER: 60/ 085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011

Qy	2	EET-----PPTPDTS-----EEVTI-----KANLI FANGSTOAPKRGTFEK	40
Db	62	EETPKAELQPETPATDKVASLPKTBEKPQEVSSTPSDKAEVV-----TPTSABKETANK	118
Qy	41	ATSEAYAYADTLKK-DNGEYTVDVADK	66
Db	117	KAEAEASPKEEAKEVDKSNTDKTDK	143

```
RESULT 9
US-10-273-573-8150
; Sequence 8150, Application US/10273573
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: US/10/273,573
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 8150
; LENGTH: 1372
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (795)..(810)
; OTHER INFORMATION: WILM'S TUMOUR PROTEIN SIGNATURE domain identified by eMATRIX,
; OTHER INFORMATION: accession number PR00049D, p-value=7.500e-10, raw score of 0.00
US-10-273-573-8150

Query Match 15.8%; Score 61.5; DB 6; Length 1372;
Best Local Similarity 24.4%; Pred. No. 1.2e+02;
Matches 19; Conservative 12; Mismatches 26; Indels 21; Gaps 2;

QY 1 KETPTPTD-----SEEVTKANLIFANGSTOTAEKGFKA 41
Db 35 EEEPRLPDGLGVPWKEAVRIHALLKKGSEEE--LEASKSPGNGNEEEEEEEYEE 92

QY 42 TSEAYAYADTLKKDNGEY 59
Db 93 EEDYDEEEESSEGEY 110

RESULT 10
US-10-273-573-8152
; Sequence 8152, Application US/10273573
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: US/10/273,573
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 8152
; LENGTH: 1377
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (795)..(810)
; OTHER INFORMATION: WILM'S TUMOUR PROTEIN SIGNATURE domain identified by eMATRIX,
; OTHER INFORMATION: accession number PR00049D, p-value=7.500e-10, raw score of 0.00
US-10-273-573-8152

Query Match 15.8%; Score 61.5; DB 6; Length 1377;
Best Local Similarity 24.4%; Pred. No. 1.3e+02;
Matches 19; Conservative 12; Mismatches 26; Indels 21; Gaps 2;

QY 1 KETPTPTD-----SEEVTKANLIFANGSTOTAEKGFKA 41
Db 35 EEEPRLPDGLGVPWKEAVRIHALLKKGSEEE--LEASKSPGNGNEEEEEEEYEE 92
```

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QY 42 TSEAYAYADTLKKDNGEY 59
Db 93 EEDYDEEEESSEGEY 110

RESULT 11
US-09-897-516A-7245
; Sequence 7245, Application US/09897516A
; GENERAL INFORMATION:
; APPLICANT: Corbin, David R.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Huesing, Joseph E.
; APPLICANT: Malvar, Thomas M.
; APPLICANT: Krasomil-Osterfeld, Karina C.
; APPLICANT: Slater, Steven C.
; APPLICANT: Spiridonov, Sergei
; TITLE OF INVENTION: Xenorhabdus sp. Genome Sequences And Uses Thereof
; FILE REFERENCE: 38-21(51847)B
; CURRENT APPLICATION NUMBER: US/09/897,516A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,161
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 8415
; SEQ ID NO 7245
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Xenorhabdus sp.
US-09-897-516A-7245

Query Match 15.7%; Score 61; DB 5; Length 253;
Best Local Similarity 31.3%; Pred. No. 16;
Matches 26; Conservative 9; Mismatches 18; Indels 30; Gaps 6;

QY 9 ETDSEEV-----IKANLIFANGSTOTAEKGFKAATSEAYAYADTLKKDNGEY 60
Db 53 DTDSDSEIVATSKSVKAYDLANSANQNA-----SSANDNATLSKDRNG---- 99

QY 61 VDVADE-----GYTLNIRF 74
Db 100 ADIPDKTNELKNIGLGETANVR 122

RESULT 12
US-10-617-320-2862
; Sequence 2862, Application US/10617320
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIA
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/617,320
; FILING DATE: 10-Jul-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
```

```
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 2862:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 311 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (B) LOCATION 1...311
; SEQUENCE DESCRIPTION: SEQ ID NO: 2862:
US-10-617-320-2862
```

```
Query Match 15.7%; Score 61; DB 6; Length 311;
Best Local Similarity 30.0%; Pred. No. 23;
Matches 18; Conservative 7; Mismatches 33; Indels 2; Gaps 1;
```

```
QY 10 TDSSEVITKANLIFANGSTQTAETFEKATSEAYAYADTLKKDNGEYTVADVADKGYT 69
Db 112 TDSIEIVNPDHYLFTIG--EGSSLKATMTVNSGRGVVPADENKKDNAPVGTGLAVDSIYT 169
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```
RESULT 13
US-10-640-833-4119
; Sequence 4119, Application US/10640833
; GENERAL INFORMATION:
; APPLICANT: Doucette-Stamm, Lynn
; APPLICANT: Bush, David
; APPLICANT: Zeng, Qiaodong
; APPLICANT: Opperman, Timothy
; APPLICANT: Houseweart, Chad Eric
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH03-15
; CURRENT APPLICATION NUMBER: US/10/640,833
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: US 09/583,110
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 4119
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-640-833-4119
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```
Query Match 15.7%; Score 61; DB 6; Length 311;
Best Local Similarity 30.0%; Pred. No. 23;
Matches 18; Conservative 7; Mismatches 33; Indels 2; Gaps 1;
```

```
QY 10 TDSSEVITKANLIFANGSTQTAETFEKATSEAYAYADTLKKDNGEYTVADVADKGYT 69
Db 112 TDSIEIVNPDHYLFTIG--EGSSLKATMTVNSGRGVVPADENKKDNAPVGTGLAVDSIYT 169
```

```
RESULT 14
US-10-299-636-32
; Sequence 32, Application US/10299636
```

```
; GENERAL INFORMATION:
; APPLICANT: Briles, David E
; APPLICANT: McDaniel, Larry S
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Crain, Marilyn J
; APPLICANT: Hollingshead, Susan
; APPLICANT: Tart, Rebecca
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF
; FILE REFERENCE: 57909/361
; CURRENT APPLICATION NUMBER: US/10/299,636
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 08/714,741
; PRIOR FILING DATE: 1996-09-16
; PRIOR APPLICATION NUMBER: 08/529,055
; PRIOR FILING DATE: 1995-09-15
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-299-636-32
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Query Match 15.6%; Score 60.5; DB 6; Length 130;
Best Local Similarity 50.0%; Pred. No. 9.3;
Matches 17; Conservative 2; Mismatches 14; Indels 1; Gaps 1;
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```
QY 22 LIFANGSTQTAETFEKATSEAYAYADTLKKD 55
Db 28 LVRAEESPOQVVE--KSSLEKRYEEAKAKADTAKKD 60
```

```
RESULT 15
US-10-221-131-95
; Sequence 95, Application US/10221131
; GENERAL INFORMATION:
; APPLICANT: FUKUSHIMA, NAOSHI
; APPLICANT: TSUCHIYA, MASAYUKI
; APPLICANT: OH-EDA, MASAYOSHI
; APPLICANT: UNO, SHINSUKE
; APPLICANT: KIKUCHI, YASUFUMI
; TITLE OF INVENTION: POLYPEPTIDE INDUCING APOPTOSIS
; FILE REFERENCE: 065678/0106
; CURRENT APPLICATION NUMBER: US/10/221,131
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: PCT/JP01/01912
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 09/523,095
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: JP 2000-115246
; PRIOR FILING DATE: 2000-04-17
; PRIOR APPLICATION NUMBER: JP 2000-321822
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 95
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: pscM1. MABL1-scfv
US-10-221-131-95
```

```
Query Match 15.6%; Score 60.5; DB 6; Length 271;
Best Local Similarity 27.3%; Pred. No. 23;
Matches 18; Conservative 12; Mismatches 23; Indels 13; Gaps 2;
```

```
QY 24 FANGSTQTAETFG---TFEKTSEAYAYADTLKKDN-----CEYTVADVADKGYTL 70
Db 76 INDGTYNEKFKGATLTSKSSSAAYWELSSLAESDSAVYCARGGYISYDDWGQQTTL 135
```

QY 71 NIKFAG 76
Db 136 TVSSGG 141

Search completed: September 3, 2003, 11:40:55
Job time : 11.6712 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:14:37 ; Search time 17.9589 Seconds
(without alignments)
406.975 Million cell updates/sec

Title: US-08-325-278B-1_COPY_5_80

Perfect score: 399

Sequence: 1 KEETPETDSEEEVTKA.....GEYTVADKGYTLNIKFPAG 76

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_76.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	389	100.0	455	2 A45063	immunoglobulin-bi
2	389	100.0	719	2 A42808	Ig light chain-bin
3	298.5	76.7	992	2 S54396	protein L precursor
4	144.5	37.1	74	2 A34483	Ig light chain-bin
5	85	21.9	1576	2 A80249	probable hemolysin
6	74	19.0	529	2 S62194	hypothetical prote
7	72	18.5	487	2 T10215	hypothetical prote
8	71	18.3	528	2 D83874	nickel ABC transpo
9	71	18.3	929	2 T51932	kinesin [imported]
10	69.5	17.9	292	2 AG1457	p45 related protei
11	69	17.7	123	2 T80601	hypothetical prote
12	69	17.7	341	2 S67641	hypothetical prote
13	67.5	17.4	1056	2 B82557	hypothetical prote
14	67.5	17.4	1876	2 E97944	zinc metalloprotei
15	67	17.2	571	2 A43507	streptolysin O pre
16	67	17.2	779	2 T05990	hypothetical prote
17	67	17.2	890	2 S22452	surface exclusion
18	67	17.2	891	2 G41662	130K surface exclu
19	66.5	17.1	255	2 F89769	hypothetical prote
20	66.5	17.1	642	2 H81868	probable virulence
21	66.5	17.1	840	2 S48975	hypothetical prote
22	66.5	17.1	843	2 S72375	surface exclusion
23	66	17.0	183	2 E83809	hypothetical prote
24	66	17.0	498	2 A86014	cell division memb
25	66	17.0	498	2 A91168	cell division memb
26	66	17.0	653	2 F70383	organic solvent to
27	65.5	16.8	313	2 T33391	hypothetical prote
28	64.5	16.6	273	2 T47891	hypothetical prote
29	64	16.5	298	2 T47760	hypothetical prote

30 64 16.5 299 2 T33390
31 64 16.5 316 2 G71600
32 64 16.5 478 2 AF1758
33 64 16.5 582 2 S42613
34 64 16.5 583 2 F69153
35 63.5 16.3 442 1 IEEC41
36 63.5 16.3 568 2 E97066
37 63.5 16.3 744 2 F95013
38 63 16.2 285 2 C89959
39 63 16.2 636 2 H70184
40 63 16.2 799 2 T02456
41 63 16.2 815 2 T46169
42 63 16.2 954 2 I51703
43 63 16.2 3063 2 S55505
44 63 16.2 3562 2 A47171
45 62.5 16.1 280 2 I55577

hypothetical prote
rifin PF81005w - m
chitinase and chit
membrane protein p
conserved hypothet
transposase insg f
membrane associate
pneumococcal surfa
conserved hypothet
methyl-accepting c
protein kinase hom
CD48-like protein
c-kit-related kina
fatty-acid synthas
chondroitin sulfat
Fc gamma (IgG) rec

ALIGNMENTS

RESULT 1

A45063

immunoglobulin-binding protein LG - Peptostreptococcus magnus

C:Species: Peptostreptococcus magnus

C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 15-Oct-1999

C:Accession: A45063

R:Kihlberg, B.M.; Sjoeborg, U.; Kastern, W.; Bjoerck, L.

J. Biol. Chem. 267, 25583-25588, 1992

A:Title: Protein LG: a hybrid molecule with unique immunoglobulin binding properties.

A:Reference number: A45063; MUID:93094283; PMID:1460053

A:Accession: A45063

A:Status: preliminary

A:Molecule type: mRNA; protein

A:Residues: 1-455 <KIH>

A:Cross-references: GB:S50809; NID:g261705; PIDN:AAA03280.1; PID:g261706

A:Note: sequence extracted from NCBI backbone (NCBIN:120302, NCBI:120303)

Query Match 100.0%; Score 389; DB 2; Length 455;
Best Local Similarity 100.0%; Pred. No. 2.e-31;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEETPETDSEEEVTKANLIFANGSTQTAFFKGTPEKATSEAYAYADTLKKONGEY 60
DB 26 KEETPETDSEEEVTKANLIFANGSTQTAFFKGTPEKATSEAYAYADTLKKONGEY 85
QY 61 DVADKGYTLNIKFPAG 76
DB 86 DVADKGYTLNIKFPAG 101

RESULT 2

A42808

Ig light chain-binding protein precursor - Peptostreptococcus magnus

N:Alternate names: protein L

C:Species: Peptostreptococcus magnus

C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999

C:Accession: A42808; A41493

R:Kastern, W.; Sjoeborg, U.; Bjoerck, L.

J. Biol. Chem. 267, 12820-12825, 1992

A:Title: Structure of peptostreptococcal protein L and identification of a repeated i

A:Reference number: A42808; MUID:92316971; PMID:1618782

A:Accession: A42808

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-719 <KAS>

A:Cross-references: GB:M86697

R:Kastern, W.; Holst, E.; Nielsen, E.; Sjoeborg, U.; Bjoerck, L.

Infect. Immun. 58, 1217-1222, 1990

A:Title: Protein L, a bacterial immunoglobulin-binding protein and possible virulence

A:Reference number: A41493; MUID:90215984; PMID:2108927

A:Accession: A41493

A:Status: preliminary

A: Accession: J13932
A: Status: preliminary; translated from GB/EMBL/DDBJ
A: Molecule type: DNA
A: Molecule type: DNA
A: Residues: 1-939 <WUO>
A: Cross-references: EMBL:U8521; PIDN:AAB47851.1
A: Experimental source: strain T213 mating population VI
C: Genetics:
A: Gene: NhkIN1

Query Match

Query Match 17.78; Score 69; DB 2; Length 123;

[illegible]

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:04:52 ; Search time 9.63014 Seconds
(without alignments)
371.130 Million cell updates/sec

Title: US-08-325-278B-1_COPY_5_80

Perfect score: 389

Sequence: 1 KEETPETPETDEEVTIKA.....GETYVDVADKGYTLNIKIFAG 76

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	73	18.8	634	1	GYRB_BORHE
2	69	17.7	123	1	DP30_CAEEL
3	68	17.5	574	1	TACY_STRCB
4	68	17.5	574	1	TACY_STRCB
5	67	17.2	571	1	TACY_STRPY
6	66.5	17.1	840	1	YHT1_YEAST
7	66	17.0	418	1	PGK_EUPCR
8	64.5	16.6	300	1	JAM1_MOUSE
9	64.5	16.6	446	1	GBAL_KLULA
10	64	16.5	544	1	CAR9_CANAL
11	63.5	16.3	442	1	INSG_ECOLI
12	63.5	16.3	1409	1	HAP1_HAEIN
13	63	16.2	815	1	C48D_ARATH
14	63	16.2	3562	1	PGCV_CHICK
15	62.5	16.1	190	1	HBPI_RHAP
16	62.5	16.1	269	1	LTSL_STRFI
17	62.5	16.1	374	1	FCG1_HUMAN
18	62	15.9	199	1	PVAA_STRP8
19	62	15.9	644	1	YHOB_DROME
20	61.5	15.8	404	1	HUTI_TREVO
21	61.5	15.8	516	1	YDDS_ECOLI
22	61.5	15.8	646	1	DHSA_CAEEL
23	61.5	15.8	1139	1	LI25_CAEEL
24	61	15.7	311	1	RPOA_STRPN
25	61	15.7	688	1	EFG_CLOPE
26	61	15.7	1120	1	STFR_ECOLI
27	61	15.7	1167	1	SCA2_STRPY
28	61	15.7	1181	1	SCA2_STRPY
29	60.5	15.6	514	1	YJJI_HAEIN
30	60.5	15.6	613	1	DNAK_LACSK
31	60.5	15.6	625	1	HTPG_BUCAP
32	60.5	15.6	1176	1	SLAP_BACSH
33	60	15.4	497	1	FTSY_ECOLI

RESULT 1

GYRB_BORHE 34 60 15.4 588 1 PPCK_THEAC
ID GYRB_BORHE STANDARD; PRT; 634 AA.
AC Q9ZFK1; 35 60 15.4 1655 1 OMPB_RICCN
36 60 15.4 2464 1 MAPB_MOUSE
37 60 15.4 2472 1 NCR2_MOUSE
38 60 15.4 3079 1 IRA2_YEAST
39 59.5 15.3 261 1 RNPH_THETN
40 59.5 15.3 344 1 CD2_RAT
41 59.5 15.3 398 1 RPC4_HUMAN
42 59.5 15.3 444 1 SLAP_LACAC
43 59.5 15.3 472 1 IFT2_HUMAN
44 59.5 15.3 480 1 TGN2_HUMAN
45 59.5 15.3 496 1 AGP2_MOUSE

ALIGNMENTS

OS Borrelia hermsii.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=140;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HS1;
RA Samuels D.S., Kimmel B.J., Huang W.M.;
RT "Mutations in Borrelia hermsii gyrB confer resistance to coumermycin
Al.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: DNA GYRASE NEGATIVELY SUPERCOILS CLOSED CIRCULAR DOUBLE-
CC STRANDED DNA IN AN ATP-DEPENDENT MANNER AND ALSO CATALYZES THE
CC INTERCONVERSION OF OTHER TOPOLOGICAL ISOMERS OF DOUBLE-STRANDED
CC DNA RINGS, INCLUDING CATENANES AND KNOTTED RINGS.
CC -!- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC -!- SUBUNIT: MADE UP OF TWO CHAINS. THE A CHAIN IS RESPONSIBLE FOR DNA
CC BREAKAGE AND REJOINING; THE B CHAIN CATALYZES ATP HYDROLYSIS. THE
CC ENZYME FORMS AN A2B2 TETRAMER.
CC -!- SIMILARITY: Belongs to the type II topoisomerase family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF098862; AAC72846.1; -
CC HSSP; P06982; IAJ6.
CC InterPro; IPR003594; ATPbind_ATPase.
CC InterPro; IPR002288; DNA_gyraseB_C.
CC InterPro; IPR000565; DNA_gyrb.
CC InterPro; IPR001241; DNA_topoisomII.
CC InterPro; IPR006171; Toprim_dom.
CC Pfam; PF00204; DNA_gyraseB; 1.
CC Pfam; PF00986; DNA_gyraseB_C; 1.
CC Pfam; PF02518; HATPase_C; 1.
CC Pfam; PF01751; Toprim; 1.
CC PRINTS; PR00418; TP12FAMILY.
CC ProDom; PD149633; DNA_gyraseB_C; 1.
CC SMART; SM00387; HATPase_C; 1.
CC SMART; SM00433; TOP2c; 1.
CC TIGRFAMs; TIGR01059; gyrB; 1.
CC PROSITE; PS00177; TOPOISOMERASE-II; 1.
CC Topoisomerase; Isomerase; ATP-binding.
KW

O9hlv2 thermoplas
O9kka3 r outer mem
P14873 mus musculu
O9wu42 mus musculu
P19158 saccharomyc
Q8rc30 thermoanaer
P08921 rattus norv
P05423 homo sapien
P35829 lactobacill
P09913 homo sapien
O43493 homo sapien
O35608 mus musculu

```

Db          74 LDSTVVPILQGLGAKDRPENPIE 99
::          |  ||  |  ::
RESULT 3
TACY_STRCB
ID TACY_STRCB STANDARD; PRT; 574 AA.
AC Q53957;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Streptolysin O precursor (Thiol-activated cytolysin).
GN SLO.
OS Streptococcus canis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1329;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95102113; PubMed=7803818;
RA Okumura K., Hara A., Tanaka T., Nichiguchi I., Minamide W.,
RA Igarashi H., Yutsudo T.;
RT "Cloning and sequencing the streptolysin O genes of group C and group
RT G streptococci.";
RL DNA Seq. 4:325-328(1994).
CC -1- FUNCTION: SULHYDRYL-ACTIVATED TOXIN. IS ABLE TO LYSE CHOLESTEROL
CC CONTAINING MEMBRANES. CAN BE REVERSIBLY INACTIVATED BY OXIDATION.
CC CHOLESTEROL IS THE RECEPTOR FOR THE BINDING OF THESE TOXINS TO
CC EUKARYOTIC CELL MEMBRANES.
CC -1- SIMILARITY: BELONGS TO THE THIOL-ACTIVATED CYTOLYSIN FAMILY.
-----
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CC or send an email to license@isb-sib.ch).
-----
CC EMBL; D16825; BAA04105.1; -
CC HSP; P19995; LPFO.
DR InterPro: IPR001869; Thiol_cytolysin.
DR Pfam: PF01289; Thiol_cytolysin; 1.
DR PRINTS; PR01400; TACYPOLYSIN.
DR ProDom; PD007082; Thiol_cytolysin; 1.
DR PROSITE; PS00481; THIOL_CYTOLYSINS; 1.
KW Toxin; Hemolysis; Cytolysis; Signal.
FT SIGNAL 1 36
FT CHAIN 37 574
FT ACT_SITE 533 533
FT ACT_SITE 533 533
SQ SEQUENCE 574 AA; 63911 MW; C84D2036908329AF CRC64;
Query Match 17.5%; Score 68; DB 1; Length 574;
Best Local Similarity 30.1%; Pred. No. 17;
Matches 22; Conservative 13; Mismatches 32; Indels 6; Gaps 2;
QY 4 TPTPTDSEEVTIKA-----NLIFANGSTOAEFGTFEKATSPAYADTLKKDNGE 58
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 49 TNEQPKPESELTTERKAGOMDDMLNSNDWIKLAPKEMPLESAEKEKKSEDN-KKSEED 107
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 59 YTFVDVADKGYTLN 71
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 108 HTEEINDKIYSLN 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
RESULT 4
TACY_STRCB
ID TACY_STRCB STANDARD; PRT; 574 AA.
AC Q54114;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Streptolysin O precursor (Thiol-activated cytolysin).

```



```

QY 59 YTVDAVKGYTLN 71
DE : : | | | |
DB 105 HTEINDKIYSLN 117

RESULT 6
YHTL_YEAST STANDARD; PRT; 840 AA.
AC P38835;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Hypothetical 95.1 kDa protein in ACT5-YCK1 intergenic region.
GN YHR131C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / AB972;
RX MEDLINE=94378003; PubMed=8091229;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
RA Du Z., Favell A., Fulton L., Gattung S., Geisel C., Kirsten J.,
RA Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
RA Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
RA Nham M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
RA Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,
RA Vaudin M.;
RT *Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
RT VIII.
RL Science 265:2077-2082(1994).
CC -1- SIMILARITY: TO YEAST YNL144C.
CC -----
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CC -----
CC EMBL; U10398; AAB68414.1; -.
CC HSSP; S48975; S48975.
CC PIR; S48975; S48975.
CC HSSP; Q00963; IDRO.
CC SGD; S0001173; YHR131C.
CC InterPro: IPR001849; PH.
CC Pfam; PF00169; PH; 1.
CC SMART; SM00233; PH; 1.
CC KX Hypothetical protein.
FT DOMAIN 312 325 POLY-ARG.
FT DOMAIN 788 840 ASP/GLU-RICH (HIGHLY ACIDIC).
SQ SEQUENCE 840 AA; 95058 MW; 3A86717D3332A0DF CRC64;

Query Match 17.1%; Score 66.5; DB 1; Length 840;
Best Local Similarity 29.9%; Pred. No. 37;
Matches 23; Conservative 13; Mismatches 28; Indels 13; Gaps 4;

QY 9 ETDSEEVTKANLIFANGSTQTAEFK-----GTFEKATSEAYAYADTLKNDGEY 59
DE : : | | | | : : | | | | : : | | | |
DB 176 ETKSEKEDRIHSDLVHRSQSLHRLHRLTLPTRSAEFKKAQERISY--RVKDRSRV 233

QY 60 TVDVA-DKGYTL-NIKF 74
DE : : | | | | : : | | | | : : | | | |
DB 234 LTDEALYKSFLLQNAKF 250

RESULT 7
PGK_EUPCR
ID PGK_EUPCR STANDARD; PRT; 418 AA.
AC Q02608;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)

QY 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phosphoglycerate kinase (EC 2.7.2.3).
OS PGK.
OC Eukaryota; Alveolata; Ciliophora; Spirotrichea; Hypotrichia;
OC Euplotida; Euplotidae; Moneuplotes.
OX NCBI_TaxID=5936;
RN [1]
RP SEQUENCE FROM N.A.
RA Pearlman R.E.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + 3-phospho-D-glycerate -> ADP + 3-
CC phospho-D-glyceroyl phosphate.
CC -1- PATHWAY: Second phase of glycolysis; second step.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to the phosphoglycerate kinase family.
CC -----
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CC -----
CC EMBL; U97355; AAB58162.1; -.
CC HSSP; P00560; IOPG.
CC InterPro: IPR001576; PGK.
CC Pfam; PF00162; PGK; 1.
CC PRINTS; PR00477; PGLYCKINASE.
CC PROSITE; PS00111; PGLYCERATE_KINASE; 1.
KW Transferase; Kinase; Glycolysis.
SQ SEQUENCE 418 AA; 45601 MW; D1FEC7D9F850F29D CRC64;

Query Match 17.0%; Score 66; DB 1; Length 418;
Best Local Similarity 39.3%; Pred. No. 19;
Matches 24; Conservative 7; Mismatches 26; Indels 4; Gaps 3;

QY 12 SEEVTKANLIFANGSTQTAEFKGTFERKATSEAYAYADTLKNDGEYTVDAVKGYTLN 71
DE : : | | | | : : | | | | : : | | | |
DB 322 SFDEIVRRNTLFWNGPSGVFEWK-NFAKG-SHAMLQAVTESTKNG--TVSVCGGGDTLN 377

QY 72 I 72
DE :
DB 378 L 378

RESULT 8
JAML_MOUSE STANDARD; PRT; 300 AA.
ID JAML_MOUSE
AC Q88752;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Junctional adhesion molecule 1 precursor (JAM).
GN F11R OR JAM1 OR JCAM1 OR JCAM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98327120; PubMed=9660867;
RA Martin-Padura I., Lostaglio S., Schneemann M., Williams L., Romano M.,
RA Fruscella P., Panzeri C., Stoppacciaro A., Ruco L., Villa A.,
RA Simmons D., Dejana E.;
RT "Junctional adhesion molecule, a novel member of the immunoglobulin
RT superfamily that distributes at intercellular junctions and modulates
RT monocyte transmigration."
RL J. Cell Biol. 142:117-127(1998).
RN [2]
RP INTERACTION WITH PAR3.
RX PubMed=11447115;

```



```
CAR9_CANAL
ID CAR9_CANAL STANDARD; PRT; 544 AA.
AC Q42779;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Candidapepsin 9 precursor (EC 3.4.23.24) (Aspartate protease 9)
DE (ACP 9) (Secreted aspartic protease 9).
GN SAP9.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C74;
RX MEDLINE=99018822; PubMed=9802014;
RA Monod M., Hube B., Hess D., Sanglard D.;
RT "Differential regulation of SAP8 and SAP9, which encode two new
RT members of the secreted aspartic proteinase family in Candida
RT albicans.";
RL Microbiology 144:2731-2737(1998).
CC -I- CATALYTIC ACTIVITY: Preferential cleavage at the carboxyl of
CC hydrophobic amino acids, but fails to cleave 15-Leu-1-Tyr-16, 16-
CC Tyr-1-Leu-17 and 24-Phe-1-Phe-25 of insulin B chain. Activates
CC trypsinogen, and degrades keratin.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
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CC EMBL; AF043331; AAC69996.1; -.
CC HSPSP; P28871; IEAG.
CC MEROPS; A01.0PW; -.
CC InterPro; IPR001969; Aspprotease_site.
CC InterPro; IPR001461; AspproteaseA1.
CC Pfam; PF00026; asp; 1.
CC PROSITE; PS00141; ASP_PROTEASE; 1.
KW Hydrolase; Aspartyl protease; Glycoprotein; Zymogen; Signal;
KW Multigene family.
FT SIGNAL 1 17 POTENTIAL.
FT PROPEP 18 ? POTENTIAL.
FT CHAIN 2 544 CANDIDAPEPSIN 9.
FT ACT_SITE 167 167 BY SIMILARITY.
FT ACT_SITE 371 371 BY SIMILARITY.
FT DISULFID 406 441 BY SIMILARITY.
FT CARBOHYD 212 212 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 240 240 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 252 252 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 422 422 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 499 499 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 544 AA; 58624 MW; E6D755A46040A486 CRC64;

Query Match 16.5%; Score 64; DB 1; Length 544;
Best Local Similarity 27.6%; Pred. No. 41;
Matches 21; Conservative 18; Mismatches 19; Indels 18; Gaps 4;

QY 18 IKANLIFANGSTQTAFFKGT-----FEKATSEAYAYADTL-----KKDNGEYT----- 60
Db 347 LKIDVSSSGST-TNLSGTTGWLDTGSLTVSVFSDTLQSLGKALNGQYSNVGAYVYN 405
QY 61 VDVADEGYTLNFKFG 76
Db 406 CNLADSSRTVDIEFGG 421

CAR9_CANAL
ID INSG_ECOLI STANDARD; PRT; 442 AA.
AC P03835;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Transposase insg for insertion sequence element IS4.
DE INSG OR B4278.
GN Escherichia coli.
OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=82012962; PubMed=6268937;
RA Klaer R., Kuhn S., Tillmann E., Fritz H.-J., Starlinger P.;
RT "The sequence of IS4.";
RL Mol. Gen. Genet. 181:169-175(1981).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=95334362; PubMed=7610040;
RA Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
RA Blattner F.R.;
RT "Analysis of the Escherichia coli genome VI: DNA sequence of the
RT region from 92.8 through 100 minutes.";
RL Nucleic Acids Res. 23:2105-2119(1995).
CC -I- FUNCTION: INVOLVED IN THE TRANSPOSITION OF THE INSERTION
CC SEQUENCE IS4.
CC -I- SIMILARITY: BELONGS TO THE TRANSPOSASE FAMILY 11.
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CC EMBL; J01733; -. NOT_ANNOTATED_CDS.
CC EMBL; U14003; AAA97174.1; -.
CC EMBL; AE000498; AAC77234.1; -.
CC FIR; A04463; IIEC41.
CC EcoGene; EG40007; insG.
CC InterPro; IPR002559; Transposase_11.
CC Pfam; PF01609; Transposase_11; 1.
KW Transposase element; Transposition; DNA-binding; DNA recombination;
KW Complete proteome.
SQ SEQUENCE 442 AA; 50385 MW; 0B9CAAA0FFAC724E CRC64;

Query Match 16.3%; Score 63.5; DB 1; Length 442;
Best Local Similarity 25.6%; Pred. No. 37;
Matches 20; Conservative 14; Mismatches 27; Indels 17; Gaps 3;

QY 4 TPETPTDSE-----EVTIKANLIFANGSTQTAFFKGTSEAYAYAD 50
Db 139 TPTDTPDAAFPQTHAGNPALYPQVKVCMQELTSHLLTAAAF-GTMKNSENE---LAE 194
QY 51 TLKKDNGEYTVDAKGY 68
Db 195 QLIEQTGDNLTLMKGY 212

RESULT 12
ID HAP1_HAEIN STANDARD; PRT; 1409 AA.
AC P44596;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adhesion and penetration protein precursor (EC 3.4.21.-).
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DR InterPro: IPR003338; ATPaseVAT_N.
DR Pfam: PF00004; AAA; 2.
DR Pfam: PF02359; cdc48_N; 1.
DR SMART: SM00382; AAA; 2.
DR TIGRPFAMs: TIGR01243; CDC48; 1.
DR PROSITE: PS00674; AAA; 2.
KW Hypothetical protein; Cell division; Cell cycle; Transport;
KW Protein transport; Nuclear protein; ATP-binding; Repeat;
KW Multigene family.
FT NP_BIND 249 256 ATP (POTENTIAL).
FT NP_BIND 522 529 ATP (POTENTIAL).
SQ SEQUENCE 815 AA; 90340 MW; 8F2817396748B6CC CRC64;

Query Match 16.2%; Score 63; DB 1; Length 815;
Best Local Similarity 28.6%; Pred. No. 80;
Matches 22; Conservative 12; Mismatches 27; Indels 16; Gaps 3;

QY 1 KEETPTPTDSEEVTKA-----NLIFANGSTQAEFGKTFERATSEAYAYADTLKKD 55
DB 717 RAESPAMEDEETAEIKAGHFESMKYARRSVSDAIR-----KYQAFQOTLQOS 768

QY 56 NG---EYTVDVADKGYT 69
DB 769 RGFGEFRFPDAPTGT 785

RESULT 14
PGCV_CHICK STANDARD; PRT; 3562 AA.
AC Q90953; Q90945;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Versican core protein precursor (Large fibroblast proteoglycan)
DE (Chondroitin sulfate proteoglycan core protein 2) (PG-M).
GN CP5G2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxId=9031;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS V0 AND V1).
RC STRAIN=White leghorn; TISSUE=Limb bud;
RX MEDLINE=93300846; PubMed=8314802;
RA Shinomura T., Nishida Y., Ito K., Kimata K.;
RT "cDNA cloning of PG-M, a large chondroitin sulfate proteoglycan
RT expressed during chondrogenesis in chick limb buds. Alternative
RT spliced multi-forms of PG-M and their relationships to versican.";
RL J. Biol. Chem. 268:14461-14469(1993).
CC -!- FUNCTION: May play a role in intercellular signaling and in
CC connecting cells with the extracellular matrix. May take part in
CC the regulation of cell motility, growth and differentiation. Binds
CC hyaluronic acid.
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=V0;
CC IsoId=Q90953-1; Sequence=Displayed;
CC Name=V1;
CC IsoId=Q90953-2; Sequence=VSP_003093;
CC -!- TISSUE SPECIFICITY: Prechondrogenic condensation area of
CC developing limb buds.
CC -!- DEVELOPMENTAL STAGE: Disappears after the cartilage development
CC (By similarity).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 link domains.
CC -!- SIMILARITY: Contains 2 EGF-like domains.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.
CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.
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CC -----
CC EMBL; X60226; CAA42787.1; -.
CC EMBL; D13542; BAA02742.1; -.
CC PIR; A47171; A47171.
CC HSSP; P00740; 1EDM.
CC InterPro: IPR000152; ASX_hydroxyl.
CC InterPro: IPR000742; EGF_2.
CC InterPro: IPR001881; EGF_Ca.
CC InterPro: IPR006209; EGF_like.
CC InterPro: IPR007110; Ig-like.
CC InterPro: IPR003599; Ig.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR001304; Lectin_C.
CC InterPro: IPR000538; Link.
CC InterPro: IPR000436; Sushi_SCR_CCP.
CC Pfam: PF00008; EGF; 2.
CC Pfam: PF00047; ig; 1.
CC Pfam: PF00059; lectin_c; 1.
CC Pfam: PF00084; sushi; 1.
CC Pfam: PF00193; Xlink; 2.
CC PRINTS; PR01265; LINKMODULE.
CC ProDom; PD000918; Link; 2.
CC SMART; SM00032; CCP; 1.
CC SMART; SM00034; CLECT; 1.
CC SMART; SM00179; EGF_CA; 1.
CC SMART; SM00409; Ig; 1.
CC SMART; SM00445; LINK; 2.
CC PROSITE; PS00010; ASX_HYDROXYL; 1.
CC PROSITE; PS00615; C-TYPE LECTIN_1; 1.
CC PROSITE; PS00041; C-TYPE LECTIN_2; 1.
CC PROSITE; PS00022; EGF_1; 2.
CC PROSITE; PS01186; EGF_2; 1.
CC PROSITE; PS01187; EGF_CA; 1.
CC PROSITE; PS00835; IG_LIKE; 1.
CC PROSITE; PS01241; LINK; 2.
KW Glycoprotein; Proteoglycan; Lectin; Extracellular matrix; Sushi;
KW Signal; Repeat; EGF-like domain; Calcium; Immunoglobulin domain;
KW Hyaluronic acid; Alternative splicing.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 3562 VERSICAN CORE PROTEIN.
FT DOMAIN 27 143 IG-LIKE V-TYPE.
FT DOMAIN 166 243 LINK 1.
FT DOMAIN 264 345 LINK 2.
FT DOMAIN 3234 3290 EGF-LIKE 1.
FT DOMAIN 3292 3328 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 3341 3455 C-TYPE LECTIN.
FT DOMAIN 3460 3518 SUSHI.
FT DISULFID 44 129 BY SIMILARITY.
FT DISULFID 171 242 BY SIMILARITY.
FT DISULFID 195 216 BY SIMILARITY.
FT DISULFID 269 344 BY SIMILARITY.
FT DISULFID 293 314 BY SIMILARITY.
FT DISULFID 3258 3269 BY SIMILARITY.
FT DISULFID 3263 3278 BY SIMILARITY.
FT DISULFID 3280 3289 BY SIMILARITY.
FT DISULFID 3296 3307 BY SIMILARITY.
FT DISULFID 3301 3316 BY SIMILARITY.
FT DISULFID 3318 3327 BY SIMILARITY.
FT DISULFID 3334 3345 BY SIMILARITY.
FT DISULFID 3362 3454 BY SIMILARITY.
FT DISULFID 3430 3446 BY SIMILARITY.
FT DISULFID 3461 3504 BY SIMILARITY.
FT DISULFID 3490 3517 BY SIMILARITY.
FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 529 529 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 709 709 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 948 948 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1409 1409 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1479 1479 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1523 1523 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1530 1530 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1625 1625 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1751 1751 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1988 1988 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2088 2088 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2089 2089 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2507 2507 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2642 2642 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2679 2679 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2748 2748 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2762 2762 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 3069 3069 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 3194 3194 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 3232 3232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 3545 3545 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 485 1411 Missing (in isoform V1).
FT SQ SEQUENCE 3562 AA; 388078 MW; 9BC565E88C1602D2 CRC64;
Query Match 16.2%; Score 63; DB 1; Length 3562;
Best Local Similarity 28.6%; Pred. No. 3.9e+02;
Matches 26; Conservative 13; Mismatches 30; Indels 22; Gaps 5;
QY 6 ETPEPDSREVTIKANLIFANGSTQTAEFKGT--FEKAT-----SEAYAYADTLKKDNG 57
DB 863 ERAETESDEV-VSADFDTGKTGVTFVHTSSLDLEKFTLSKIPEDSSATVKFSFSSSG 921
QY 58 -----EYTVDVADK--GYTLNIRKA 75
DB 922 TVLPATVATVLEVTDEHDETSGYVNLMTFS 952
RESULT 15
HBPL_RHIAP STANDARD; PRT; 190 AA.
AC Q77420;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Female-specific histamine-binding protein 1 precursor (FS-HBPL).
OS Rhipicephalus appendiculatus (Brown ear tick).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Rhipicephalus.
OX NCBI_TaxID=34631;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary gland;
RX MEDLINE=99288454; PubMed=10360182;
RA Paesen G.C., Adams P.L., Harlos K., Nuttall P.A., Stuart D.I.;
RT "Tick histamine-binding proteins: isolation, cloning, and three-dimensional structure."
RL Mol. Cell 3:661-671(1999).
CC -!- FUNCTION: BINDS HISTAMINE WITH A HIGH-AFFINITY. THE ABILITY TO
CC OUTCOMPETE HISTAMINE RECEPTORS INDICATES THAT ITS FUNCTION IS TO
CC SUPPRESS INFLAMMATION DURING BLOOD FEEDING.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -----
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CC -----
DR EMBL: U96080; AAC63106.1; -
DR HSSP: O77421; 1QFT.
DR InterPro: IPR002970; His_binding.

DR Pfam: PF02098; His_binding; 1.
DR ProDom: PD152455; His_binding; 1.
KW SIGNAL. 1 18 POTENTIAL.
FT CHAIN 19 190 FEMALE-SPECIFIC HISTAMINE-BINDING PROTEIN
FT DISULFID 66 187 BY SIMILARITY.
FT DISULFID 137 166 BY SIMILARITY.
SQ SEQUENCE 190 AA; 21370 MW; 855BE151A90053B1 CRC64;
Query Match 16.1%; Score 62.5; DB 1; Length 190;
Best Local Similarity 31.6%; Pred. No. 19;
Matches 18; Conservative 13; Mismatches 19; Indels 7; Gaps 3;
QY 12 SEEEVTKANLIFANGSTQTAEFKGTFEKAT-SEAYAY----ADTLKKDNGEYTVDV 63
DB 75 NEDEKNVEAFWFMNNAIV--YQHTFEKATPKMYGKKNNAITVQTEGGQVLTDV 129
Search completed: September 3, 2003, 11:20:02
Job time : 11.6301 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:04:17 ; Search time 48.3288 Seconds
(without alignments)
236.470 Million cell updates/sec

Title: US-08-325-278b-1_COPY_81_152

Perfect score: 371

Sequence: 1 KEKTEPKKEVTIKANLIY.....GEYTVDVADKGYTLNPKFAG 72

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_19Jun03.*
1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	371	100.0	72	21	Peptostreptococcus
2	371	100.0	305	14	Immunoglobulin lig
3	371	100.0	367	21	Expression vector
4	371	100.0	434	14	Sequence encoding
5	371	100.0	467	22	Amino acid sequenc
6	352	94.9	72	21	Peptostreptococcus
7	322	86.8	72	21	Peptostreptococcus
8	314	84.6	76	21	Peptostreptococcus
9	308	83.0	75	21	Peptostreptococcus

10	308	83.0	291	14	AA42204
11	308	83.0	1027	14	AA42203
12	308	83.0	1027	14	AA42203
13	299	80.6	182	18	AAW32479
14	299	80.6	182	20	AAW06907
15	292.5	78.8	71	21	AA82542
16	291	78.4	178	18	AAW32486
17	291	78.4	178	20	AAW06913
18	291	78.4	198	18	AAW32481
19	291	78.4	198	20	AAW06910
20	291	78.4	342	18	AAW32482
21	291	78.4	342	20	AAW06909
22	291	78.4	482	20	AAW06915
23	291	78.4	495	18	AAW32480
24	291	78.4	495	20	AAW06908
25	289.5	78.0	71	21	AA82541
26	286	77.1	82	21	AA82536
27	283	76.3	74	21	AA82543
28	279	75.2	82	21	AA82545
29	279	75.2	82	21	AA82548
30	277	74.7	82	21	AA82546
31	273	73.6	82	21	AA82547
32	90.5	24.4	395	22	ABG11860
33	89.5	24.1	463	22	ABG23272
34	73	19.7	588	22	AB43638
35	69.5	18.7	279	23	ABG77964
36	68.5	18.5	261	20	AA33183
37	68.5	18.5	344	17	AA91439
38	68.5	18.5	374	17	AAW00859
39	68.5	18.5	374	19	AAW0448
40	68.5	18.5	374	19	AAW97833
41	68.5	18.5	374	19	AAW97833
42	68.5	18.5	374	21	AA96226
43	68.5	18.5	399	21	AA43683
44	68.5	18.5	399	22	AAW75008
45	67.5	18.2	344	13	AA22549

ALIGNMENTS

RESULT 1

AA82538
ID AA82538 standard; Protein; 72 AA.

XX AA82538;

XX AC

XX DT

XX 20-JUL-2000 (first entry)

XX DE

XX Peptostreptococcus strain 312 protein L domain B2 protein sequence.

XX KW

XX Immunoglobulin light chain binding protein; PpL; protein L;

XX KW Peptostreptococcus; human immunoglobulin kappa chain;

XX KW immunoaffinity chromatography.

XX OS

XX Peptostreptococcus sp.

XX PN

XX WO200015803-A1.

XX PD

XX 23-MAR-2000.

XX PF

XX 14-SEP-1999; 99WO-GB03048.

XX PR

XX 14-SEP-1998; 98GB-0019998.

XX PR

XX 26-APR-1999; 99GB-0009578.

XX (ACTI-) ACTINOVA LTD.

XX PI

XX Gore MG, Beckingham JA, Roberts SE;

XX WPI; 2000-271441/23.

XX DR

XX N-PSDB; AAA08427.

XX XX

PT New modified immunoglobulin light chain binding protein, useful in
PT immunoaffinity chromatography, has a dissociation constant of 400 nM or
PT more at pH8 with respect to human immunoglobulin kappa-chain -
XX
XX
PS Disclosure; Page 42; 56pp; English.
XX
XX The present invention describes an immunoglobulin (Ig) light chain
CC binding protein (PI) which has been modified by one or more amino acid
CC substitutions such that the dissociation constant (Kd) of the protein
CC with respect to human Ig kappa-chain is 400 nM or more at pH8. PI is
CC useful in immunoaffinity chromatography. The present sequence is a
CC Peptostreptococcus protein L Ig light chain binding domain, which is
CC given in the disclosure of the present invention.
XX
XX Sequence 72 AA;
SQ
Query Match 100.0%; Score 371; DB 21; Length 72;
Best Local Similarity 100.0%; Pred. No. 2.4e-37;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KETPEEPKEEVTIKANLIYADGKTQTAEFKGTFFETAAYRYADALKKNGEYTDVA 60
Db 1 KETPEEPKEEVTIKANLIYADGKTQTAEFKGTFFETAAYRYADALKKNGEYTDVA 60
QY 61 DKGYTLNIRKFA 72
Db 61 DKGYTLNIRKFA 72
RESULT 2
AAR42993
ID AAR42993 standard; Protein; 305 AA.
AC
AC AAR42993;
XX
XX 25-MAR-2003 (updated)
DT 16-MAY-1994 (first entry)
XX
XX Immunoglobulin light chain binding protein (Protein L).
DE
XX Immunoglobulin; light chain; binding; identification; purification;
KW separation.
KW
XX
XX E. coli LE392/PHDL, DSM 7054.
OS
XX
XX Key Location/Qualifiers
FH Domain 5..305
FT /label= B1 immunoglobulin light chain binding
FT domain.
FT Domain 81..305
FT /label= B2 immunoglobulin light chain binding
FT domain.
FT Domain 153..305
FT /label= B3 immunoglobulin light chain binding
FT domain.
FT Domain 225..305
FT /label= B4 immunoglobulin light chain binding
FT domain.
FT Domain 297..305
FT /label= B5 immunoglobulin light chain binding
FT domain.
XX
XX WO9322342-A1.
PN
XX
XX 11-NOV-1993.
PD
XX
XX 28-APR-1993; 93WO-SR00375.
PF
XX
XX 28-APR-1992; 92SE-0001331.
PR
XX (HIGH-) HIGHTECH RECEPTOR AB.
PA
XX Bjoerck L, Sjoerbring U;
PI

XX
DR WPI; 1993-368722/46.
DR N-PSDB; AAQ50452.
XX
XX New protein L binding light chains of all immunoglobulin classes
PT - for binding purifying and identifying immunoglobulin, also
PT related DNA, vectors and host cells
XX
XX Claim 1; Page 36; 71pp; English.
XX
CC The protein (Protein L) is capable of binding to immunoglobulin G
CC light chains. It is useful for binding, separating (purifying) and
CC identifying immunoglobulin and for removing immunoglobulin molecules
CC from serum. Hybrid proteins of the L protein can bind all human
CC immunoglobulin classes and many immunoglobulins from other species.
CC They are highly soluble and retain their binding activity at high
CC temperatures over a pH range of 3-10. They can be immobilised
CC without loss of activity.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 305 AA;
SQ
Query Match 100.0%; Score 371; DB 14; Length 305;
Best Local Similarity 100.0%; Pred. No. 1.6e-36;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KETPEEPKEEVTIKANLIYADGKTQTAEFKGTFFETAAYRYADALKKNGEYTDVA 60
Db 81 KETPEEPKEEVTIKANLIYADGKTQTAEFKGTFFETAAYRYADALKKNGEYTDVA 140
QY 61 DKGYTLNIRKFA 72
Db 141 DKGYTLNIRKFA 152
RESULT 3
AAB10432
ID AAB10432 standard; Protein; 367 AA.
XX
XX AAB10432;
AC
XX
XX 01-DEC-2000 (first entry)
DT
XX
XX Expression vector pSEX11L4 protein G.
DE
XX
XX Expression vector; antibody binding protein; monoclonal antibody; Neo-R;
KW B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.
XX
XX Synthetic.
XX
XX DE19900635-A1.
PN
XX
XX 13-JUL-2000.
PD
XX
XX 11-JAN-1999; 99DE-1000635.
PF
XX
XX 11-JAN-1999; 99DE-1000635.
PR
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA
XX Breitling F, Poustka A, Moldenhauer G;
PI
XX
XX WPI: 2000-499832/45.
DR N-PSDB; AAA71428.
XX
XX Selecting monoclonal antibodies, by expressing them on the surface of
PT hybridomas attached to antibody-binding protein, then reaction with
PT antibody library
XX
XX Claim 16; Fig 1; 22pp; German.
PS
XX
XX This invention describes a novel method for the selection of monoclonal
CC antibodies (Mab) which comprises (i) fusing B lymphocytes with myeloma

CC cells to produce antibody-producing hybridomas such that the antibodies
 CC are presented at the surface of the hybridomas by an antibody-binding
 CC protein (I); and (ii) binding the antibody to antigens (Ag). The
 CC invention also describes antibody-binding proteins (I) that comprise a
 CC combination of the signal peptide of a murine immunoglobulin (Ig) kappa
 CC chain or a murine MHC (major histocompatibility complex) class I k(k)
 CC molecule; an antibody-binding site of proteins A, G, I or IG, and the
 CC transmembrane domain of PDGFR (platelet-derived growth factor receptor)
 CC or CD52. The method is used to select MAB with specificity for particular
 CC antigens. MAB can be selected without separate culture of hybridomas,
 CC and selection can be made against many antigens in a library, optionally
 CC on the basis of strength of affinity for a particular antigen. Complex
 CC mixtures of hybridomas can be used for selection, reducing the time and
 CC cost involved in MAB selection. This sequence represents the protein G
 CC contained in the expression vector pSEX114 which contains the protein G,
 CC Neo-R and the bla protein described in the method of the invention.

XX SQ Sequence 367 AA;

Query Match 100.0%; Score 371; DB 21; Length 367;
 Best Local Similarity 100.0%; Pred. NO. 2.1e-36;
 Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEKTPPEKPEEVTKANLIYADGKTQTAEFGTFEEATAEAYRYADALKKDNGEYTVDA 60
 DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 25 KEKTPPEKPEEVTKANLIYADGKTQTAEFGTFEEATAEAYRYADALKKDNGEYTVDA 84
 QY 61 DKGYTLNIRFAG 72
 DB ||||||||||||
 85 DKGYTLNIRFAG 96

RESULT 4
 AAR42994
 ID AAR42994 standard; Protein; 434 AA.

XX AC AAR42994;

XX DT 25-MAR-2003 (updated)
 XX DT 16-MAY-1994 (first entry)

XX Sequence encoding immunoglobulin light chain binding protein.

KW Immunoglobulin; light chain; binding; identification; purification;
 KW separation; ss.

XX OS E. coli L392/pHDLG, DSM 7055.

XX FH Key Location/Qualifiers
 FT Domain 5..305
 FT /label= B1 immunoglobulin light chain binding
 FT domain.
 FT Domain 81..305
 FT /label= B2 immunoglobulin light chain binding
 FT domain.
 FT Domain 153..305
 FT /label= B3 immunoglobulin light chain binding
 FT domain.
 FT Domain 225..305
 FT /label= B4 immunoglobulin light chain binding
 FT domain.
 FT Domain 297..305
 FT /label= B5 immunoglobulin light chain binding
 FT domain.
 FT Domain 309..434
 FT /label= C1 immunoglobulin heavy chain binding
 FT domain.
 FT Domain 364..434
 FT /label= D intermediate immunoglobulin heavy
 FT chain binding domain.
 FT Domain 379..434
 FT /label= C2 immunoglobulin heavy chain binding
 FT domain.

XX WO9322342-A1.
 PN 11-NOV-1993.
 PD 28-APR-1993; 93WO-SE00375.
 XX 28-APR-1992; 92SE-0001331.
 PR (HIGH-) HIGHTECH RECEPTOR AB.
 XX Bjoerck L, Sjoerbring U;
 PI WPI; 1993-368722/46.
 XX P-PSDB; AAR42994.
 DR New protein L binding light chains of all immunoglobulin classes
 XX - for binding purifying and identifying immunoglobulin, also
 PT related DNA, vectors and host cells
 PS Claim 6; Page 39-40; 71pp; English.
 XX Protein L (AAR42993) is capable of binding to immunoglobulin G light
 CC chains. It is useful for binding, separating (purifying) and
 CC identifying immunoglobulin and for removing immunoglobulin molecules
 CC from serum. This is the coding sequence of one hybrid protein of
 CC the L protein. The hybrid proteins can bind all human
 CC immunoglobulin classes and many immunoglobulins from other species.
 CC They are highly soluble and retain their binding activity at high
 CC temperatures over a pH range of 3-10. They can be immobilised
 CC without loss of activity.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX SQ Sequence 434 AA;

Query Match 100.0%; Score 371; DB 14; Length 434;
 Best Local Similarity 100.0%; Pred. NO. 2.6e-36;
 Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEKTPPEKPEEVTKANLIYADGKTQTAEFGTFEEATAEAYRYADALKKDNGEYTVDA 60
 DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 81 KEKTPPEKPEEVTKANLIYADGKTQTAEFGTFEEATAEAYRYADALKKDNGEYTVDA 140
 QY 61 DKGYTLNIRFAG 72
 DB ||||||||||||
 141 DKGYTLNIRFAG 152

RESULT 5
 AAB31372
 ID AAB31372 standard; Protein; 467 AA.

XX AC AAB31372;

XX DT 20-APR-2001 (first entry)

XX Amino acid sequence of protein L/CBD cex/ER retaining peptide fusion.
 DE Protein production; food processing; protein antibiotic; feed enzyme;
 KW protein L; CBD cex protein; cell signal peptide.
 XX Synthetic.

OS WO200077174-A1.

XX PN 21-DEC-2000.

XX 07-JUN-2000; 2000WO-IL00330.

XX 10-JUN-1999; 99US-0329234.

XX (CBDT-) CBD TECHNOLOGIES LTD.
 PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.

XX Shani Z, Shoseyov O;
 XX WPI; 2001-112219/12.
 DR N-PSDB; AAF24730.
 XX
 XX Expressing and isolating recombinant protein in a plant, useful for
 PT producing large quantities of recombinant proteins, by expressing a
 PT fusion protein including a cellulose binding peptide fused to a
 PT recombinant protein -
 XX
 XX Example; Fig 2a; 87pp; English.
 XX
 CC The specification describes a method for expressing and isolating
 CC a recombinant protein in a plant. The method comprising expressing a
 CC fusion protein including the recombinant protein and a cellulose
 CC binding peptide fused to it, where the fusion protein is
 CC compartmentalised and sequestered within plant cells, plant derived
 CC tissue or cultured plant cells. The method is useful for obtaining large
 CC quantities of the recombinant proteins and protein products in a simple
 CC and cost-effective manner. Recombinant proteins may be used commercially,
 CC such as in the food processing industry, e.g. glucoamylases and glucose
 CC isomerases are used for converting starch to high fructose corn syrup,
 CC proteinases for the hydrolysis of high molecular weight proteins and in
 CC manufacturing leather or alcoholic beverages, pectinesterases for
 CC pectin hydrolysis in food industry, lipases for cleaving ester linkage
 CC in triglycerides, and for effluent treatment. The recombinant proteins
 CC may further be used to produce protein antibiotics, which can be used
 CC in healing processes, and to produce animal feed enzymes. The present
 CC sequence represents a fusion protein of the invention, and comprises a
 CC fusion of a cell signal peptide, protein L, CBD cex, and an endoplasmic
 CC reticulum retaining peptide.
 XX
 SQ Sequence 467 AA;
 Query Match 100.0%; Score 371; DB 22; Length 467;
 Best Local Similarity 100.0%; Pred. No. 2.9e-36;
 Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KETPEPEKEEVTIKANLIYADGKTQTAEFGTFFETAEAYRYADALKKDNGEYTVDA 60
 Db 120 KETPEPEKEEVTIKANLIYADGKTQTAEFGTFFETAEAYRYADALKKDNGEYTVDA 179
 QY 61 DKGYTLNIRFAG 72
 Db 180 DKGYTLNIRFAG 191
 RESULT 6
 AAY82539
 ID AAY82539 standard; Protein; 72 AA.
 AC AAY82539;
 XX
 XX 20-JUL-2000 (first entry)
 DT
 DE Peptostreptococcus strain 312 protein L domain B3 protein sequence.
 XX
 KW Immunoglobulin light chain binding protein; PpL; protein L;
 KW Peptostreptococcus; human immunoglobulin kappa chain;
 KW Immunoaffinity chromatography.
 XX
 OS Peptostreptococcus sp.
 XX
 PN WO200015803-A1.
 XX
 PD 23-MAR-2000.
 PF 14-SEP-1999; 99WO-GB03048.
 XX
 PR Immunoglobulin light chain binding protein; PpL; protein L;
 PR Peptostreptococcus; human immunoglobulin kappa chain;
 PR Immunoaffinity chromatography.
 XX
 OS Peptostreptococcus sp.
 XX
 PN WO200015803-A1.
 XX
 PD 23-MAR-2000.
 PF 14-SEP-1999; 99WO-GB03048.
 XX
 PR 14-SEP-1998; 98GB-0019998.
 PR 26-APR-1999; 99GB-0009578.
 XX
 XX

PA (ACTI-) ACTINOVA LTD.
 XX
 PI Gore MG, Beckingham JA, Roberts SE;
 XX
 XX WPI; 2000-271441/23.
 DR N-PSDB; AAA08428.
 XX
 XX New modified immunoglobulin light chain binding protein, useful in
 PT immunoaffinity chromatography, has a dissociation constant of 400 nM or
 PT more at pH8 with respect to human immunoglobulin kappa-chain -
 XX
 XX Disclosure; Page 43; 56pp; English.
 XX
 CC The present invention describes an immunoglobulin (Ig) light chain
 CC binding protein (P1) which has been modified by one or more amino acid
 CC substitutions such that the dissociation constant (Kd) of the protein
 CC with respect to human Ig kappa-chain is 400 nM or more at pH8. P1 is
 CC useful in immunoaffinity chromatography. The present sequence is a
 CC Peptostreptococcus protein L Ig light chain binding domain, which is
 CC given in the disclosure of the present invention.
 XX
 SQ Sequence 72 AA;
 Query Match 94.9%; Score 352; DB 21; Length 72;
 Best Local Similarity 94.4%; Pred. No. 4.8e-35;
 Matches 68; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 KETPEPEKEEVTIKANLIYADGKTQTAEFGTFFETAEAYRYADALKKDNGEYTVDA 60
 Db 1 KETPEPEKEEVTIKANLIYADGKTQTAEFGTFFETAEAYRYADALKKDNGEYTVDA 60
 QY 61 DKGYTLNIRFAG 72
 Db 61 DKGYTLNIRFAG 72
 RESULT 7
 AAY82540
 ID AAY82540 standard; Protein; 72 AA.
 XX
 AC AAY82540;
 XX
 XX 20-JUL-2000 (first entry)
 DT
 DE Peptostreptococcus strain 312 protein L domain B4 protein sequence.
 XX
 KW Immunoglobulin light chain binding protein; PpL; protein L;
 KW Peptostreptococcus; human immunoglobulin kappa chain;
 KW Immunoaffinity chromatography.
 XX
 OS Peptostreptococcus sp.
 XX
 PN WO200015803-A1.
 XX
 PD 23-MAR-2000.
 PF 14-SEP-1999; 99WO-GB03048.
 XX
 PR 14-SEP-1998; 98GB-0019998.
 PR 26-APR-1999; 99GB-0009578.
 XX
 XX (ACTI-) ACTINOVA LTD.
 XX
 PI Gore MG, Beckingham JA, Roberts SE;
 XX
 XX WPI; 2000-271441/23.
 DR N-PSDB; AAA08429.
 XX
 XX New modified immunoglobulin light chain binding protein, useful in
 PT immunoaffinity chromatography, has a dissociation constant of 400 nM or
 PT more at pH8 with respect to human immunoglobulin kappa-chain -
 XX
 XX Disclosure; Page 44-45; 56pp; English.
 XX

XX The present invention describes an immunoglobulin (Ig) light chain
CC binding protein (PI) which has been modified by one or more amino acid
CC substitutions such that the dissociation constant (Kd) of the protein
CC with respect to human Ig kappa-chain is 400 nM or more at pH8. PI is
CC useful in immunoaffinity chromatography. The present sequence is a
CC Peptostreptococcus protein L Ig light chain binding domain, which is
CC given in the disclosure of the present invention.
XX
SQ Sequence 72 AA;

Query Match 86.8%; Score 322; DB 21; Length 72;
Best Local Similarity 84.7%; Pred. No. 2.1e-31;
Matches 61; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 KEKTPPEEVTIKANLIYADGKTQTAEFGKTFEATAEAYRYADALKKNGEYTVDA 60
DB 1 KEKTPPEEVTIKANLIYADGKTQTAEFGKTFEATAEAYRYADALKKNGEYTVDA 60
QY 61 DRGYTLNIRFAG 72
DB 61 DGYTLNIRFAG 72

RESULT 8
AAY82537
ID AAY82537 standard; Protein; 76 AA.
XX
AC AAY82537;
XX
DT 20-JUL-2000 (first entry)
XX
DE Peptostreptococcus strain 312 protein L domain B1 protein sequence.
XX
KW Immunoglobulin light chain binding protein; PpL; protein L;
KW Peptostreptococcus; human immunoglobulin kappa chain;
KW immunoaffinity chromatography.
XX
OS Peptostreptococcus sp.
XX
PN WO200015803-A1.
XX
PD 23-MAR-2000.
XX
PF 14-SEP-1999; 99WO-GB03048.
XX
PR 14-SEP-1998; 98GB-0019998.
PR 26-APR-1999; 99GB-0009578.
XX
PA (ACTI-) ACTINOVA LTD.
XX
PI Gore MG, Beckingham JA, Roberts SE;
XX
DR WPI; 2000-271441/23.
DR N-PSDB; AAA08426.
XX
PT New modified immunoglobulin light chain binding protein, useful in
PT immunoaffinity chromatography, has a dissociation constant of 400 nM or
PT more at pH8 with respect to human immunoglobulin kappa-chain -
XX
PS Disclosure; Page 40-41; 56pp; English.
XX
PI Gore MG, Beckingham JA, Roberts SE;
XX
DR WPI; 2000-271441/23.
DR N-PSDB; AAA08426.
XX
PT New modified immunoglobulin light chain binding protein, useful in
PT immunoaffinity chromatography, has a dissociation constant of 400 nM or
PT more at pH8 with respect to human immunoglobulin kappa-chain -
XX
PS Disclosure; Page 40-41; 56pp; English.

XX The present invention describes an immunoglobulin (Ig) light chain
CC binding protein (PI) which has been modified by one or more amino acid
CC substitutions such that the dissociation constant (Kd) of the protein
CC with respect to human Ig kappa-chain is 400 nM or more at pH8. PI is
CC useful in immunoaffinity chromatography. The present sequence is a
CC Peptostreptococcus protein L Ig light chain binding domain, which is
CC given in the disclosure of the present invention.
XX
SQ Sequence 76 AA;

Query Match 84.6%; Score 314; DB 21; Length 76;

Best Local Similarity 81.6%; Pred. No. 2.1e-30;
Matches 62; Conservative 6; Mismatches 4; Indels 4; Gaps 1;

QY 1 KEKTPPEEVTIKANLIYADGKTQTAEFGKTFEATAEAYRYADALKKNGEYTV 56
DB 1 KEKTPPEEVTIKANLIYADGKTQTAEFGKTFEATAEAYRYADALKKNGEYTV 60
QY 57 VDVAADKGYTLNIRFAG 72
DB 61 VDVAADKGYTLNIRFAG 76

RESULT 9
AAY82544
ID AAY82544 standard; Protein; 75 AA.
XX
AC AAY82544;
XX
DT 20-JUL-2000 (first entry)
XX
DE Peptostreptococcus strain 3316 protein L domain C4 protein sequence.
XX
KW Immunoglobulin light chain binding protein; PpL; protein L;
KW Peptostreptococcus; human immunoglobulin kappa chain;
KW immunoaffinity chromatography.
XX
OS Peptostreptococcus sp.
XX
PN WO200015803-A1.
XX
PD 23-MAR-2000.
XX
PF 14-SEP-1999; 99WO-GB03048.
XX
PR 14-SEP-1998; 98GB-0019998.
PR 26-APR-1999; 99GB-0009578.
XX
PA (ACTI-) ACTINOVA LTD.
XX
PI Gore MG, Beckingham JA, Roberts SE;
XX
DR WPI; 2000-271441/23.
DR N-PSDB; AAA08433.
XX
PT New modified immunoglobulin light chain binding protein, useful in
PT immunoaffinity chromatography, has a dissociation constant of 400 nM or
PT more at pH8 with respect to human immunoglobulin kappa-chain -
XX
PS Disclosure; Page 49-50; 56pp; English.
XX
CC The present invention describes an immunoglobulin (Ig) light chain
CC binding protein (PI) which has been modified by one or more amino acid
CC substitutions such that the dissociation constant (Kd) of the protein
CC with respect to human Ig kappa-chain is 400 nM or more at pH8. PI is
CC useful in immunoaffinity chromatography. The present sequence is a
CC Peptostreptococcus protein L Ig light chain binding domain, which is
CC given in the disclosure of the present invention.
XX
SQ Sequence 75 AA;

Query Match 83.0%; Score 308; DB 21; Length 75;
Best Local Similarity 84.3%; Pred. No. 1.1e-29;
Matches 59; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 3 KPEEPKEEVTIKANLIYADGKTQTAEFGKTFEATAEAYRYADALKKNGEYTVDA 62
DB 5 ETPPEEKEEVTIKANLIYADGKTQTAEFGKTFEATAEAYRYADALKKNGEYTVDA 64
QY 63 GYTLNIRFAG 72
DB 65 GYTLNIRFAG 74

```

RESULT 10
AAR42204
ID AAR42204 standard; Protein; 291 AA.
XX AC
XX AAR42204;
XX AC
XX 25-MAR-2003 (updated)
XX DT 18-MAY-1994 (first entry)
XX DT
XX XX Immunoglobulin binding protein derived from protein L.
XX DE
XX KW Peptide; immunoglobulin; binding; analysis; purification; ELISA;
XX KW enzyme linked immunoabsorbant assay.
XX KW Synthetic.
XX OS
XX XX WO9322439-A1.
XX PN
XX XX 11-NOV-1993.
XX PD
XX PF 07-MAY-1993; 93WO-GB00950.
XX PR
XX PR 07-MAY-1992; 92GB-0009804.
XX PR 24-DEC-1992; 92GB-0026928.
XX XX (PUBL-) PUBLIC HEALTH LAB SERVICE BOARD.
XX PA
XX PI Atkinson A, Duggieby CJ, Murphy JP, Trowern AR;
XX XX WPI; 1993-368798/46.
XX DR N-PSDB; AAQ50947.
XX DR
XX XX New immunoglobulin binding proteins derived from Protein L -
XX PT which bind immunoglobulin kappa light chains but not albumin or
XX PT cell walls
XX PS Claim 12; Figure 2; 28pp; English.
XX CC The synthetic immunoglobulin binding proteins derived from protein
XX CC L comprise repeated sequences from protein L which bind
XX CC immunoglobulin kappa light chains. They can be used in protein
XX CC analysis, purification procedures and other biochemical processes e.
XX CC g. ELISA. The synthetic molecules are of particular advantage if
XX CC they are free of regions in protein L which exhibit albumin and cell
XX CC wall binding.
XX CC (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 291 AA;
XX Query Match 83.0%; Score 308; DB 14; Length 291;
XX Best Local Similarity 84.3%; Pred. No. 6.5e-29;
XX Matches 59; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 3 KTPEEPKEVTIKANLIYADGKTQTAEFGTTEATAEAYRYADALKDNGEYTVDVADK 62
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 221 ETPEEPKEVTIKVNLIFADGKTQTAEFGTTEATAEAYRYADLLAKVNGEYTDLEGG 280.
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 63 GYTLNIKFPAG 72
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 281 GYTINIKFPAG 290
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
AAR42203
ID AAR42203 standard; Protein; 1027 AA.
XX AC
XX AAR42203;
XX AC
XX 25-MAR-2003 (updated)
XX DT 18-MAY-1994 (first entry)
XX DT
XX XX Protein L.
XX DE
XX OS Peptococcus magnus.
XX XX

KW Peptide; immunoglobulin; binding; analysis; purification; ELISA;
KW enzyme linked immunoabsorbant assay.
KW Peptococcus magnus.
KW OS
KW FH Location/Qualifiers
KW FT 36..59
KW FT /label= Signal sequence.
KW FT 60..968
KW FT /label= Mature protein L.
KW XX
KW PN WO9322439-A1.
KW XX
KW PD 11-NOV-1993.
KW XX
KW PF 07-MAY-1993; 93WO-GB00950.
KW PR
KW PR 07-MAY-1992; 92GB-0009804.
KW PR 24-DEC-1992; 92GB-0026928.
KW XX
KW PA (PUBL-) PUBLIC HEALTH LAB SERVICE BOARD.
KW XX
KW PI Atkinson A, Duggieby CJ, Murphy JP, Trowern AR;
KW XX
KW WPI; 1993-368798/46.
KW DR N-PSDB; AAQ50946.
KW DR
KW XX New immunoglobulin binding proteins derived from Protein L -
KW PT which bind immunoglobulin kappa light chains but not albumin or
KW PT cell walls
KW PS Disclosure; Figure 1; 28pp; English.
KW CC The synthetic immunoglobulin binding proteins derived from protein
KW CC L correspond to the repeated sequences in protein L which bind
KW CC immunoglobulin kappa light chains. They can be used in protein
KW CC analysis, purification procedures and other biochemical processes e.
KW CC g. ELISA. The synthetic molecules are of particular advantage if
KW CC they are free of regions in protein L which exhibit albumin and cell
KW CC wall binding.
KW CC (Updated on 25-MAR-2003 to correct PN field.)
KW SQ Sequence 1027 AA;
KW Query Match 83.0%; Score 308; DB 14; Length 1027;
KW Best Local Similarity 84.3%; Pred. No. 3.5e-28;
KW Matches 59; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 3 KTPEEPKEVTIKANLIYADGKTQTAEFGTTEATAEAYRYADALKDNGEYTVDVADK 62
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 503 ETPEEPKEVTIKVNLIFADGKTQTAEFGTTEATAEAYRYADLLAKVNGEYTDLEGG 562
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 63 GYTLNIKFPAG 72
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 563 GYTINIKFPAG 572
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
AAR43699
ID AAR43699 standard; Protein; 1027 AA.
XX AC
XX AAR43699;
XX AC
XX 25-MAR-2003 (updated)
XX DT 18-MAY-1994 (first entry)
XX DT
XX XX Protein L.
XX DE
XX KW Protein; immunoglobulin; binding; immobilisation; light chains;
KW KW antibodies; diagnosis; pharmaceutical; ss.
XX OS
XX OS Peptococcus magnus.
XX XX

```

[illegible]

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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:16:02 ; Search time 15.7808 Seconds
(without alignments)
193.043 Million cell updates/sec

Title: US-08-325-278B-1_COPY_81_152

Perfect score: 371
Sequence: 1 KEKTPPEKEVTVKANLIY.....GEYTVDVADKGYTLNIKTAG 72

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	371	100.0	305	2	US-08-795-475-1
2	371	100.0	434	2	US-08-795-475-3
3	308	83.0	75	3	US-08-446-137B-8
4	308	83.0	291	3	US-08-446-137B-4
5	308	83.0	1027	3	US-08-446-137B-2
6	299	80.6	182	3	US-08-828-741B-2
7	299	80.6	182	4	US-09-160-567-2
8	299	80.6	182	4	US-09-710-299-2
9	292.5	78.8	71	3	US-08-446-137B-6
10	291	78.4	178	3	US-08-828-741B-13
11	291	78.4	178	4	US-09-160-567-13
12	291	78.4	178	4	US-09-710-299-13
13	291	78.4	198	3	US-08-828-741B-8
14	291	78.4	198	4	US-09-160-567-8
15	291	78.4	198	4	US-09-710-299-8
16	291	78.4	342	3	US-08-828-741B-6
17	291	78.4	342	4	US-09-160-567-6
18	291	78.4	342	4	US-09-710-299-6
19	291	78.4	495	3	US-08-828-741B-4
20	291	78.4	495	4	US-09-160-567-4
21	291	78.4	495	4	US-09-710-299-4
22	288.5	77.8	71	3	US-08-446-137B-5
23	283	76.3	74	3	US-08-446-137B-7
24	69.5	18.7	279	4	US-09-314-701-60
25	66.5	17.9	138	6	5218099-1
26	65	17.5	419	4	US-09-134-001C-3441
27	64	17.3	262	3	US-08-961-083-98

28	64	17.3	262	4	US-09-536-784-98	Sequence 98, Appl
29	64	17.3	270	3	US-08-961-083-206	Sequence 206, App
30	64	17.3	270	4	US-09-536-784-206	Sequence 206, App
31	64	17.3	600	6	5240706-1	Patent No. 5240706
32	63	17.0	289	1	US-08-072-070-4	Sequence 4, Appl
33	63	17.0	289	1	US-08-469-434-4	Sequence 4, Appl
34	63	17.0	289	1	US-08-214-222-4	Sequence 4, Appl
35	63	17.0	289	2	US-08-467-852A-5	Sequence 5, Appl
36	63	17.0	289	2	US-08-468-718-4	Sequence 4, Appl
37	63	17.0	289	2	US-08-247-491A-5	Sequence 5, Appl
38	60.5	16.3	109	4	US-09-405-743A-7	Sequence 7, Appl
39	60.5	16.3	155	4	US-09-252-991A-24006	Sequence 24006, A
40	60.5	16.3	288	3	US-08-312-949-4	Sequence 4, Appl
41	60.5	16.3	288	3	US-08-446-201-4	Sequence 4, Appl
42	60.5	16.3	619	1	US-08-465-746-2	Sequence 2, Appl
43	60.5	16.3	619	1	US-08-214-164-2	Sequence 2, Appl
44	60.5	16.3	619	2	US-08-467-852A-3	Sequence 3, Appl
45	60.5	16.3	619	2	US-08-246-636-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-795-475-1
; Sequence 1, Application US/08795475
; Patent No. 5965390
; GENERAL INFORMATION:
; APPLICANT: Bjvick, Lars
; APPLICANT: Sjvbring, Ulf
; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,475
; FILING DATE: 11-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 100084.402d1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 305 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli LE392/pHDL, DSM 7054
US-08-795-475-1

Query Match 100.0%; Score 371; DB 2; Length 305;
Best Local Similarity 100.0%; Pred. No. 3.4e-38;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KEKTPPEKEVTVKANLIYADKGTQTAEFGTFEATAEAYADALKKNGEYTVDA 60
|||||

Db 81 KKTPEEPKEVTIRANLIYADGKTQTAEFKGTAEATAEAYRYADALKKONGEYTVDA 140

QY 61 DKGYTLINIKFAG 72

Db 141 DKGYTLINIKFAG 152

RESULT 2

US-08-795-475-3

; Sequence 3, Application US/08795475

; Patent No. 5965390

; GENERAL INFORMATION:

; APPLICANT: Bjvrck, Lars

; APPLICANT: Sjvbring, Ulf

; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SEED and BERRY LLP

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; CITY: Seattle

; STATE: Washington

; COUNTRY: USA

; ZIP: 98104-7092

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/795,475

; FILING DATE: 11-FEB-1997

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Mcmasters, David D.

; REGISTRATION NUMBER: 33,963

; REFERENCE/DOCKET NUMBER: 100084.402D1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 622-4900

; TELEFAX: (206) 682-6031

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 434 amino acids

; TYPE: amino acid

; STRANDEDNESS: unknown

; TOPOLOGY: unknown

; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

; ORIGINAL SOURCE:

; ORGANISM: Escherichia coli LE392/pHDLG, DSM 7055

US-08-795-475-3

Query Match 100.0%; Score 371; DB 2; Length 434;

Best Local Similarity 100.0%; Pred. No. 5.5e-38;

Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKTPEEPKEVTIRANLIYADGKTQTAEFKGTAEATAEAYRYADALKKONGEYTVDA 60

Db 81 KKTPEEPKEVTIRANLIYADGKTQTAEFKGTAEATAEAYRYADALKKONGEYTVDA 140

QY 61 DKGYTLINIKFAG 72

Db 141 DKGYTLINIKFAG 152

RESULT 3

US-08-446-137B-8

; Sequence 8, Application US/08446137B

; Patent No. 6162903

; GENERAL INFORMATION:

; APPLICANT: Trowern, Angus R.

; APPLICANT: Atkinson, Anthony

; APPLICANT: Murphy, Jonathan P.

; APPLICANT: Laurence, Oliver S.

; APPLICANT: Duggieby, Clive J.

; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEINS DERIVED

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SEED and BERRY LLP

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; CITY: Seattle

; STATE: Washington

; COUNTRY: USA

; ZIP: 98104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/446,137B

; FILING DATE: 22-MAY-1995

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Mcmasters, David D.

; REGISTRATION NUMBER: 33,963

; REFERENCE/DOCKET NUMBER: 100084.406

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 622-4900

; TELEFAX: (206) 682-6031

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 75 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

US-08-446-137B-8

Query Match 83.0%; Score 308; DB 3; Length 75;

Best Local Similarity 84.3%; Pred. No. 3.6e-31;

Matches 59; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 3 KTTPEEPKEVTIRANLIYADGKTQTAEFKGTAEATAEAYRYADALKKONGEYTVDA 62

Db 5 ETPEEPKEVTIKVNLIFADGKTQTAEFKGTAEATAEAYRYADLLAKVNGEYTDLEDG 64

QY 63 GYTLINIKFAG 72

Db 65 GYTLINIKFAG 74

RESULT 4

US-08-446-137B-4

; Sequence 4, Application US/08446137B

; Patent No. 6162903

; GENERAL INFORMATION:

; APPLICANT: Trowern, Angus R.

; APPLICANT: Atkinson, Anthony

; APPLICANT: Murphy, Jonathan P.

; APPLICANT: Laurence, Oliver S.

; APPLICANT: Duggieby, Clive J.

; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEINS DERIVED

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SEED and BERRY LLP

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; CITY: Seattle

; STATE: Washington

; COUNTRY: USA

; ZIP: 98104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30


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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,137B
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McWaters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 100084.406
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 291 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-446-137B-4

Query Match      83.0%; Score 308; DB 3; Length 291;
Best Local Similarity 84.3%; Pred. No. 2.2e-30;
Matches 59; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 3 KTPPEPKKEVTIKANLIYADGKTQTAEFKGTFFETAEAYRYADALKKNGEYTVADVADK 62
Db 221 ETPEEPKEEVTIKVNLIFADGKTQTAEFKGTFFETAEAYRYADLLAKVNGEYTVADLE 280
QY 63 GYTLNFKFAG 72
Db 281 GYTINIKFAG 290

RESULT 5
US-08-446-137B-2
; Sequence 2, Application US/08446137B
; Patent No. 6162903
; GENERAL INFORMATION:
; APPLICANT: Trower, Angus R.
; APPLICANT: Atkinson, Anthony
; APPLICANT: Murphy, Jonathan P.
; APPLICANT: Laurence, Oliver S.
; APPLICANT: Dugleby, Clive J.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEINS DERIVED
; FROM L PROTEIN AND THEIR USES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,137B
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McWaters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 100084.406
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 682-6031
; TELEFAX: (206) 622-4900
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,137B-2
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McWaters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 100084.406
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 682-6031
; TELEFAX: (206) 622-4900
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 291 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-446-137B-2

Query Match      83.0%; Score 308; DB 3; Length 291;
Best Local Similarity 84.3%; Pred. No. 2.2e-30;
Matches 59; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 3 KTPPEPKKEVTIKANLIYADGKTQTAEFKGTFFETAEAYRYADALKKNGEYTVADVADK 62
Db 221 ETPEEPKEEVTIKVNLIFADGKTQTAEFKGTFFETAEAYRYADLLAKVNGEYTVADLE 280
QY 63 GYTLNFKFAG 72
Db 281 GYTINIKFAG 290

RESULT 6
US-08-828-741B-2
; Sequence 2, Application US/08828741B
; Patent No. 6043069
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Sues, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treuclien, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
; PRODUCING SAME
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,741B
; FILING DATE: 26-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10591
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 182 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-828-741B-2

Query Match      80.6%; Score 299; DB 3; Length 182;
Best Local Similarity 80.3%; Pred. No. 1.5e-29;
Matches 57; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 2 EKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFFETAEAYRYADALKKNGEYTVADVAD 61
Db 20 QAPKONTEEVTIKANLIYADGKTQTAEFKGTFFETAEAYRYADLLAKVNGEYTVADVAD 79
QY 62 KGYTLNFKFAG 72
Db 80 KGYTLNFKFAG 90
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RESULT 7
US-09-160-567-2
; Sequence 2, Application US/09160567
; Patent No. 6326179
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlington, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
; TITLE OF INVENTION: PRODUCING SAME
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/160,567
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,741
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10591
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 182 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-160-567-2

Query Match 80.6%; Score 299; DB 4; Length 182;
Best Local Similarity 80.3%; Pred. No. 1.5e-29;
Matches 57; Conservative 7; Mismatches 0; Gaps 0;

QY 2 EKTPEPKKEVTIKANLIYADGKTQTAEFKGTFEEATAYADALKKDNGETYVDVAD 61
Db 20 QAPKDNTEEVTKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVAD 79

QY 62 KGYTLNKFAG 72
Db 80 KGYTLNKFAG 90

US-09-160-567-2

Query Match 80.6%; Score 299; DB 4; Length 182;
Best Local Similarity 80.3%; Pred. No. 1.5e-29;
Matches 57; Conservative 7; Mismatches 0; Gaps 0;

QY 2 EKTPEPKKEVTIKANLIYADGKTQTAEFKGTFEEATAYADALKKDNGETYVDVAD 61
Db 20 QAPKDNTEEVTKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVAD 79

QY 62 KGYTLNKFAG 72
Db 80 KGYTLNKFAG 90

US-09-160-567-2

RESULT 8
US-09-710-299-2
; Sequence 2, Application US/09710299
; Patent No. 6521741
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlington, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
; TITLE OF INVENTION: PRODUCING SAME
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/710,299
; FILING DATE: 09-No. 6521741-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,741
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10591
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 182 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-710-299-2

Query Match 80.6%; Score 299; DB 4; Length 182;
Best Local Similarity 80.3%; Pred. No. 1.5e-29;
Matches 57; Conservative 7; Mismatches 0; Gaps 0;

QY 2 EKTPEPKKEVTIKANLIYADGKTQTAEFKGTFEEATAYADALKKDNGETYVDVAD 61
Db 20 QAPKDNTEEVTKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVAD 79

QY 62 KGYTLNKFAG 72
Db 80 KGYTLNKFAG 90

US-09-710-299-2

RESULT 9
US-08-446-137B-6
; Sequence 6, Application US/08446137B
; Patent No. 6162903
; GENERAL INFORMATION:
; APPLICANT: Trowern, Angus R.
; APPLICANT: Atkinson, Anthony
; APPLICANT: Murphy, Jonathan P.
; APPLICANT: Laurence, Oliver J.
; APPLICANT: Dugglesby, Clive J.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEINS DERIVED
; TITLE OF INVENTION: FROM L PROTEIN AND THEIR USES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
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[illegible]

Db 72 FAG 74

RESULT 12

US-09-710-299-13

; Sequence 13, Application US/09710299

; Patent No. 6521741

; GENERAL INFORMATION:

APPLICANT: Koentgen, Frank
 Suess, Gabriele M.
 Tarlington, David M.
 Treutlein, Herbert R.

TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF

PRODUCING SAME

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER

STREET: 400 Garden City Plaza

CITY: Garden City

STATE: New York

COUNTRY: United States of America

ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/710,299

FILING DATE: 09-No. 6521741-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/828,741

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Digiglio, Frank S.

REGISTRATION NUMBER: 31,346

REFERENCE/DOCKET NUMBER: 10591

TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 742-4343

TELEFAX: (516) 742-4366

TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 178 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-09-710-299-13

Query Match

Best Local Similarity 78.4%; Score 291; DB 4; Length 178;

Matches 56; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 10 EEVTKANLIYADCKTQTAFFKGTPEATAEAYRYADALKKNGEYTVADVADKGYTLNIK 69

Db 12 EEVTKANLIYADCKTQTAFFKGTPEATAEAYRYADALKKNGEYTVADVADKGYTLNIK 71

QY 70 FAG 72

Db 72 FAG 74

RESULT 13

US-08-828-741B-8

; Sequence 8, Application US/08828741B

; Patent No. 6043069

; GENERAL INFORMATION:

APPLICANT: Koentgen, Frank

APPLICANT: Suess, Gabriele M.

APPLICANT: Tarlington, David M.

APPLICANT: Treutlein, Herbert R.

TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
 TITLE OF INVENTION: PRODUCING SAME

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER

STREET: 400 Garden City Plaza

CITY: Garden City

STATE: New York

COUNTRY: United States of America

ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/828,741B

FILING DATE: 26-MAR-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Digiglio, Frank S.

REGISTRATION NUMBER: 31,346

REFERENCE/DOCKET NUMBER: 10591

TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 742-4343

TELEFAX: (516) 742-4366

TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 198 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-828-741B-8

Query Match

Best Local Similarity 78.4%; Score 291; DB 3; Length 198;

Matches 56; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 10 EEVTKANLIYADCKTQTAFFKGTPEATAEAYRYADALKKNGEYTVADVADKGYTLNIK 69

Db 32 EEVTKANLIYADCKTQTAFFKGTPEATAEAYRYADALKKNGEYTVADVADKGYTLNIK 91

QY 70 FAG 72

Db 92 FAG 94

RESULT 14

US-09-160-567-8

; Sequence 8, Application US/09160567

; Patent No. 6326179

; GENERAL INFORMATION:

APPLICANT: Koentgen, Frank

APPLICANT: Suess, Gabriele M.

APPLICANT: Tarlington, David M.

APPLICANT: Treutlein, Herbert R.

TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF

TITLE OF INVENTION: PRODUCING SAME

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER

STREET: 400 Garden City Plaza

CITY: Garden City

STATE: New York

COUNTRY: United States of America

ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/160,567
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,741
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10591
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 198 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-160-567-8

Query Match 78.4%; Score 291; DB 4; Length 198;
Best Local Similarity 88.9%; Pred. No. 1.7e-28;
Matches 56; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

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DB 32 EEVTKANLIFANGSTQTAEFKGTFFEKATSEAYAYADTLKKNGETVDVADKGYTLNIK 91

QY 70 FAG 72
|||
DB 92 FAG 94

RESULT 15
US-09-710-299-8
; Sequence 8, Application US/09710299
; Patent No. 6521741
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; Suess, Gabriele M.
; Tarlinton, David M.
; Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
; PRODUCING SAME
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/710,299
; FILING DATE: 09-NO. 6521741-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,741
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10591
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366

; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 198 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-710-299-8

Query Match 78.4%; Score 291; DB 4; Length 198;
Best Local Similarity 88.9%; Pred. No. 1.7e-28;
Matches 56; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 10 EEVTKANLIYADGKTQTAEFKGTFFEEATAEAYRYADALKKDNGETVDVADKGYTLNIK 69
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 32 EEVTKANLIFANGSTQTAEFKGTFFEKATSEAYAYADTLKKNGETVDVADKGYTLNIK 91

QY 70 FAG 72
|||
DB 92 FAG 94

Search completed: September 3, 2003, 11:25:36
Job time : 16.7808 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:23:22 ; Search time 26.6301 Seconds
(without alignments)
371.228 Million cell updates/sec

Title: US-08-325-278B-1_COPY_81_152

Perfect score: 371
Sequence: 1 KKTPEPKKEVTIKANLIY.....GEYTVDAKGYTLNKFAG 72

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513375 seqs, 137303645 residues

Total number of hits satisfying chosen parameters: 513375

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA.*

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	371	100.0	72	10	US-09-808-212A-6
2	371	100.0	305	8	US-08-325-278-1
3	371	100.0	434	8	US-08-325-278-3
4	352	94.9	72	10	US-09-808-212A-8
5	322	86.8	72	10	US-09-808-212A-10
6	314	84.6	76	10	US-09-808-212A-4
7	308	83.0	75	10	US-09-808-212A-18
8	299	80.6	182	12	US-10-345-618-2
9	292.5	78.8	71	10	US-09-808-212A-14
10	291	78.4	178	12	US-10-345-618-13
11	291	78.4	198	12	US-10-345-618-8
12	291	78.4	342	12	US-10-345-618-6
13	291	78.4	482	12	US-10-345-618-16
14	291	78.4	495	12	US-10-345-618-4
15	289.5	78.0	71	10	US-09-808-212A-12

16	286	77.1	82	10	US-09-808-212A-2	Sequence 2, Appli
17	283	76.3	74	10	US-09-808-212A-16	Sequence 16, Appl
18	69.5	18.7	279	14	US-10-059-964-60	Sequence 60, Appl
19	69.5	18.7	279	15	US-10-314-639-60	Sequence 60, Appl
20	68.5	18.5	261	10	US-09-245-764-7	Sequence 7, Appli
21	68.5	18.5	399	9	US-09-925-301-1128	Sequence 1128, Ap
22	68.5	18.5	399	15	US-10-106-698-5782	Sequence 5782, Ap
23	65.5	17.7	829	9	US-09-815-242-11216	Sequence 11216, A
24	64	17.3	262	9	US-09-765-272-98	Sequence 98, Appl
25	64	17.3	270	9	US-09-765-272-206	Sequence 206, App
26	64	17.3	448	12	US-10-342-224-82	Sequence 82, Appl
27	63.5	17.1	1588	12	US-10-154-419-37	Sequence 37, Appl
28	63.5	17.1	1588	14	US-10-002-769-5	Sequence 5, Appli
29	63	17.0	179	10	US-09-738-626-4795	Sequence 4795, Ap
30	62	16.7	841	9	US-09-815-242-5779	Sequence 5779, Ap
31	62	16.7	841	9	US-09-815-242-12751	Sequence 12751, A
32	61	16.4	836	10	US-09-858-525A-10	Sequence 10, Appl
33	61	16.4	871	10	US-09-858-525A-2	Sequence 2, Appli
34	60.5	16.3	109	10	US-09-816-989A-7	Sequence 7, Appli
35	60.5	16.3	271	15	US-10-138-505-30	Sequence 30, Appl
36	60.5	16.3	274	15	US-10-138-505-26	Sequence 26, Appl
37	60.5	16.3	619	11	US-09-882-774-1	Sequence 1, Appli
38	60.5	16.3	637	9	US-09-815-242-12058	Sequence 12058, A
39	60.5	16.3	637	15	US-10-127-032-168	Sequence 168, App
40	60	16.2	1001	15	US-10-128-714-3240	Sequence 3240, Ap
41	59.5	16.0	455	9	US-09-191-989-4	Sequence 4, Appli
42	59	15.9	102	15	US-10-016-516-12	Sequence 12, Appl
43	59	15.9	300	10	US-09-953-499-10	Sequence 10, Appl
44	59	15.9	1098	10	US-09-797-862-32	Sequence 32, Appl
45	58.5	15.8	191	9	US-09-815-242-14038	Sequence 14038, A

ALIGNMENTS

RESULT 1

US-09-808-212A-6
; Sequence 6, Application US/09808212A
; Patent No. US20020137918A1
; GENERAL INFORMATION:
; APPLICANT: Gore, Michael Graham
; APPLICANT: Beckingham, Jennifer Ann
; APPLICANT: Roberts, Sian Eleri
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN
; FILE REFERENCE: 100084.41AUS
; CURRENT APPLICATION NUMBER: US/09/808,212A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Peptostreptococcus sp.
US-09-808-212A-6

Query Match	100.0%	Score 371;	DB 10;	Length 72;
Best Local Similarity	100.0%	Pred. No. 1.6e-35;		
Matches 72;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	KKTPEPKKEVTIKANLIYADGKTQTAEFKGTFEETATAEAYADALKKDNGEYTVDA	60	
DB	1	KKTPEPKKEVTIKANLIYADGKTQTAEFKGTFEETATAEAYADALKKDNGEYTVDA	60	
QY	61	DKGYTLNKFAG 72		
DB	61	DKGYTLNKFAG 72		
RESULT 2				
US-08-325-278-1				
; Sequence 1, Application US/08325278				
; Publication No. US20030027283A1				
; GENERAL INFORMATION:				

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; APPLICANT: Bjvrck, Lars
; APPLICANT: SJvdring, Ulf
; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,278
; FILING DATE: 26-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 450023.401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 305 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli LE392/pHDL, DSM 7054
; US-08-325-278-1

Query Match 100.0%; Score 371; DB 8; Length 305;
Best Local Similarity 100.0%; Pred. No. 1e-34;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKTPEEPKEEVTIRKANLIYADGKTQTAEFKGTFFETAEAYRYADALKKNGEYTDVA 60
Db 81 KKTPEEPKEEVTIRKANLIYADGKTQTAEFKGTFFETAEAYRYADALKKNGEYTDVA 140

QY 61 DKGYTLNKFAG 72
Db 141 DKGYTLNKFAG 152

RESULT 3
US-08-325-278-3
; Sequence 3, Application US/08325278
; Publication No. US20030027283A1
; GENERAL INFORMATION:
; APPLICANT: Bjvrck, Lars
; APPLICANT: SJvdring, Ulf
; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,278
; FILING DATE: 26-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 450023.401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 434 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli LE392/pHDLG, DSM 7055
; US-08-325-278-3

Query Match 100.0%; Score 371; DB 8; Length 434;
Best Local Similarity 100.0%; Pred. No. 1.6e-34;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 81 KKTPEEPKEEVTIRKANLIYADGKTQTAEFKGTFFETAEAYRYADALKKNGEYTDVA 140

QY 61 DKGYTLNKFAG 72
Db 141 DKGYTLNKFAG 152

RESULT 4
US-08-808-212A-8
; Sequence 8, Application US/09808212A
; Patent No. US20020137918A1
; GENERAL INFORMATION:
; APPLICANT: Gore, Michael Graham
; APPLICANT: Beckingham, Jennifer Ann
; APPLICANT: Roberts, Sian Eleri
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN
; FILE REFERENCE: 100084.414US
; CURRENT APPLICATION NUMBER: US/09/808,212A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Peptostreptococcus sp.
; US-08-808-212A-8

Query Match 94.9%; Score 352; DB 10; Length 72;
Best Local Similarity 94.4%; Pred. No. 2.5e-33;
Matches 68; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Db 1 KKTPEEPKEEVTIRKANLIYADGKTQTAEFKGTFFETAEAYRYADALKKNGEYTDVA 60

QY 61 DKGYTLNKFAG 72
Db 61 DKGYTLNKFAG 72

RESULT 5
US-09-808-212A-10
; Sequence 10, Application US/09808212A
; Patent No. US20020137918A1

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```
; GENERAL INFORMATION:
; APPLICANT: Gore, Michael Graham
; APPLICANT: Beckingham, Jennifer Ann
; APPLICANT: Roberts, Sian Eleri
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN
; FILE REFERENCE: 100084.414US
; CURRENT APPLICATION NUMBER: US/09/808,212A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0.
; SEQ ID NO 10
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Peptostreptococcus sp.
; US-09-808-212A-10

Query Match      86.8%; Score 322; DB 10; Length 72;
Best Local Similarity 84.7%; Pred. No. 7e-30;
Matches 61; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 KETPEEPKEEVTIKANLIYADGKTQTAEFKGTFEATAYADALKKDNGEYTDVA 60
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QY 61 DKGTYLNIRFAG 72
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Db 61 DGGTYNIRFAG 72

RESULT 6
US-09-808-212A-4
; Sequence 4, Application US/09808212A
; Patent No. US20020137918A1
; GENERAL INFORMATION:
; APPLICANT: Gore, Michael Graham
; APPLICANT: Beckingham, Jennifer Ann
; APPLICANT: Roberts, Sian Eleri
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN
; FILE REFERENCE: 100084.414US
; CURRENT APPLICATION NUMBER: US/09/808,212A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Peptostreptococcus sp.
; US-09-808-212A-4

Query Match      84.6%; Score 314; DB 10; Length 76;
Best Local Similarity 81.6%; Pred. No. 6.2e-29;
Matches 62; Conservative 6; Mismatches 4; Indels 4; Gaps 1;

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QY 57 VDVAADKGTYLNIRFAG 72
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Db 61 VDVAADKGTYLNIRFAG 76

RESULT 7
US-09-808-212A-18
; Sequence 18, Application US/09808212A
; Patent No. US20020137918A1
; GENERAL INFORMATION:
; APPLICANT: Gore, Michael Graham
; APPLICANT: Beckingham, Jennifer Ann
; APPLICANT: Roberts, Sian Eleri
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN
; FILE REFERENCE: 100084.414US
; CURRENT APPLICATION NUMBER: US/09/808,212A
; CURRENT FILING DATE: 2001-03-13
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; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Peptostreptococcus sp.
; US-09-808-212A-18

Query Match      83.0%; Score 308; DB 10; Length 75;
Best Local Similarity 84.3%; Pred. No. 3e-28;
Matches 59; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

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Db 5 ETEPEEPKEEVTIKVNLIFADGKTQTAEFKGTFEATAYADLLAKVNGEYTDLEDG 64

QY 63 GYTINIKFAG 72
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Db 65 GYTINIKFAG 74

RESULT 8
US-10-345-618-2
; Sequence 2, Application US/10345618
; Publication No. US20030148484A1
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF PRODUCING SAME
; FILE REFERENCE: 13474
; CURRENT APPLICATION NUMBER: US/10/345,618
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US/09/509,031
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:LHL protein
; OTHER INFORMATION: sequence
; US-10-345-618-2

Query Match      80.6%; Score 299; DB 12; Length 182;
Best Local Similarity 80.3%; Pred. No. 9.9e-27;
Matches 57; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 2 EKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEATAYADALKKDNGEYTDVAD 61
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QAPKNDTEEVTIKANLIYADGKTQTAEFKGTFEATSEAYADTLKKNGEYTDVAD 79

QY 62 KGYTLNIRFAG 72
   :|||||:|||||
Db 80 KGYTLNIRFAG 90

RESULT 9
US-09-808-212A-14
; Sequence 14, Application US/09808212A
; Patent No. US20020137918A1
; GENERAL INFORMATION:
; APPLICANT: Gore, Michael Graham
; APPLICANT: Beckingham, Jennifer Ann
; APPLICANT: Roberts, Sian Eleri
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN
; FILE REFERENCE: 100084.414US
; CURRENT APPLICATION NUMBER: US/09/808,212A
; CURRENT FILING DATE: 2001-03-13
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; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: fastseq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Peptostreptococcus sp.
US-09-808-212A-14

Query Match
Best Local Similarity 78.8%; Score 292.5; DB 10; Length 71;
Matches 58; Conservative 5; Mismatches 8; Indels 1; Gaps 1;

QY 1 KEKTPPEEVTIKANLIYADGKTQTAEFGTPEEATAEAYRYADALKKNGEYTVDA 60
Db 1 KEK-PEEPEEVTIKVNLIFADGKTQTAEFGTPEEATAKAYAYADLLAKENGEXTADLE 59
QY 61 DRGYTLNIRFAG 72
Db 60 DSGNTINIRFAG 71

RESULT 10
US-10-345-618-13
; Sequence 13, Application US/10345618
; Publication No. US20030148484A1
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF PRODUCING SAME
; FILE REFERENCE: 13474
; CURRENT APPLICATION NUMBER: US/10/345,618
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US/09/509,031
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:LHL-omp
; OTHER INFORMATION: protein sequence
US-10-345-618-13

Query Match
Best Local Similarity 78.4%; Score 291; DB 12; Length 178;
Matches 56; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 10 EEVTIKANLIYADGKTQTAEFGTPEEATAEAYRYADALKKNGEYTVDAKGYTLNK 69
Db 12 EEVTIKANLIFANGSTQTAEFGTPEKATSEAYAYADTLKDKNGEYTVDAKGYTLNK 71
QY 70 FAG 72
Db 72 FAG 74

RESULT 11
US-10-345-618-8
; Sequence 8, Application US/10345618
; Publication No. US20030148484A1
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF PRODUCING SAME
; FILE REFERENCE: 13474
; CURRENT APPLICATION NUMBER: US/10/345,618
; CURRENT FILING DATE: 2003-01-16

; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:LHL.seq
; OTHER INFORMATION: protein sequence
US-10-345-618-8

Query Match
Best Local Similarity 78.4%; Score 291; DB 12; Length 198;
Matches 56; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 10 EEVTIKANLIYADGKTQTAEFGTPEEATAEAYRYADALKKNGEYTVDAKGYTLNK 69
Db 32 EEVTIKANLIFANGSTQTAEFGTPEKATSEAYAYADTLKDKNGEYTVDAKGYTLNK 91
QY 70 FAG 72
Db 92 FAG 94

RESULT 12
US-10-345-618-6
; Sequence 6, Application US/10345618
; Publication No. US20030148484A1
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF PRODUCING SAME
; FILE REFERENCE: 13474
; CURRENT APPLICATION NUMBER: US/10/345,618
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US/09/509,031
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:TLHL protein
; OTHER INFORMATION: sequence
US-10-345-618-6

Query Match
Best Local Similarity 78.4%; Score 291; DB 12; Length 342;
Matches 56; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 10 EEVTIKANLIYADGKTQTAEFGTPEEATAEAYRYADALKKNGEYTVDAKGYTLNK 69
Db 176 EEVTIKANLIFANGSTQTAEFGTPEKATSEAYAYADTLKDKNGEYTVDAKGYTLNK 235
QY 70 FAG 72
Db 236 FAG 238

RESULT 13
US-10-345-618-16
; Sequence 16, Application US/10345618
; Publication No. US20030148484A1
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlinton, David M.
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; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF PRODUCING SAME
; FILE REFERENCE: 13474
; CURRENT APPLICATION NUMBER: US/10/345,618
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US/09/509,031
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ccMTLgI protein
US-10-345-618-16

Query Match 78.4%; Score 291; DB 12; Length 482;
Best Local Similarity 88.9%; Pred. No. 2.8e-25;
Matches 56; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 10 EETIKANLIYADGKTQTAEFGTTEATAEAYRYADALKKDNGETVDVADKGYTLNIK 69
Db 323 EETIKANLIYADGKTQTAEFGTTEATAEAYRYADALKKDNGETVDVADKGYTLNIK 382
QY 70 FAG 72
Db 383 FAG 385

RESULT 14
US-10-345-618-4
; Sequence 4, Application US/10345618
; Publication No. US20030148484A1
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF PRODUCING SAME
; FILE REFERENCE: 13474
; CURRENT APPLICATION NUMBER: US/10/345,618
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US/09/509,031
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:CATAB-TEV
US-10-345-618-4

Query Match 78.4%; Score 291; DB 12; Length 495;
Best Local Similarity 88.9%; Pred. No. 2.9e-25;
Matches 56; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 10 EETIKANLIYADGKTQTAEFGTTEATAEAYRYADALKKDNGETVDVADKGYTLNIK 69
Db 176 EETIKANLIYADGKTQTAEFGTTEATAEAYRYADALKKDNGETVDVADKGYTLNIK 235
QY 70 FAG 72
Db 236 FAG 238

RESULT 15
US-09-808-212A-12
; Sequence 12, Application US/09808212A

; Patent No. US20020137918A1
; GENERAL INFORMATION:
; APPLICANT: Gore, Michael Graham
; APPLICANT: Beckingham, Jennifer Ann
; APPLICANT: Roberts, Sian Eleri
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN
; FILE REFERENCE: 100084.414US
; CURRENT APPLICATION NUMBER: US/09/808,212A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Peptostreptococcus sp.
US-09-808-212A-12

Query Match 78.0%; Score 289.5; DB 10; Length 71;
Best Local Similarity 80.3%; Pred. No. 3.7e-26;
Matches 57; Conservative 7; Mismatches 6; Indels 1; Gaps 1;
QY 2 EKTPEEPKEEVTIKANLIYADGKTQTAEFGTTEATAEAYRYADALKKDNGETVDVAD 61
Db 1 KETP-EPEEEVTIKANLIYADGKTQTAEFGTTEATAEAYRYADALKKDNGETVDVAD 59
QY 62 KGYTLNIKFAG 72
Db 60 KGLTLNIKFAG 70

Search completed: September 3, 2003, 11:42:50
Job time : 26.6301 secs

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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:19:27; Search time 213.041 Seconds
(without alignments)
294.149 Million cell updates/sec

Title: US-08-325-278B-1_COPY_81_152

Perfect score: 371
Sequence: 1 KKTPEPKREVTIKANLIY.....GEYTVADKGYTLNIKFAG 72

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 5580241 seqs, 870357830 residues

Total number of hits satisfying chosen parameters: 5580241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Pending Patents_AA_Main:*

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- 2: /cgn2_6/ptodata/1/paa/US06_COMB.pep.*
- 3: /cgn2_6/ptodata/1/paa/US07_COMB.pep.*
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- 5: /cgn2_6/ptodata/1/paa/US081_COMB.pep.*
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- 10: /cgn2_6/ptodata/1/paa/US086_COMB.pep.*
- 11: /cgn2_6/ptodata/1/paa/US087_COMB.pep.*
- 12: /cgn2_6/ptodata/1/paa/US088_COMB.pep.*
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- 25: /cgn2_6/ptodata/1/paa/US099B_COMB.pep.*
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- 27: /cgn2_6/ptodata/1/paa/US101_COMB.pep.*
- 28: /cgn2_6/ptodata/1/paa/US102_COMB.pep.*
- 29: /cgn2_6/ptodata/1/paa/US103_COMB.pep.*
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- 31: /cgn2_6/ptodata/1/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	371	100.0	72	23	US-09-808-212A-6
2	371	100.0	305	7	US-08-325-278-1

3	371	100.0	305	7	US-08-325-278A-1	Sequence 1, Appli
4	371	100.0	305	7	US-08-325-278B-1	Sequence 1, Appli
5	371	100.0	367	23	US-09-889-182A-4	Sequence 4, Appli
6	371	100.0	434	7	US-08-325-278-3	Sequence 3, Appli
7	371	100.0	434	7	US-08-325-278A-3	Sequence 3, Appli
8	371	100.0	434	7	US-08-325-278B-3	Sequence 3, Appli
9	371	100.0	467	25	US-09-980-469-12	Sequence 12, Appli
10	371	100.0	719	22	US-09-791-537-10210	Sequence 10210, A
11	371	100.0	719	22	US-09-791-537-96101	Sequence 96101, A
12	352	94.9	72	23	US-09-808-212A-8	Sequence 8, Appli
13	322	86.8	72	23	US-09-808-212A-10	Sequence 10, Appli
14	314	84.6	76	23	US-09-808-212A-4	Sequence 4, Appli
15	314	84.6	78	22	US-09-791-537-22553	Sequence 22553, A
16	308	83.0	75	23	US-09-808-212A-18	Sequence 18, Appli
17	308	83.0	291	8	US-08-446-137A-4	Sequence 4, Appli
18	308	83.0	992	22	US-09-791-537-88366	Sequence 88366, A
19	308	83.0	1027	7	US-08-331-637-2	Sequence 2, Appli
20	308	83.0	1027	8	US-08-446-137A-2	Sequence 2, Appli
21	308	83.0	1027	15	US-09-187-295-2	Sequence 2, Appli
22	299	80.6	182	19	US-09-509-031-2	Sequence 2, Appli
23	299	80.6	182	23	US-09-820-048A-2	Sequence 2, Appli
24	292.5	78.8	71	23	US-09-808-212A-14	Sequence 14, Appli
25	291	78.4	178	19	US-09-509-031-13	Sequence 13, Appli
26	291	78.4	178	23	US-09-820-048A-13	Sequence 13, Appli
27	291	78.4	198	19	US-09-509-031-8	Sequence 8, Appli
28	291	78.4	198	23	US-09-820-048A-8	Sequence 8, Appli
29	291	78.4	342	19	US-09-509-031-6	Sequence 6, Appli
30	291	78.4	342	23	US-09-820-048A-6	Sequence 6, Appli
31	291	78.4	482	19	US-09-509-031-16	Sequence 16, Appli
32	291	78.4	495	19	US-09-509-031-4	Sequence 4, Appli
33	291	78.4	495	23	US-09-820-048A-4	Sequence 4, Appli
34	289.5	78.0	71	23	US-09-808-212A-12	Sequence 12, Appli
35	286	77.1	82	23	US-09-808-212A-2	Sequence 2, Appli
36	283	76.3	74	23	US-09-808-212A-16	Sequence 16, Appli
37	90.5	24.4	395	1	PCT-US01-08631-42219	Sequence 42219, A
38	90.5	24.4	395	19	US-09-538-092-857	Sequence 857, App
39	89.5	24.1	463	1	PCT-US01-08631-53631	Sequence 53631, A
40	72.5	19.5	301	27	US-10-179-131-7741	Sequence 7741, Ap
41	72.5	19.5	536	22	US-09-791-537-9081	Sequence 9081, Ap
42	72	19.4	1447	30	US-10-437-963-198658	Sequence 198658,
43	71	19.1	634	22	US-09-791-537-126395	Sequence 126395,
44	69.5	18.7	130	21	US-09-708-427-40518	Sequence 40518, A
45	69.5	18.7	172	21	US-09-708-427-40517	Sequence 40517, A

ALIGNMENTS

RESULT 1
US-09-808-212A-6
; Sequence 6, Application US/09808212A
; GENERAL INFORMATION:
; APPLICANT: Gore, Michael Graham
; APPLICANT: Beckingham, Jennifer Ann
; APPLICANT: Roberts, Sian Eleri
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN
; FILE REFERENCE: 100084.414US
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Peptostreptococcus sp.
US-09-808-212A-6

Query Match 100.0%; Score 371; DB 23; Length 72;
Best Local Similarity 100.0%; Pred. No. 4.8e-36;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKTPEPKREVTIKANLIYADGKTQTAEKFGTFEATAYAYDAALKKDNGEYTVDA 60
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Db 1 KKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEATAEAYRYADALKKDNGETVDVA 60
QY 61 DRGYTLNIFAG 72
| | | | | | | | | |
Db 61 DRGYTLNIFAG 72

RESULT 2
US-08-325-278-1
; Sequence 1, Application US/08325278
; GENERAL INFORMATION:
; APPLICANT: Bjorck, Lars
; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,278
; FILING DATE: 26-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 450023.401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 305 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli LE392/pHDL, DSM 7054
; US-08-325-278-1

Query Match 100.0%; Score 371; DB 7; Length 305;
Best Local Similarity 100.0%; Pred. No. 3.5e-35;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEATAEAYRYADALKKDNGETVDVA 60
| | | | | | | | | |
Db 81 KKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEATAEAYRYADALKKDNGETVDVA 140

QY 61 DRGYTLNIFAG 72
| | | | | | | | | |
Db 141 DRGYTLNIFAG 152

RESULT 3
US-08-325-278A-1
; Sequence 1, Application US/08325278A
; GENERAL INFORMATION:
; APPLICANT: Bjorck, Lars
; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed IP Law Group
```

```
; STREET: 701 Fifth Avenue Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,278A
; FILING DATE: 26-Oct-1994
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 100084.402
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 305 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli LE392/pHDL, DSM 7054
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
; US-08-325-278A-1

Query Match 100.0%; Score 371; DB 7; Length 305;
Best Local Similarity 100.0%; Pred. No. 3.5e-35;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEATAEAYRYADALKKDNGETVDVA 60
| | | | | | | | | |
Db 81 KKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEATAEAYRYADALKKDNGETVDVA 140

QY 61 DRGYTLNIFAG 72
| | | | | | | | | |
Db 141 DRGYTLNIFAG 152

RESULT 4
US-08-325-278B-1
; Sequence 1, Application US/08325278B
; GENERAL INFORMATION:
; APPLICANT: Bjorck, Lars
; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed IP Law Group
; STREET: 701 Fifth Avenue Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,278B
; FILING DATE: 26-Oct-1994
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.
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;
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 100084.402
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 305 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli LE392/pHDL, DSM 7054
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-08-325-278b-1

Query Match 100.0%; Score 371; DB 7; Length 305;
Best Local Similarity 100.0%; Pred. No. 3.5e-35;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKTPEEPKEEVTIRKANLIYADGKTQTAEFGTFFETAEAYRYADALKKNGEYTDVA 60
   |||||||
Db 81 KKTPEEPKEEVTIRKANLIYADGKTQTAEFGTFFETAEAYRYADALKKNGEYTDVA 140
   |||||||

QY 61 DKGYTLNIRKAG 72
   |||||||
Db 141 DKGYTLNIRKAG 152

RESULT 5
US-09-889-182A-4
; Sequence 4, Application US/09889182A
; GENERAL INFORMATION:
; APPLICANT: Breittling, Frank
; TITLE OF INVENTION: SELECTION OF MONOCLONAL ANTIBODIES
; FILE REFERENCE: 4121-126
; CURRENT APPLICATION NUMBER: US/09/889,182A
; PRIOR FILING DATE: 2000-01-11
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-889-182A-4

Query Match 100.0%; Score 371; DB 23; Length 367;
Best Local Similarity 100.0%; Pred. No. 4.6e-35;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKTPEEPKEEVTIRKANLIYADGKTQTAEFGTFFETAEAYRYADALKKNGEYTDVA 60
   |||||||
Db 25 KKTPEEPKEEVTIRKANLIYADGKTQTAEFGTFFETAEAYRYADALKKNGEYTDVA 84
   |||||||

QY 61 DKGYTLNIRKAG 72
   |||||||
Db 85 DKGYTLNIRKAG 96

RESULT 6
US-08-325-278-3
; Sequence 3, Application US/08325278
; GENERAL INFORMATION:
; APPLICANT: Björck, Lars
; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
; NUMBER OF SEQUENCES: 14
```

```
;
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,278
; FILING DATE: 26-Oct-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 450023.401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 434 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli LE392/pHDLG, DSM 7055
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-325-278-3

Query Match 100.0%; Score 371; DB 7; Length 434;
Best Local Similarity 100.0%; Pred. No. 5.7e-35;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKTPEEPKEEVTIRKANLIYADGKTQTAEFGTFFETAEAYRYADALKKNGEYTDVA 60
   |||||||
Db 81 KKTPEEPKEEVTIRKANLIYADGKTQTAEFGTFFETAEAYRYADALKKNGEYTDVA 140
   |||||||

QY 61 DKGYTLNIRKAG 72
   |||||||
Db 141 DKGYTLNIRKAG 152

RESULT 7
US-08-325-278A-3
; Sequence 3, Application US/08325278A
; GENERAL INFORMATION:
; APPLICANT: Björck, Lars
; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed IP Law Group
; STREET: 701 Fifth Avenue Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,278A
; FILING DATE: 26-Oct-1994
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
```

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; NAME: Potter, Jane E. R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 100084.402
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 434 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli LE392/pHDLG, DSM 7055
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-325-278A-3

Query Match 100.0%; Score 371; DB 7; Length 434;
Best Local Similarity 100.0%; Pred. No. 5.7e-35;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEKTPPEKPEEVTIKANLIYADGKTQTAEFKGTFFEAATAEAYRYADALKKDNGETVDVA 60
Db 81 KEKTPPEKPEEVTIKANLIYADGKTQTAEFKGTFFEAATAEAYRYADALKKDNGETVDVA 140
QY 61 DKGYTLNKFAG 72
Db 141 DKGYTLNKFAG 152

RESULT 9
US-09-980-469-12
; Sequence 12, Application US/09980469
; GENERAL INFORMATION:
; APPLICANT: Shoseyov, Oded
; TITLE OF INVENTION: PROCESS OF EXPRESSING AND ISOLATING RECOMBINANT PROTEINS AND R
; FILE REFERENCE: 01/22924
; CURRENT APPLICATION NUMBER: US/09/980,469
; CURRENT FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: pUC19-cell1-ProtL-cexNG-HDEL fusion encoded product
US-09-980-469-12

Query Match 100.0%; Score 371; DB 25; Length 467;
Best Local Similarity 100.0%; Pred. No. 6.3e-35;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEKTPPEKPEEVTIKANLIYADGKTQTAEFKGTFFEAATAEAYRYADALKKDNGETVDVA 60
Db 120 KEKTPPEKPEEVTIKANLIYADGKTQTAEFKGTFFEAATAEAYRYADALKKDNGETVDVA 179
QY 61 DKGYTLNKFAG 72
Db 180 DKGYTLNKFAG 191

RESULT 10
US-09-791-537-10210
; Sequence 10210, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10210
; LENGTH: 719
; TYPE: PRT
; ORGANISM: Peptostreptococcus magnus
US-09-791-537-10210

Query Match 100.0%; Score 371; DB 22; Length 719;
Best Local Similarity 100.0%; Pred. No. 1.1e-34;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db	1	KETPPEPKEEVTIKANLIYADGKTQTAEFKTTFEATAEAYRYADLLAKENGKYTVDA	60
Qy	61	DKGYTLNIRFAG	72
Db	61	DKGYTLNIRFAG	72

RESULT 15
US-09-791-537-22553
; Sequence 22553, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biomimix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22553
; LENGTH: 78
; TYPE: PRT
; ORGANISM: pdb 2PTL
US-09-791-537-22553

Query Match 84.6%; Score 314; DB 22; Length 78;
Best Local Similarity 81.6%; Pred. No. 3.3e-29;
Matches 62; Conservative 6; Mismatches 4; Indels 4; Gaps 1;
QY 1 KEKTPPEP---KEEVTKANLIYADGKQTOTAEFKGTPEATAEAYRYADALKKDNGEYT 56
Db 3 KEETPETPTDSEEEVTKANLIFANGSTQTAEFKGTPEKATSEAYAYADTLKKDNGEYT 62
QY 57 VDVADKGYTLNIKFAG 72
Db 63 VDVADKGYTLNIKFAG 78

Search completed: September 3, 2003, 11:40:07
Job time : 213.041 secs

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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:20:12 ; Search time 10.1096 Seconds
(without alignments)
223.701 Million cell updates/sec

Title: US-08-325-278b-1_copy_81_152

Perfect score: 371

Sequence: 1 KEKTEPEKKEVTKANLIY.....GEYTVADVADKGYTLNKRFG 72

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 148256 seqs, 31410045 residues

Total number of hits satisfying chosen parameters: 148256

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 2: /cgn2_6/prodata/1/paa/US06_NEW_COMB.pcp.*
- 3: /cgn2_6/prodata/1/paa/US07_NEW_COMB.pcp.*
- 4: /cgn2_6/prodata/1/paa/US08_NEW_COMB.pcp.*
- 5: /cgn2_6/prodata/1/paa/US09_NEW_COMB.pcp.*
- 6: /cgn2_6/prodata/1/paa/US10_NEW_COMB.pcp.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	17.3	291	6	US-10-640-833-4201
2	64	17.3	328	6	US-10-617-320-3318
3	63.5	17.1	914	6	US-10-631-467-789
4	63.5	17.1	1019	1	PCT-US03-21510-62
5	62.5	16.8	157	5	US-09-897-516A-8199
6	62	16.7	930	5	US-09-200-650E-3
7	61	16.4	728	6	US-10-467-534-81
8	61	16.4	977	6	US-10-293-244-1201
9	61	16.4	977	7	US-60-490-890-580
10	61	16.4	1003	6	US-10-293-244-3169
11	60.5	16.3	271	6	US-10-221-131-95
12	60.5	16.3	271	6	US-10-221-131-96
13	60.5	16.3	354	6	US-10-299-636-105
14	60.5	16.3	588	6	US-10-299-636-96
15	60	16.2	247	6	US-10-408-765A-1338
16	60	16.2	1166	5	US-09-200-650E-7
17	59.5	16.0	1849	6	US-10-637-544-2
18	59.5	16.0	2315	6	US-10-603-114-5434
19	59	15.9	102	6	US-10-016-516A-12
20	59	15.9	242	5	US-09-674-548A-244
21	59	15.9	300	5	US-09-397-243D-12
22	59	15.9	300	6	US-10-633-008-10
23	58.5	15.8	383	6	US-10-613-520-1853
24	58.5	15.8	592	1	PCT-US02-21936-30
25	58.5	15.8	634	6	US-10-613-520-1103
26	58.5	15.8	636	6	US-10-613-520-1638

ALIGNMENTS

RESULT 1

US-10-640-833-4201
; Sequence 4201, Application US/10640833

; GENERAL INFORMATION:

; APPLICANT: Doucette-Stamm, Lynn

; APPLICANT: Bush, David

; APPLICANT: Zeng, Qiangdong

; APPLICANT: Opperman, Timothy

; APPLICANT: Houseweart, Chad Eric

; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics

; FILE REFERENCE: PATH03-15

; CURRENT APPLICATION NUMBER: US/10/640,833

; CURRENT FILING DATE: 2003-08-14

; PRIOR APPLICATION NUMBER: US 09/583,110

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/107,433

; PRIOR FILING DATE: 1998-06-30

; PRIOR APPLICATION NUMBER: US 60/085,131

; PRIOR FILING DATE: 1998-05-12

; PRIOR APPLICATION NUMBER: US 60/051,553

; PRIOR FILING DATE: 1997-07-02

; NUMBER OF SEQ ID NOS: 5322

; SEQ ID NO 4201

; LENGTH: 291

; TYPE: PRT

; ORGANISM: Streptococcus pneumoniae

US-10-640-833-4201

Query Match

Best Local Similarity 17.3%; Score 64; DB 6; Length 291;

Matches 17; Conservative 9; Mismatches 17; Indels 22; Gaps 2;

QY 20 YADGKTQTAEFK-----GTFEATAEAYRYADALKKNGEYTVADVADK 63

Db 165 FIEAKTETETYSQHLGKLSVVGSTSVSLMEKLAAY-----KKENPEVITDITSG 218

QY 64 YTLNI 68

Db 219 SSAGI 223

RESULT 2

US-10-617-320-3318

; Sequence 3318, Application US/10617320

; GENERAL INFORMATION:

; APPLICANT: Lynn A Doucette-Stamm and David Bush

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID

; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIA

```

; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/617,320
; FILING DATE: 10-Jul-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 3318:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 328 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...328
; SEQUENCE DESCRIPTION: SEQ ID NO: 3318:
US-10-617-320-3318

Query Match 17.3%; Score 64; DB 6; Length 328;
Best Local Similarity 26.2%; Pred. No. 5.8;
Matches 17; Conservative 9; Mismatches 17; Indels 22; Gaps 2;

QY 20 YADGKTQTAEFK-----GTFEATAEAYRYADALKKNGEYTVDVADKG 63
Db 202 FTEAKTETETYSQHLGKGLSVGTSVSSLKLAAY-----KKENPEYTVIDITNSG 255
QY 64 YTLNI 68
Db 256 SSAGI 260

RESULT 3
US-10-631-467-789
; Sequence 789, Application US/10631467
; GENERAL INFORMATION:
; APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive
; FILE OF INVENTION: disease
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
; PRIOR FILING DATE: 2002-08-06

; THERAPEUTICS
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 789
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-631-467-789

Query Match 17.1%; Score 63.5; DB 6; Length 914;
Best Local Similarity 40.5%; Pred. No. 23;
Matches 17; Conservative 5; Mismatches 19; Indels 1; Gaps 1;

QY 3 KTPPEPKKEVTIKANLIYADGKTQTAEFKGTTFEATAEAYRY 44
Db 434 KTPSITSEAVVPEAGLV-IDGKTLNAIFQGLKLEKFLQY 474

RESULT 4
PCT-US03-21510-62
; Sequence 62, Application PC/TUS0321510
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: MP21S AS MODIFIERS OF THE p21 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX03-046C-PC
; CURRENT APPLICATION NUMBER: PCT/US03/21510
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US 60/394,795
; PRIOR FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US 60/401,739
; PRIOR FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US 60/411,010
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 60/437,158
; PRIOR FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
; LENGTH: 1019
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-21510-62

Query Match 17.1%; Score 63.5; DB 1; Length 1019;
Best Local Similarity 40.5%; Pred. No. 27;
Matches 17; Conservative 5; Mismatches 19; Indels 1; Gaps 1;

QY 3 KTPPEPKKEVTIKANLIYADGKTQTAEFKGTTFEATAEAYRY 44
Db 539 KTPSITSEAVVPEAGLV-IDGKTLNAIFQGLKLEKFLQY 579

RESULT 5
US-09-897-516A-8199
; Sequence 8199, Application US/09897516A
; GENERAL INFORMATION:
; APPLICANT: Corbin, David R.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Huesing, Joseph E.
; APPLICANT: Malvar, Thomas M.
; APPLICANT: Krasomil-Osterfeld, Karina C.
; APPLICANT: Slater, Steven C.
; APPLICANT: Spiridonov, Sergei
; TITLE OF INVENTION: Xenorhabdus sp. Genome Sequences And Uses Thereof
; FILE REFERENCE: 38-21(51847)B
; CURRENT APPLICATION NUMBER: US/09/897,516A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,161
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 8415
; SEQ ID NO 8199
; LENGTH: 157
; TYPE: PRT
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US-10-467-534-81

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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 580
; LENGTH: 977
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-490-890-580

Query Match      16.4%; Score 61; DB 7; Length 977;
Best Local Similarity 34.5%; Pred. No. 49;
Matches 19; Conservative 6; Mismatches 22; Indels 8; Gaps 2;

QY      4 TPEEPKEE---VTIKANL-----IVADGKTQTAEFKGTFEEATAEAYRYADALKK 50
      :||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      844 SPEAPPAEQDPVOLKLTQLEWTEAILEDQTRQKLMAEFEFAQTSACRLQEELEK 898

RESULT 10
US-10-293-244-3169
; Sequence 3169, Application US/10293244
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-029
; CURRENT APPLICATION NUMBER: US/10/293,244
; PRIOR FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: Not yet Assigned
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 09/728,422
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 09/693,325
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/663,561
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/654,936
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 09/620,325
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/598,075
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 3960
; SOFTWARE: Custom
; SEQ ID NO 3169
; LENGTH: 1003
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-244-3169

Query Match      16.4%; Score 61; DB 6; Length 1003;
Best Local Similarity 34.5%; Pred. No. 51;
Matches 19; Conservative 6; Mismatches 22; Indels 8; Gaps 2;

QY      4 TPEEPKEE---VTIKANL-----IVADGKTQTAEFKGTFEEATAEAYRYADALKK 50
      :||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      870 SPEAPPAEQDPVOLKLTQLEWTEAILEDQTRQKLTAEFEFAQTSACRLQEELEK 924

RESULT 11
US-10-221-131-95
; Sequence 95, Application US/10221131
; GENERAL INFORMATION:
; APPLICANT: FUKUSHIMA, NAOSHI
; APPLICANT: TSUCHIYA, MASAYUKI
; APPLICANT: OH-EDA, MASAYOSHI
; APPLICANT: UNO, SHINSUKE
; APPLICANT: KIKUCHI, YASUFUMI
; TITLE OF INVENTION: POLYPEPTIDE INDUCING APOPTOSIS
; FILE REFERENCE: 065678/0106
; CURRENT APPLICATION NUMBER: US/10/221,131
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; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: PCT/JP01/01912
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 09/523,095
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: JP 2000-115246
; PRIOR FILING DATE: 2000-04-17
; PRIOR APPLICATION NUMBER: JP 2000-321822
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 95
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: pscml. MABL1-scfv
US-10-221-131-95

Query Match      16.3%; Score 60.5; DB 6; Length 271;
Best Local Similarity 27.3%; Pred. No. 12;
Matches 18; Conservative 11; Mismatches 24; Indels 13; Gaps 2;

QY      20 YADGKTQTAEFKG-----TFEEATAEAYRYADALKKDN-----GEYTVADVADKGYTL 66
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      76 YNDGTYNEKFKGKATLTSEKSSAAYMELSLASEDSAVYYCARGGYSYDDWGQGTTL 135

QY      67 NIKFAG 72
      : |
Db      136 TVSSGG 141

RESULT 12
US-10-221-131-96
; Sequence 96, Application US/10221131
; GENERAL INFORMATION:
; APPLICANT: FUKUSHIMA, NAOSHI
; APPLICANT: TSUCHIYA, MASAYUKI
; APPLICANT: OH-EDA, MASAYOSHI
; APPLICANT: UNO, SHINSUKE
; APPLICANT: KIKUCHI, YASUFUMI
; TITLE OF INVENTION: POLYPEPTIDE INDUCING APOPTOSIS
; FILE REFERENCE: 065678/0106
; CURRENT APPLICATION NUMBER: US/10/221,131
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: PCT/JP01/01912
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 09/523,095
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: JP 2000-115246
; PRIOR FILING DATE: 2000-04-17
; PRIOR APPLICATION NUMBER: JP 2000-321822
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 96
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: pscml. MABL1-scfv
US-10-221-131-96

Query Match      16.3%; Score 60.5; DB 6; Length 271;
Best Local Similarity 27.3%; Pred. No. 12;
Matches 18; Conservative 11; Mismatches 24; Indels 13; Gaps 2;

QY      20 YADGKTQTAEFKG-----TFEEATAEAYRYADALKKDN-----GEYTVADVADKGYTL 66
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      73 YNDGTYNEKFKGKATLTSEKSSAAYMELSLASEDSAVYYCARGGYSYDDWGQGTTL 132

QY      67 NIKFAG 72
      : |
```


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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:14:37 ; Search time 17.0137 Seconds
(without alignments)
406.975 Million cell updates/sec

Title: US-08-325-278b-1_copy_81_152
Perfect score: 371
Sequence: 1 KEKTEPEKKEVTIKANLIY.....GEYTVDAKGYTLNIKIFAG 72

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	371	100.0	455	2 A45063	immunoglobulin-bin
2	371	100.0	719	2 A42808	Ig light chain-bin
3	308	83.0	992	2 S54396	protein L precursor
4	171.5	46.2	74	2 A34483	Ig light chain-bin
5	90.5	24.4	395	2 A43700	BNS1 protein - hum
6	89.5	24.1	1576	2 AE0249	probable hemolysin
7	69.5	18.7	256	2 S54803	merozoite surface
8	69	18.6	529	2 S62194	hypothetical prote
9	68.5	18.5	243	2 F72719	hypothetical prote
10	68.5	18.5	279	2 S67132	hypothetical prote
11	68.5	18.5	280	2 I55577	Fc gamma (IgG) rec
12	68.5	18.5	344	2 A41357	Fc gamma (IgG) rec
13	68.5	18.5	374	1 A39878	Fc gamma (IgG) rec
14	66.5	17.9	160	2 I47163	cytolytic trigger
15	66	17.8	448	2 H84782	late embryogenesis
16	65.5	17.7	718	2 F90512	hypothetical prote
17	65.5	17.7	829	2 E64114	translation initia
18	65.5	17.7	458	2 C82199	RTX toxin RtxA Vcl
19	64	17.3	291	2 G95243	hypothetical prote
20	64	17.3	312	2 D98108	hypothetical prote
21	64	17.3	448	2 JC6171	late embryogenesis
22	64	17.3	929	2 T51932	kinesin [imported]
23	63.5	17.1	255	2 F83769	hypothetical prote
24	63.5	17.1	436	2 T18638	hypothetical prote
25	63.5	17.1	582	2 A32613	membrane protein p
26	63.5	17.1	796	2 S50672	hypothetical prote
27	63	17.0	401	2 AH0364	probable HlyD fami
28	63	17.0	499	2 T10680	cytochrome P450 mo
29	63	17.0	950	2 B87611	TonB-dependent rec

30	62.5	16.8	280	2 S35103	bone sialoprotein
31	62.5	16.8	451	1 D84424	tLGD homolog Mj099
32	62.5	16.8	476	1 W2EC	tryptophanase (EC
33	62.5	16.8	476	2 E91209	tryptophanase [imp
34	62.5	16.8	476	2 H86055	tryptophanase [imp
35	62.5	16.8	487	2 B71873	hypothetical prote
36	62.5	16.8	1179	2 T35093	DNA-directed DNA p
37	62	16.7	266	2 A12289	hypothetical prote
38	62	16.7	384	2 G86287	hypothetical prote
39	62	16.7	455	2 D81284	probable fumarate
40	62	16.7	516	2 B64902	probable oligopept
41	62	16.7	658	2 S37494	squalene-hopane cy
42	62	16.7	871	2 D86355	protein T16E15.12
43	61.5	16.6	334	2 C84117	cell shape determi
44	61.5	16.6	479	2 T47561	late embryogenesis
45	61.5	16.6	528	2 D83874	nickel ABC transpo

ALIGNMENTS

RESULT 1
A45063
immunoglobulin-binding protein LG - Peptostreptococcus magnus
C:Species: Peptostreptococcus magnus
C>Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 15-Oct-1999
C:Accession: A45063
R:Kihlberg, B.M.; Sjoerding, U.; Kastern, W.; Bjorck, L.
J. Biol. Chem. 267, 25583-25588, 1992
A:Title: Protein LG: a hybrid molecule with unique immunoglobulin binding properties.
A:Reference number: A45063; MUID:93094283; PMID:1460053
A:Accession: A45063
A:Status: preliminary
A:Molecule type: mRNA; protein
A:Residues: 1-455 <KIR>
A:Cross-references: GB:S50809; NID:q261705; PIDN:AAA03280.1; PID:q261706
A>Note: sequence extracted from NCBI backbone (NCBIN:120302, NCBI:120303)

Query Match 100.0%; Score 371; DB 2; Length 455;
Best Local Similarity 100.0%; Pred. No. 6.6e-30;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	KEKTEPEKKEVTIKANLIYADGKTQTAEFKGTFFETAETAEAYRYADALKKNGEYTVDA 60
DB	102	KEKTEPEKKEVTIKANLIYADGKTQTAEFKGTFFETAETAEAYRYADALKKNGEYTVDA 161
QY	61	DKGYTLNIKIFAG 72
DB	162	DKGYTLNIKIFAG 173

RESULT 2
A42808
Ig light chain-binding protein precursor - Peptostreptococcus magnus
N:Alternate names: protein L
C:Species: Peptostreptococcus magnus
C>Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999
C:Accession: A42808; A41493
R:Kastern, W.; Sjoerding, U.; Bjorck, L.
J. Biol. Chem. 267, 12820-12825, 1992
A:Title: Structure of peptostreptococcal protein L and identification of a repeated i
A:Reference number: A42808; MUID:92316971; PMID:1618782
A:Accession: A42808
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-719 <KAS>
A:Cross-references: GB:M86697
R:Kastern, W.; Holst, E.; Nielsen, E.; Sjoerding, U.; Bjorck, L.
Infect. Immun. 58, 1217-1222, 1990
A:Title: Protein L, a bacterial immunoglobulin-binding protein and possible virulence
A:Reference number: A41493; MUID:90215984; PMID:2108927
A:Accession: A41493
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 202-275 <RA2>
C:Keywords: immunoglobulin

Query Match 100.0%; Score 371; DB 2; Length 719;
Best Local Similarity 100.0%; Pred. No. 1.1e-29;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEKTEPEEKEEVIKANIYADGKTQTAEFGKTFEATAEAYRYADALKKNGEYTVDA 60
|||||
Db 174 KEKTEPEEKEEVIKANIYADGKTQTAEFGKTFEATAEAYRYADALKKNGEYTVDA 233
|||||
QY 61 DKGYTLNKFAG 72
|||||
Db 234 DKGYTLNKFAG 245
|||||

RESULT 3
S54396
protein L precursor - Peptostreptococcus magnus (strain 3316)
C:Species: Peptostreptococcus magnus
A:Variety: Strain 3316
C:Date: 27-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 15-Oct-1999
C:Accession: S54396
R:Murphy, J.P.; Duggleby, C.J.; Atkinson, M.A.; Trowern, A.R.; Atkinson, T.; Goward, C.F.
Mol. Microbiol. 12, 911-920, 1994
A:Title: The functional units of a peptostreptococcal protein L.
A:Reference number: S54396; MUID:95020613; PMID:7934898
A:Accession: S54396
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-992 <MUR>
A:Cross-references: EMBL:L04466; NID:g150673; PIDN:AAA67503.1; PID:g150674

Query Match 83.0%; Score 308; DB 2; Length 992;
Best Local Similarity 84.3%; Pred. No. 3.5e-23;
Matches 59; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 3 KTEPEEKEEVIKANIYADGKTQTAEFGKTFEATAEAYRYADALKKNGEYTVDA 62
:|||||
Db 468 ETEPEEKEEVIKANIYADGKTQTAEFGKTFEATAEAYRYADALKKNGEYTVDA 527
:|||||
QY 63 GYTLNKFAG 72
|||||
Db 528 GYTLNKFAG 537
|||||

RESULT 4
A34483
Ig light chain-binding protein L - Peptostreptococcus magnus (fragments)
C:Species: Peptostreptococcus magnus
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 16-Aug-1996
C:Accession: A34483
R:Akerstroem, B.; Bjoerck, L.
J. Biol. Chem. 264, 19740-19746, 1989
A:Title: Protein L: an immunoglobulin light chain-binding bacterial protein. Characteriz
A:Reference number: A34483; MUID:90062074; PMID:2479638
A:Accession: A34483
A:Molecule type: protein
A:Residues: 1-74 <AKE>
C:Keywords: immunoglobulin

Query Match 46.2%; Score 171.5; DB 2; Length 74;
Best Local Similarity 58.2%; Pred. No. 1.3e-10;
Matches 39; Conservative 5; Mismatches 4; Indels 19; Gaps 2;

QY 2 EKTPEEKEEVIKANIYADGKTQTAEFGKTFEATAEAYRYADALKKNGEYTVDA 45
|||||
Db 9 ETTPEEKEEVIKANIYADGKTQTAEFGKTFEATAEAYRYADALKKNGEYTVDA 65
:|||||
QY 46 DALKNDN 52
:|||||
Db 66 EALKND 72
:|||||

RESULT 5
A43700
BNS1 protein - human
C:Species: Homo sapiens (man)
C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 21-Jul-2000
C:Accession: A43700
R:Ittmann, M.; Greco, A.; Basilico, C.
Mol. Cell. Biol. 7, 3386-3393, 1987
A:Title: Isolation of the human gene that complements a temperature-sensitive cell cy
A:Reference number: A43700; MUID:88065472; PMID:3683386
A:Accession: A43700
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-395 <ITT>
A:Cross-references: GB:M17754; NID:g179512; PIDN:AAA51838.1; PID:g179513
C:Genetics:
A:Gene: GDB:BNS1T
A:Cross-references: GDB:l19728; OMIM:187280
A:Map position: 8pter-8q24

Query Match 24.4%; Score 90.5; DB 2; Length 395;
Best Local Similarity 33.3%; Pred. No. 0.13;
Matches 27; Conservative 10; Mismatches 25; Indels 19; Gaps 3;

QY 3 KTEPEEKEEVIKANIYADGKTQTAEFGKTFEATAEAYRYADALKK 50
|||||
Db 63 KIKEPEKEEVIKKEKRRDRDRQREHGHRGRREVIQSHSIFQGGAEEMK 117
:|||||
QY 51 DNGEYTVDAKGG--YTLNIK 69
:|||||
Db 118 GNWDKTVDSMDGSPSHIINIK 138
:|||||

RESULT 6
AE0249
probable hemolysin YP02045 [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C:Accession: AE0249
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.
ll, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AE0249
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1576 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC90857.1; PID:g15980056; GSPDB:GN00175
C:Genetics:
A:Gene: YPO2045

Query Match 24.1%; Score 89.5; DB 2; Length 1576;
Best Local Similarity 27.5%; Pred. No. 0.7;
Matches 30; Conservative 11; Mismatches 25; Indels 43; Gaps 4;

QY 1 KEKTEPEEKEEVIKANIYADGKTQTAEFGKTFEATAEAYRYADALKKNGEYTVDA 36
|||||
Db 1001 KANTEQEKEVSLRG-----GMTATQEIKGHLGVKAETSGQDSYAEMLVGNINAKSG 1054
:|||||
QY 37 ----ATAPAYRYADALKKNGEYTVDA-----VADKGYTLNKFAG 72
:|||||
Db 1055 VSIKTTGAYYATNIEGNGDITIDAGNNLYFDQVQDSQRSSNIKFSG 1103
:|||||

RESULT 7
S54803
merozoite surface glycoprotein precursor - Theileria parva (fragment)
C:Species: Theileria parva
C:Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Sep-1997

Query Match 18.5%; Score 68.5; DB 2; Length 243;
Best Local Similarity 28.4%; Pred. No. 12;
Matches 19; Conservative 14; Mismatches 33; Indels 1; Gaps 1;

QY 6 EEPKEEVTIKANLIYADGKTQTAEFGTTEEAETAAAYRYADALKKONGEYTVDVADKGYT 65
: : : : : | : : : : : | : : : : : | : : : : :
Db 134 DAPLDVSVKADSGVKGRSKIRPGGVVYEADSSGVKLAI A-PATRGEYWIDVDKSSG 192
: : : : : | : : : : : | : : : : : | : : : : :
QY 66 LNIKFAG 72
: : : : : | : : : : : | : : : : : | : : : : :
Db 193 VTIEFEG 199

RESULT 10
S67132
hypothetical protein YOR239w - yeast (*Saccharomyces cerevisiae*)
N:Alternate names: hypothetical protein O5240
C:Species: *Saccharomyces cerevisiae*
C>Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002
C:Accession: S67132
R:Boyer, J.; Fairhead, C.; Gaillon, L.; Galisson, F.; Michaux, G.; Thierry, A.; DuJon submitted to the Protein Sequence Database, July 1996
A:Reference number: S67104
A:Accession: S67132
A:Molecule type: DNA
A:Residues: 1-279 <BO>
A:CROSS-references: EMBL:Z75147; NID:g1420546; PID:e252406; PID:g1420547; GSPDB:GN000
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:ABP140; MIPS:YOR239W
A:CROSS-references: SGD:S0005765
A:Map position: 15R

Query Match 18.5%; Score 68.5; DB 2; Length 279;
Best Local Similarity 27.5%; Pred. No. 14;
Matches 19; Conservative 14; Mismatches 27; Indels 9; Gaps 1;

QY 1 KEPTPEPKREVTIKANLIYADGKT-----QTAEFGTTEEAETAAAYRYADALKKD 51
: : : : : | : : : : : | : : : : : | : : : : :
Db 81 KPETNEEDEEGSMENKIYSKGENADINVDVFQYKEMENTGAEVLAASSVEESDAIQEG 140
: : : : : | : : : : : | : : : : : | : : : : :
QY 52 NGELYVDVA 60
: : : : : | : : : : : | : : : : : | : : : : :
Db 141 VAEETEGIA 149

RESULT 11
I5577
Fc gamma (IgG) receptor I-B splice form 1 precursor - human
N:Alternate names: CD64
N:Contains: Fc-gamma (IgG) receptor I-B splice form 2
C:Species: *Homo sapiens* (man)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C:Accession: I5577; I70303
R:Porges, A.J.; Redecha, P.B.; Dosbeile, R.; Pan, L.C.; Salmon, J.E.; Kimberly, R.P.
J. Clin. Invest. 90, 2102-2109, 1992
A>Title: Novel Fc gamma receptor I family gene products in human mononuclear cells.
A:Reference number: I5577; MUID:93055454; PMID:1430234
A:Accession: I5577
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-280 <RES>
A:CROSS-references: GB:L03419; NID:g182460; PIDN:AAA35825.1; PID:g292023
A>Note: splice form B1
A:Accession: I70303
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-10,103-153,'A',155-280 <RE2>
A:CROSS-references: GB:L03420; NID:g182461; PIDN:AAA35826.1; PID:g292024
A:Experimental source: mononuclear cells
A>Note: splice form B2
C:Comment: This receptor does not bind monomeric IgG with high affinity.
C:Genetics:

A;Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-374 <RES>
A:Cross-references: GB:I03418; NID:g184840; PIDN:AAA36049.1; PID:g292169
R:Allen, J.M.; Seed, B.
Science 243, 378-381, 1989
A:title: Isolation and expression of functional high-affinity Fc receptor complementa
A:Reference number: A41357; MUID:R9100284; PMID:29111749
A:Accession: B41357
A:Molecule type: mRNA
A:Residues: 1-24,'S','26-337','T','339-374 <AL1>
A:Cross-references: GB:X14356; GB:M21091; NID:g31331; PIDN:CAA32537.1; PID:g31332
R:Allen, J.M.; Seed, B.
Nucleic Acids Res. 16, 11824, 1988
A:title: Nucleotide sequence of three cDNAs for the human high affinity Fc receptor (F
A:Reference number: S03018; MUID:R9098339; PMID:2974947
A:Accession: S03018
A:Molecule type: mRNA
A:Residues: 1-24,'S','26-337','T','339-374 <AL2>
A:Cross-references: EMBL:X14356; NID:g31331; PIDN:CAA32537.1; PID:g31332
R:Perez, C.; Wietzerbin, J.; Benach, P.D.
Mol. Cell. Biol. 13, 2182-2192, 1993
A:title: Two cis-DNA elements involved in myeloid-cell-specific expression and gamma
ism.
A:Reference number: I57525; MUID:93204964; PMID:8455606
A:Accession: I57525
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-8 <RE2>
A:Cross-references: GB:S57204; NID:g298692; PIDN:AAD13887.1; PID:g4261587
C:Genetics:
A:Gene: GDB:FCGR1A; CD64
A:Cross-references: GDB:135911; OMIM:146760
A:Map position: lq21-lq21
C:Superfamily: Fc gamma receptor I; immunoglobulin homology
C:Keywords: alternative splicing; glycoprotein; immunoglobulin receptor; transmembran
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-292/Domain: extracellular #status predicted <EXT>
F:117-170/Domain: immunoglobulin homology <IMM2>
F:293-313/Domain: transmembrane #status predicted <TMW>
F:59,78,152,159,163,195,240/Binding site: carbohydrate (Asn) (covalent) #status predi

Query Match 18.5%; Score 68.5; DB 1; Length 374;
Best Local Similarity 31.2%; Pred. No. 20;
Matches 15; Conservative 10; Mismatches 22; Indels 1; Gaps 1;

QY 9 KEVTTKANLIYADGKTQAEF-KGTFEATATAEAYRYADAKKDNGEY 55
:| |: ::: :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 36 EETVTLHCEVLHLPGSSSTOWFLNGTATQTSTPSYRITSASVNDSEY 83
:| |: ::: :|| :|| :|| :|| :|| :|| :|| :|| :||

RESULT 14
I47163
cytolytic trigger molecule G7 - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47163
R:Halloran, P.J.; Sweeney, S.E.; Strohmaier, C.M.; Kim, Y.B.
J. Immunol. 153, 2631-2641, 1994
A:title: Molecular cloning and identification of the porcine cytolytic trigger molecu
A:Reference number: I47163; MUID:94358430; PMID:8077673
A:Accession: I47163
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-160 <HAL>
A:Cross-references: EMBL:U08991; NID:g476167; PIDN:AAA57188.1; PID:g476168
C:Superfamily: Fc gamma receptor III; immunoglobulin homology
F:14-65/Domain: immunoglobulin homology <IMW>

Query Match 17.9%; Score 66.5; DB 2; Length 160;
Best Local Similarity 34.7%; Pred. No. 13;
Matches 17; Conservative 6; Mismatches 25; Indels 1; Gaps 1;

RESULT 15

R.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999

A;Accession: H84782

A; Molecule type: DNA

A: Cross-references: GB: A

A: Gene. At2g36640

A; Map position: 2
C: Superfamily: pea seed

Quarry Match

Best Local Similarity

100

—
..
—
—
..
—

1

—

Search completed: September 3, 2003, 11:24:29
Job time : 18.0137 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:04:52 ; Search time 9.12329 Seconds
(without alignments)
371.130 Million cell updates/sec

Title: US-08-325-278B-1_COPY_81_152

Perfect score: 371

Sequence: 1 KEKTEPKKEVTIKANLIY.....GEYTVDVADKGYTLNIKFAK 72

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 segs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98.5	26.5	398	1	RPC4_HUMAN
2	93.5	25.2	398	1	RPC4_MOUSE
3	72.5	19.5	536	1	INR2_SHEEP
4	71	19.1	634	1	GYYR_BORHE
5	68.5	18.5	374	1	FCGI_HUMAN
6	68.5	18.5	627	1	ABPX_YEAST
7	65.5	17.7	829	1	IF2_HAEN
8	64.5	17.4	370	1	MYOM_APLCA
9	64	17.3	600	1	DNAK_MYCHY
10	63.5	17.1	796	1	YE29_YEAST
11	63.5	17.1	1461	1	A10B_HUMAN
12	63	17.0	499	1	C831_ARATH
13	62.5	16.8	300	1	SIAL_PIG
14	62.5	16.8	451	1	Y996_METJA
15	62.5	16.8	471	1	TNAA_ECO57
16	62.5	16.8	471	1	TNAA_ECOLI
17	62.5	16.8	642	1	DNAK_FRATU
18	62.5	16.8	1179	1	DP3A_STRCO
19	62	16.7	516	1	YD05_ECOLI
20	62	16.7	658	1	SQRC_ZYMO
21	61	16.4	1410	1	RBL1_HUMAN
22	61	16.4	1433	1	SUBF_BACSU
23	60.5	16.3	444	1	SLAP_LACAC
24	60.5	16.3	637	1	DNAK_PSEAE
25	60.5	16.3	1454	1	CSP2_HUMAN
26	60.5	16.3	2805	1	MAPA_HUMAN
27	60	16.2	499	1	LEUL_PYRFU
28	60	16.2	569	1	SYR_XANAC
29	60	16.2	1829	1	Y296_HUMAN
30	59.5	16.0	269	1	T2S1_STRFI
31	59.5	16.0	350	1	Y957_METJA
32	59.5	16.0	404	1	ASSY_VIBCH
33	59.5	16.0	553	1	HIS5_EWENI

RESULT 1

RPC4_HUMAN	1176	1	SLAP_BACSH	34	59.5	16.0
ID	RPC4_HUMAN	STANDARD;	PRT; 398 AA.	35	59.5	
AC	P05423; Q9BPV7; Q9BP21; Q9BXB3;			36	59	16.0
DT	01-NOV-1988 (Rel. 09, Created)			37	59	15.9
DT	15-SEP-2003 (Rel. 42, Last sequence update)			38	59	15.9
DT	15-SEP-2003 (Rel. 42, Last annotation update)			39	59	15.9
DE	DNA-directed RNA polymerase III 47 kDa polypeptide (EC 2.7.7.6) (RNA			40	59	15.9
DE	polymerase C subunit 4) (RPC4) (RPC53) (BN51 protein).			41	59	15.9
GN	BN51T OR BN51 OR POLR3D.			42	58.5	15.8
OS	Homo sapiens (Human).			43	58.5	15.8
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			44	58.5	15.8
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			45	58.5	15.8
OX	NCBI_TaxID=9606;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=88065472; PubMed=3683386;					
RA	Ittmann M., Greco A., Basilico C.;					
RT	"Isolation of the human gene that complements a temperature-sensitive					
RL	cell cycle mutation in BHK cells.";					
RN	Mol. Cell. Biol. 7:3386-3393(1987).					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=22278866; PubMed=12391170;					
RA	Hu P., Wu S., Sun Y., Yuan C.-C., Kobayashi R., Myers M.P.,					
RT	Hernandez N.;					
RL	"Characterization of human RNA polymerase III identifies orthologues					
RN	for Saccharomyces cerevisiae RNA polymerase III subunits.";					
RP	Mol. Cell. Biol. 22:8044-8055(2002).					
RP	SEQUENCE FROM N.A.					
RX	TISSUE=Lung, and Lymph;					
RX	MEDLINE=22388257; PubMed=12477932;					
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,					
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,					
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,					
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,					
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,					
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,					
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,					
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,					
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,					
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,					
RA	Villalón D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,					
RA	Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,					
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,					
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,					
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,					
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,					
RT	Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;					
RT	"Generation and initial analysis of more than 15,000 full-length					
RL	human and mouse cDNA sequences.";					
RN	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).					
RP	SEQUENCE OF 1-50 FROM N.A.					
RX	MEDLINE=21282972; PubMed=11279001;					

P38537 bacillus sp
P32386 saccharomyc
P07891 chlamydomon
Q9pab5 ureaplasma
Q88792 mus musculus
Q8u089 pyrococcus
Q56232 thermus the
Q934g3 aquifex pyr
Q28942 sus scrofa
Q8rc30 thermoanaer
Q28938 sus scrofa


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FT DOMAIN          268      536     CYTOPLASMIC (POTENTIAL).
FT DOMAIN          358      372     3 X 5 AA TANDEM REPEATS OF S-L-E-D-C.
FT REPEAT         358      362     1.
FT REPEAT         363      367     2.
FT REPEAT         368      372     3.
FT DISULFID       85       93     BY SIMILARITY.
FT DISULFID      210      230     BY SIMILARITY.
FT CARBOHYD       58       58
FT CARBOHYD      87       87     N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD     101      101     N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD     147      147     N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD     191      191     N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE      536 AA;   60260 MW;  1055F27D80545150 CRC64;

Query Match           19.5%; Score 72.5; DB 1; Length 536;
Best Local Similarity 31.1%; Pred. No. 4.2;
Matches 23; Conservative 12; Mismatches 30; Indels 9; Gaps 4;

Qy    4 TPEEPKEVITKANLIYADGKGTQTAEPKGT---FEETAAEAYRYADAL--KKNGEVTVD 58
        :| | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db    461 SPSPPEETAVIDELDLSTESSLLIVASEGTQLPTDPDSMECLRPQDALSDKSDTSDDVD 520

Qy    59 VADKGY---TLNLIK 69
        :| | ||| :||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db    521 IGD-GYIIVQNVLNK 533

RESULT 4
GYRB_BORHE STANDARD; PRT; 634 AA.
AC Q9ZFK1;
DT 30-MAY-2000 (Rel. 39, Created)
DI 30-MAY-2000 (Rel. 39, Last sequence update)
DE DT 30-MAY-2000 (Rel. 39, Last annotation update)
GE DNA gyrase subunit B (EC 5.99.1.3).
GN GrnB.
OS Borrelia hermsii.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=140;
[1]
RN STRAIN=HSL;
RP SEQUENCE FROM N.A.
RC Samuels D.S.; Kimmel B.J., Huang W.M.;
RT "Mutations in Borrelia hermsii gyrB confer resistance to coumermycin A1."
RL Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: DNA GYRASE NEGATIVELY SUPERCOILS CLOSED CIRCULAR DOUBLE-STRANDED DNA IN AN ATP-DEPENDENT MANNER AND ALSO CATALYZES THE INTERCONVERSION OF OTHER TOPOLOGICAL ISOMERS OF DOUBLE-STRANDED DNA RINGS, INCLUDING CATENANES AND KNOTTED RINGS.
CC -!- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining of double-stranded DNA.
CC -!- SUBUNIT: MADE UP OF TWO CHAINS. THE A CHAIN IS RESPONSIBLE FOR DNA BREAKAGE AND REJOINING; THE B CHAIN CATALYZES ATP HYDROLYSIS. THE ENZYME FORMS AN A2B2 Tetramer.
CC -!- SIMILARITY: Belongs to the type II topoisomerase family.
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CC EMBL; AF098862; AAC72846.1; -.
DR HSSP; P06982; 1AJ6.
DR InterPro; IPR003594; ATpbind_Atptase.
DR InterPro; IPR002288; DNA_gyrase_C.
DR InterPro; IPR000565; DNA_gyrB.
DR InterPro; IPR001241; DNA_topoisoII.
DR InterPro; IPR006171; Toprim_dom.
DR Pfam; PF00204; DNA_gytaseB_1.
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DR Pfam: PF00986; DNA_gyraseB_C; 1.
DR Pfam: PF02518; HATPase_C; 1.
DR Pfam: PF01751; Toprim; 1.
DR PRINTS; PR00418; TPI2FAMILY.
DR ProDom; PD149633; DNA_gyraseB_C; 1.
DR SMART; SM00387; HATPase_C; 1.
DR SMART; SM00433; TOP2c; 1.
DR TIGRfams; TIGR01059; gyfB; 1.
DR PROSITE; PS00177; TOPOISOMERASE_II; 1.
DR Topoisomerase; Isomerase; ATP-binding.
SQ SEQUENCE 634 AA; 70848 MW; 5E58C5F32126833C CRC64;

Query Match          19.1%; Score 71; DB 1; Length 634;
Best Local Similarity 36.4%; Pred. No. 7.1;
Matches 20; Conservative 10; Mismatches 23; Indels 2; Gaps 1;

QY 17 NLIYADGKTQTAEFGTGFEEATAYRVADALKDNGEYTVDAVKGYT--LNLIK 69
   : : | | | | | : | : | : | : | : | : | : | : | : | : | : |
Db 270 NINTREGTHVAGFKSGFLKAMSEAFRDSKISKDVPSLTLDKFEGLTAVISIK 324

RESULT 5
FCGL_HUMAN          STANDARD;          PRT;          374 AA.
AC P12314; P12315;
DT 01-OCT-1989 (Rel. 12, Created)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE High affinity immunoglobulin gamma Fc receptor I precursor (Fc-gamma
DE RI) (FCRI) (IGG Fc receptor I) (CD64).
GN FCGRIA OR FCGRI OR FCGI OR IGFRI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89098339; PubMed=2974947;
RA Allen J.M., Seed B.;
RT "Nucleotide sequence of three cDNAs for the human high affinity Fc
RT receptor (FcRI).";
RL Nucleic Acids Res. 16:11824-11824(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89100284; PubMed=2911749;
RA Allen J.M., Seed B.;
RT "Isolation and expression of functional high-affinity Fc receptor
RT complementary DNAs.";
RL Science 243:378-381(1989).
CC 1- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULINS GAMMA. HIGH
CC 1- AFFINITY RECEPTOR.
CC 1- SUBCELLULAR LOCATION: Type I membrane protein.
CC 1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=A;
CC IsoId=P12314-1; Sequence=Displayed;
CC IsoId=P12314-2; Sequence=VSP_002637;
CC 1- TISSUE SPECIFICITY: MONOCYTE/MACROPHAGE-SPECIFIC.
CC 1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC 1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC 1- DATABASE: NAME=PROW; NOTE=CD guide CD64 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd64.htm".
CC
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CC
DR EMBL; X14356; CAA32537.1; .

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DR EMBL; X14355; CAA32536.1; .
DR HSP; P12319; IALS.
DR Genew; HGNC:3613; FCGRIA.
DR MIM; 146760; .
DR GO; GO:0005057; F:receptor signaling protein activity; TAS.
DR GO; GO:0006955; P:immune response; TAS.
DR GO; GO:0006911; P:phagocytosis, engulfment; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig.
DR Pfam; PF00047; Ig; 3.
DR Pfam; SM00409; Ig; 3.
DR PROSITE; PS00835; IG-LIKE; 3.
KW IgG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
KW Immunoglobulin domain; Repeat; Alternative splicing; Polymorphism.
FT SIGNAL 1 21
FT CHAIN 22 374
FT RECEPTOR I. HIGH AFFINITY IMMUNOGLOBULIN GAMMA FC
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM
FT DOMAIN 22 292
FT TRANSMEM 293 313
FT DOMAIN 314 374
FT DOMAIN 22 101
FT DOMAIN 95 184
FT DOMAIN 190 277
FT DISULFID 43 85
FT DISULFID 124 168
FT DISULFID 212 260
FT CARBOHYD 59 59
FT CARBOHYD 78 78
FT CARBOHYD 152 152
FT CARBOHYD 159 159
FT CARBOHYD 163 163
FT CARBOHYD 195 195
FT CARBOHYD 240 240
FT VARSPLIC 333 374
FT
FT VARIANT 26 26
FT VARIANT 59 59
FT CONFLICT 25 25
FT SEQUENCE 374 AA; 42605 MW; 2C2AA8103ECF16E6 CRC64;
Query Match          18.5%; Score 68.5; DB 1; Length 374;
Best Local Similarity 31.2%; Pred. No. 7.4;
Matches 15; Conservative 10; Mismatches 22; Indels 1; Gaps 1;

QY 9 KEEVTKANLIYADGKTQTAEF-KCTFEATATAEAYRYADALKKDNGEY 55
   : | | | : : : | : | | : : : | : | : : | : | : | : | : | : |
Db 36 EETVTLHCEVLHPLGSSSTQWFLNGTATQTSTPSYRITSASVDSNGEY 83

RESULT 6
ABPX_YEAST          STANDARD;          PRT;          627 AA.
AC Q08641; Q08644;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Actin-binding protein ABP140.
GN ABP140 OR YOR239W/YOR240W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=S288c / FY1679;
RX MEDLINE=97127829; PubMed=8972580;
RA Boyer J., Michaux G., Fairhead C., Gaillon L., Dujon B.;
RA "Sequence and analysis of a 26.9 kb fragment from chromosome XV of

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RT the yeast Saccharomyces cerevisiae. ";
RL Yeast 12:1575-1586(1996).
RN [2]
RP PARTIAL SEQUENCE FROM N.A., SEQUENCE OF 1-12; 38-72; 102-115; 244-286;
RP 560-574 AND 598-608, FUNCTION, AND SUBCELLULAR LOCATION.
RC STRAIN-BJ5457;
RX MEDLINE=96127445; PubMed=9467951;
RA Asakura T., Sasaki T., Nagano F., Satoh A., Obaishi H., Nishioka H.,
RA Imanura H., Hotta K., Tanaka K., Nakanishi H., Takai Y.;
RT "Isolation and characterization of a novel actin filament-binding
RT protein from Saccharomyces cerevisiae.";
RL Oncogene 16:121-130(1998).
CC -!- FUNCTION: Binds F-actin and shows weak F-actin crosslinking
CC activity.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and cortical cytoskeleton.
CC -!- MISCELLANEOUS: A RIBOSOMAL FRAMESHIFT OCCURS BETWEEN THE CODONS
CC FOR LEU-276 AND GLY-277.
CC -----
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CC -----
DR EMBL; Z75147; CAA99460.1; ALT-SEQ.
DR EMBL; Z75147; CAA99461.1; ALT-SEQ.
DR SGD; S0005765; ABP140.
DR GO; GO:0005884; C:actin filament; IDA.
DR GO; GO:0003780; F:actin cross-linking activity; IDA.
DR GO; GO:0030036; P:actin cytoskeleton organization and biogenesis; IDA.
DR InterPro; IPR001601; Methyltransf.
DR InterPro; IPR000051; SAM_bind.
KW Actin-binding; Cytoskeleton; Ribosomal frameshift.
FT INIT_MET 0
FT SEQUENCE 627 AA; 71354 MW; D4E55F9485412F39 CRC64;
SQ
Query Match 18.5%; Score 68.5; DB 1; Length 627;
Best Local Similarity 27.5%; Pred. No.13;
Matches 19; Conservative 14; Mismatches 27; Indels 9; Gaps 1;
QY 1 KEKTPPEKPEEYTIKANLIYADGKT-----QTAPEKGTGFEATAEAYADALKKD 51
Db 80 KPETNEDEEGSGMSNKIYSGENADINVDQYKEMTGNTGAELVSSVEESDAIOBG 139
QY 52 NGEYTVDA 60
Db 140 VAEETEGIA 148
RESULT 7
IF2_HAEIN ID IF2_HAEIN STANDARD; PRT; 829 AA.
AC P44323.
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Translation initiation factor IF-2.
GN INF OR H11284.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

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RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).
CC -!- FUNCTION: One of the essential components for the initiation of
CC protein synthesis. Protects formylmethionyl-tRNA from spontaneous
CC hydrolysis and promotes its binding to the 30S ribosomal subunits.
CC Also involved in the hydrolysis of GTP during the formation of the
CC 70S ribosomal complex.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE IF-2 FAMILY.
CC -----
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CC -----
DR EMBL; U32808; AAC22933.1; -.
DR PIR; E64114; E64114.
DR TIGR; H11284; -.
DR HAMAP; MF_00100; -.
DR InterPro; IPR000795; EF_GTPbind.
DR InterPro; IPR004161; EFTU_D2.
DR InterPro; IPR00178; IF2.
DR InterPro; IPR006847; IF2_N.
DR InterPro; IPR005325; Small_GTP.
DR Pfam; PF00009; GTP_EFTU; 1.
DR Pfam; PF03144; GTP_EFTU_D2; 2.
DR Pfam; PF04760; IF2_N; 1.
DR ProDom; PD186100; IF2; 1.
DR TIGRFAMS; TIGR00487; IF-2; 1.
DR TIGRFAMS; TIGR00231; Small_GTP; 1.
DR PROSITE; PS01176; IF2; 1.
KW Initiation factor; Protein biosynthesis; GTP-binding;
KW Complete proteome.
FT DOMAIN 331 480 G-DOMAIN.
FT NP_BIND 337 344 GTP (BY SIMILARITY).
FT NP_BIND 384 388 GTP (BY SIMILARITY).
FT NP_BIND 438 441 GTP (BY SIMILARITY).
SQ SEQUENCE 829 AA; 90551 MW; 75B20AC4CF610AF7 CRC64;
Query Match 17.7%; Score 65.5; DB 1; Length 829;
Best Local Similarity 29.1%; Pred. No.35;
Matches 25; Conservative 12; Mismatches 32; Indels 17; Gaps 3;
QY 1 KEKTPPEKPEEYTIKANLIYAD---GKTQTAPEKGTGFE-----ATAEAYRYA 45
Db 86 KAEAKPKVSAVDSRAKSVESKEKRAKAGEALRRKAEELAKQAEQARRAVEAKRYA 145
QY 46 DALKKDNGEYTVDAVKGYTLNPKFA 71
Db 146 EADSDNESSESDYSD--YNLSRYA 169
RESULT 8
MYOM_APLCA ID MYOM_APLCA STANDARD; PRT; 370 AA.
AC P15513; Q07974; Q27916;
DT 01-APR-1990 (Rel. 14, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Myomodulin neuropeptides precursor [Contains: Myomodulin A (MM-A)
DE (PMSMLRL-amide) (Neuron B16 peptide); Myomodulin B (MM-B) (GSYRMRL-
DE amide); Myomodulin D (MM-D) (GLSMLRL-amide); Myomodulin F (MM-F)
DE (SLNMLRL-amide); Myomodulin G (MM-G) (TLSMLRL-amide); Myomodulin H
DE (MM-H) (GLHMLRL-amide); Myomodulin I (MM-I) (SLSMLRL-amide)].
DE MYOMODI.
GN MYOMODI.

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OS Aplysia californica (California sea hare).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspidea;
 OC Aplousiidae; Aplysiidae; Aplysia.
 OX NCBI_TaxID=6500;
 RN [1]
 RP SEQUENCE FROM N.A., VARIANT LEU-362, AND TISSUE SPECIFICITY.
 RC TISSUE=Abdominal ganglion, Cerebral ganglion, and CNS;
 RX MEDLINE=93135828; PubMed=8422272;
 RA Lopez V., Wickham L., Desgroseillers L.;
 RT "Molecular cloning of myomodulin cDNA, a neuropeptide precursor gene
 RL expressed in neuron L10 of Aplysia californica.";
 RN DNA Cell Biol. 12:53-61(1993).
 [2]
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RC TISSUE=Buccal ganglion;
 RX MEDLINE=93340709; PubMed=8340812;
 RA Miller M.W., Reushausen S., Vittek A., Stamm S., Kupfermann I.,
 RA Brosius J., Weiss K.R.;
 RT "The myomodulin-related neuropeptides: characterization of a gene
 RL encoding a family of peptide cotransmitters in Aplysia.";
 RN J. Neurosci. 13:3358-3367(1993).
 [3]
 RP SEQUENCE OF 53-60. AMIDATION, FUNCTION, AND TISSUE SPECIFICITY.
 RC TISSUE=Buccal muscle;
 RX MEDLINE=92158798; PubMed=1788132;
 RA Cropper E.C., Vilim F.S., Alevisos A., Tenenbaum R., Kolks M.A.G.,
 RA Rosen S., Kupfermann I., Weiss K.R.;
 RT "Structure, bioactivity, and cellular localization of myomodulin B: a
 RL novel Aplysia peptide.";
 RN Peptides 12:683-690(1991).
 [4]
 RP SEQUENCE OF 203-209 AND 358-364, AND FUNCTION.
 RC TISSUE=Buccal muscle;
 RX MEDLINE=96063267; PubMed=7472354;
 RA Brezina V., Bank B., Cropper E.C., Rosen S., Vilim F.S.,
 RA Kupfermann I., Weiss K.R.;
 RT "Nine members of the myomodulin family of peptide cotransmitters at
 RL the B16-ARC neuromuscular junction of Aplysia.";
 RN J. Neurophysiol. 74:54-72(1995).
 [5]
 RP SEQUENCE OF MYOMODULIN A, AMIDATION, AND FUNCTION.
 RC TISSUE=Buccal muscle;
 RX MEDLINE=87261010; PubMed=3474664;
 RA Cropper E.C., Tenenbaum R., Kolks M.A.G., Kupfermann I., Weiss K.R.;
 RT "Myomodulin: a bioactive neuropeptide present in an identified
 RL cholinergic buccal motor neuron of Aplysia.";
 CC Proc. Natl. Acad. Sci. U.S.A. 84:5483-5486(1987).
 CC -!- FUNCTION: Exogenous application of myomodulins potentiates ARC
 CC muscle contraction.
 CC -!- TISSUE SPECIFICITY: Expressed in all ganglia of the CNS, but only
 CC in a subset of neurons including L10 in the abdominal ganglion and
 CC B16 in the buccal ganglion.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: L01421; AAA27758.1; -
 DR EMBL: S55210; AAB25131.1; -
 DR EMBL: S55211; AAB25132.1; -
 DR EMBL: S64300; AAB27697.1; -
 KW Neuropeptide; Amidation; Repeat; Cleavage on pair of basic residues;
 KW Signal.
 FT SIGNAL. 1 18 POTENTIAL.
 FT PROPEP 19 50 POTENTIAL.
 FT PEPTIDE 53 60 MYOMODULIN B.
 FT PEPTIDE 63 69 MYOMODULIN H (POTENTIAL).
 FT PROPEP 73 190 POTENTIAL.

FT PEPTIDE 193
 FT PEPTIDE 203
 FT PROPEP 213
 FT PEPTIDE 240
 FT PEPTIDE 250
 FT PEPTIDE 260
 FT PEPTIDE 270
 FT PEPTIDE 280
 FT PEPTIDE 290
 FT PEPTIDE 300
 FT PEPTIDE 310
 FT PEPTIDE 320
 FT PEPTIDE 330
 FT PEPTIDE 340
 FT PROPEP 350
 FT PROPEP 358
 FT PROPEP 368
 FT MOD_RES 60
 FT MOD_RES 69
 FT MOD_RES 199
 FT MOD_RES 209
 FT MOD_RES 246
 FT MOD_RES 256
 FT MOD_RES 266
 FT MOD_RES 276
 FT MOD_RES 286
 FT MOD_RES 296
 FT MOD_RES 306
 FT MOD_RES 316
 FT MOD_RES 326
 FT MOD_RES 336
 FT MOD_RES 346
 FT MOD_RES 364
 FT VARIANT 362
 FT CONFLICT 231
 SQ SEQUENCE 370 AA; 42253 MW; 3A792085939C88CB CRC64;
 Query Match 17.4%; Score 64.5; DB 1; Length 370;
 Best Local Similarity 29.0%; Pred. No. 19;
 Matches 27; Conservative 13; Mismatches 24; Indels 29; Gaps 6;
 QY 1 KEKTEPEPEKEVTIKR--NLI---YADGKTQTAEFGT-----FEEATAEAY-RY----- 44
 Db 71 KRGGVPEPESEENLETLLNLLQGYSDVPEPSEFDDTDLAYPYEYDAPAHPRERSTP 130
 QY 45 -----ADALKK-----DNGEYTVDVADKGY 64
 Db 131 PTDGVVAPDVLQKGSSEFEDFGDSQDSDEGY 163
 RESULT 9
 ID DNAX_MYCHY STANDARD; PRT; 600 AA.
 AC Q49539;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Chaperone protein dnax (Heat shock protein 70) (Heat shock 70 kDa
 DE protein) (HSP70) (65 kDa protein) (P65).
 GN DNAX.
 OS Mycoplasma hyopneumoniae.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2099;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=232;
 RA Chou S.Y., Shiu D.;
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.

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CC EMBL; U18922; AAB64696.1; -.
CC PIR; S50672; S50672.
CC TRANSFAC; T03423; -.
CC SGD; SO000971; RPH1.
CC DR GO; GO:0005634; C:nucleus; IC.
CC DR GO; GO:0016566; F:specific transcriptional repressor activity; IDA.
CC DR GO; GO:0006281; P:DNA repair; IMP.
CC DR GO; GO:0000122; P:negative regulation of transcription from P. .; IDA.
CC DR InterPro; IPR003347; TF_JmjC.
CC DR InterPro; IPR003349; TF_JmjN.
CC DR InterPro; IPR007087; Znf_C2H2.
CC DR Pfam; PF02373; jmjC; 1.
CC DR Pfam; PF02375; jmjN; 1.
CC DR Pfam; PF00096; zf-C2H2; 2.
CC DR ProDom; PD000003; Znf_C2H2; 1.
CC DR SMART; SM00558; JmjC; 1.
CC DR SMART; SM00545; JmjN; 1.
CC DR SMART; SM00355; Znf_C2H2; 2.
CC DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
CC DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 2.
CC KW Hypothetical protein; Nuclear protein; Zinc-finger; Metal-binding;
KW DNA-binding; Repeat.
CC FT 2N.FING 709 732 C2H2-TYPE 1.
CC FT 2N.FING 738 756 C2H2-TYPE 2.
CC SQ SEQUENCE 796 AA; 90211 MW; 606C27836E1600F5 CRC64;
Query Match 17.1%; Score 63.5; DB 1; Length 796;
Best Local Similarity 25.8%; Pred.No.53;
Matches 17; Conservative 11; Mismatches 29; Indels 9; Gaps 1;
QY 5 PESPKEVITKANLIYADGVTQTAEFKGTTEATAEAAYRADALKDNGEYTDVDADKY 64
Db 111 PEDPKARNRKGVSVKSTKLKLNPFSENFIDDFEQFR-----TETIDLSDFN 161
|::|||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 65 TLNIKF 70
|::|
Db 162 TERLKF 167
RESULT 11
A10B_HUMAN STANDARD; PRt; 1461 AA.
ID AC Q94823; Q9H725;
DT 30-MAY-2000 (Rel. 39, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Potential phospholipid-transporting ATPase VB (EC 3.6.3.1).
GN ATP10B OR ATPVB OR KIAA0715.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM B).
RC TISSUE=Amalgama;
RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
RA Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
RA Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
RA Isogai T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
[2]
RP SEQUENCE FROM N.A. (ISOFORM C).
RC TISSUE=Colon;
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Oktajari R., Ota T., Suzuki Y., Obavashi M., Nishi T., Shibahara T.,

```

FT	DOMAIN	1274	1291	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1292	1316	POTENTIAL.
FT	DOMAIN	1317	1461	CYTOPLASMIC (POTENTIAL).
FT	MOD_RES	433	433	PHOSPHORYLATION (BY SIMILARITY).
FT	METAL	1055	1055	MAGNESIUM (BY SIMILARITY).
FT	METAL	1059	1059	MAGNESIUM (BY SIMILARITY).
FT	VARSPLIC	1	156	MALVSQSSWHKQWRVDRGPHCFSESTPILLSPEKGRQSYN
FT				LTQQRVPPNSIFQDWEESRRYPGNRTCTTKYTLFTFL
FT				PRNLFQDFHRWANLYFLVLINWMPSEVFRHEITMLPLA
FT				IVLFVIMKIDGMEQFKRFDKAINCSNIYE -> MKKE
FT				GRKWKRKDKRVRVSNLLFEGWHSKPNRHRGNOIKF
FT				SKYTVLSPVKNIEQFLHRFANLYFVGIAVLNFPVNAQF
FT				PEVSMIPCVILATATKDAWEDLRRYKSDKVINRECLY
FT				S (in isoform C).
FT				/Fttid-vsp_007305.
FT	VARSPLIC	461	529	AKRLTEPKLDSGEETQYQCLFSARWAQDPATMRSQKG
FT				AQPLRRSQSARVPYIQGHYRORSMGHRES -> GIEAPKGS
FT				LSQRRKPKALLNRNEIKDILIALLEAVWHFKLLPVLWS
FT				LSQIRAVPTICKLSFVYKG (in isoform B and
FT				isoform C).
FT				/Fttid-vsp_007306.
FT	VARSPLIC	530	1461	Missing (in isoform B and isoform C).
FT				/Fttid-vsp_007307.
FT	CONFLICT	217	217	C -> R (IN REF. 1).
FT	CONFLICT	234	234	F -> S (IN REF. 2).
FT	SEQUENCE	1461 AA;	165390 MW;	2676B90416B6541 CRC64;
QY	Query Match	17.1%;	Score 63.5;	DB 1; Length 1461;
QY	Best Local Similarity	40.5%;	Pred. No. 1e+02;	
QY	Matches	17;	Conservative	5; Mismatches
QY				19; Indels
QY				1; Gaps
DB		3 KTPPEPKPEVITKANLIYADGKTQTAEFGTFEEATAEAVRY 44		
DB				
DB		981 KTPSITSEAVVPEAGLV-IDGKTLNAIFQGLKKEKLELTQY 1021		
RESULT 12				
RC831_ARATH				
ID	C831_ARATH	STANDARD;	PRT;	499 AA.
AC	O65782;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Cytochrome P450 83B1 (EC 1.14.-.-).			
DE	CP83B1 OR AF4G31500 OR F3L17.70.			
GN	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophyta;			
OC	Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsi			
OX	NCBI_TaxID=3702;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Columbia;			
RC	MEDLINE=98281573; PubMed=9620263;			
RA	Mizutani M., Ward E., Ohta D.			
RA	"Cytochrome P450 superfamily in Arabidopsis thaliana: isolation of			
RT	cDNAs, differential expression, and RFLP mapping of multiple			
RL	cytochromes P450."			
RL	Plant Mol. Biol. 37:39-52(1998).			
RP	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Columbia;			
RC	MEDLINE=20083488; PubMed=10617198;			
RA	Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,			
RA	Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,			
RA	Harris B., Ansoorge W., Brandt P., Grivell L.A., Rieger M.,			
RA	Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,			
RA	Kreis M., Delsen M., Puigdomenech P., Watson M., Schmidheini T.,			
RA	Reichert B., Portetelle D., Perez-Alonso M., Bontury M., Bancroft I.,			
RA	Vos P., Hohnel J., Zimmermann W., Wedler H., Robben J.,			
RA	Langham S.-A., McCullagh B., Billam L., Robben J.,			
RA	Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,			
RA	Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,			

RA Weitzenecker T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA Berner S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA De Keyser A., Buyschaert C., Gielen J., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLeay K., Mayes R.,
RA Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Borkova D., Bloeker H., Scharfe M., Grimm M., Loehner T., H.,
RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Partmann B., Granderath K., Dauner D., Herzl A.,
RA Neumann S., Agrifoglio A., Vitale D., Liguori R., Piravandi E.,
RA Massenet O., Quigley F., Clabaud G., Muendlein A., Feiler R.,
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Cheford F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Bagues M., Terol J., Torres A.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bielke C.,
RA Frisman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshua C.,
RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
RA Grant S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
RA Chen E., Marra M., Martienssen R., McCombie W.R.,
RA "Sequence and analysis of chromosome 4 of the plant Arabidopsis
RA thaliana.";
RA Nature 402:769-777(1999).
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
CC -----
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CC -----
DR EMBL; D78598; BAA28531.1; -;
DR EMBL; AL080283; CAB45909.1; -;
DR EMBL; AL161579; CAB79868.1; -;
DR PIR; T10680; T10680.
DR InterPro: IPR001128; Cytochrome_P450.
DR Pfam; PF00067; p450; 1.
DR PRINTS; PR00385; p450.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Transmembrane; Heme; Multigene family.
FT TRANSMEM 3 23 POTENTIAL.
FT METAL 441 441 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 499 AA; 56846 MW; CCA2D733E7D00D7B CRC64;
Query Match 17.0%; Score 63; DB 1; Length 499;
Best Local Similarity 26.8%; Pred. No. 37;
Matches 22; Conservative 7; Mismatches 31; Indels 22; Gaps 2;
QY 5 PEPKPEVTIKANLIYADGKTQTAEFKGTGFEA-----TAEA-----Y 42
Db 257 PNPKEVETESFIDLLMQIKDQFSIKFTHEVKNKMLLDIVVPGTDAARVVWVMTYLI 316
QY 43 RYADALKKNGEYTVVDADKY 64
Db 317 KYPEAMKKAQDEVRISVIGDKGY 338
RESULT 13

SIAL_PIG STANDARD; .PRT; 300 AA.
AC P31936;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bone sialoprotein II (BSP II) (Cell-binding sialoprotein) (Integrin-
DE binding sialoprotein).
GN IBSP.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Theria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE OF 1-20.
RC TISSUE=Bone;
RX MEDLINE=90237064; PubMed=2332443;
RA Zhang Q., Domenicucci C., Goldberg H.A., Wrana J.L., Sodek J.;
RT "Characterization of fetal porcine bone sialoproteins, secreted
RT phosphoprotein I (SPPI, osteopontin), bone sialoprotein, and a 23-kDa
RT glycoprotein. Demonstration that the 23-kDa glycoprotein is derived
RT from the carboxyl terminus of SPPI.";
RL J. Biol. Chem. 265:7583-7589(1990).
[2]
RP SEQUENCE OF 21-300 FROM N.A.
RX MEDLINE=94142682; PubMed=8309422;
RA Shapiro H.S., Chen J., Wrana J.L., Zhang Q., Blum M., Sodek J.;
RT "Characterization of porcine bone sialoprotein: primary structure and
RT cellular expression.";
RL Matrix 13:431-440(1993).
CC -1- FUNCTION: BINDS TIGHTLY TO HYDROXYAPATITE. APPEARS TO FORM AN
CC INTEGRAL PART OF THE MINERALIZED MATRIX. PROBABLY IMPORTANT TO
CC CELL-MATRIX INTERACTION. PROMOTES ARG-GLY-ASP-DEPENDENT CELL
CC ATTACHMENT.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MISCELLANEOUS: IT IS POSSIBLE THAT THE SEGMENTS OF CLUSTERED
CC CARBOXYL GROUPS MEDIATE THE STRONG BINDING TO HYDROXYAPATITE.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L10363; AAA19822.1; -;
DR PIR; S40032; S35103.
KW Glycoprotein; Sialic acid; Biominalization; Cell adhesion.
FT DOMAIN 49 160 GLU-RICH (ACIDIC).
FT DOMAIN 61 68 POLY-GLU.
FT DOMAIN 141 151 POLY-GLU.
FT SITE 272 274 CELL ATTACHMENT SITE.
FT CARBOHYD 94 94 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 300 AA; 33026 MW; C853E8EBDE156B6 CRC64;
Query Match 16.8%; Score 62.5; DB 1; Length 300;
Best Local Similarity 28.8%; Pred. No. 24;
Matches 17; Conservative 10; Mismatches 21; Indels 11; Gaps 3;
QY 5 PEPKPEVTIKANLIYADGKTQTAEFKGTGFEAATAAYRYADALKKNGEYTVVDADKG 63
Db 222 PTTPQD--ISGTTLPSPGKTTPEYGEYEQTAHEY-----DNG-YEYESENG 269
RESULT 14
Y996_METJA STANDARD; .PRT; 451 AA.
ID Y996_METJA
AC Q58403;
DT 15-JUL-1998 (Rel. 36, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)

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DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MJ0996.
GN MJ0996.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kervatage A.R., Dougherty B.F., Weinstock K.G., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrman J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Botodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii."
RL Science 273:1058-1073(1996).
CC -!- SIMILARITY: BELONGS TO THE TLDD/PMBA FAMILY.
CC
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CC -----
CC EMBL: U67542; AAB99001.1; ..
CC TIGR: MJ0996; ..
CC InterPro: IPR002510; Pmba_TlDD.
CC Pfam: PF01523; Pmba_TlDD; 1.
CC Hypothetical protein; Complete proteome.
SQ SEQUENCE 451 AA; 49813 MW; D5245F2E9551FB79 CRC64;
Query Match 16.8%; Score 62.5; DB 1; Length 451;
Best Local Similarity 24.7%; Pred. No. 37;
Matches 22; Conservative 13; Mismatches 25; Indels 29; Gaps 4;
QY 2 EKTREPKEVITKANLIYADGKTQAEKFGFEETAEAYAYADALKDNGEYI----- 56
Db 352 EELLEDTKEGIFLKS--RGQVDTG--KGLFQFSAVEAYLI-----ENGELTQVLKD 400
QY 57 -----VDVADRGYTLNKFAG 72
Db 401 AGLSGEILDILFKVDVATKDFELSVGYCG 429
RESULT 15
TNAAL_ECO57 STANDARD; PRT; 471 AA.
AC O8XB34;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tryptophanase (EC 4.1.99.1) (L-tryptophan indole-lyase) (TNase).
GN TNAAL OR Z5203 OR ECS4645.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA 'Groetbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:04:17 ; Search time 48.3288 Seconds
(without alignments)
236.470 Million cell updates/sec

Title: US-08-325-278b-1_COPY_225_296

Perfect score: 370

Sequence: 1 KEKTPPEPKKEVTKANLIY.....GKYTADLEGGYTNIRFAG 72

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- A_Geneseq_19Jun03.*
- 1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
 - 2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
 - 3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
 - 4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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 - 13: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
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 - 15: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
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 - 19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
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 - 21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
 - 22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
 - 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
 - 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	370	100.0	72	21	Peptostreptococcus
2	370	100.0	305	14	Immunoglobulin lig
3	370	100.0	434	14	Sequence encoding
4	370	100.0	467	22	Amino acid sequenc
5	339	91.6	72	21	Peptostreptococcus
6	329	88.9	75	21	Peptostreptococcus
7	329	88.9	291	14	Immunoglobulin bin
8	329	88.9	1027	14	Protein L. Peptoc
9	329	88.9	1027	14	Protein L. Peptoc

10	322	87.0	72	21	Peptostreptococcus
11	322	87.0	367	21	Expression vector
12	315.5	85.3	71	21	Peptostreptococcus
13	306	82.7	74	21	Peptostreptococcus
14	304	82.2	82	21	Ig light chain bin
15	297	80.3	82	21	PpL mutant protein
16	297	80.3	82	21	PpL mutant protein
17	295	79.7	82	21	PpL mutant protein
18	291	78.6	82	21	PpL mutant protein
19	269	72.7	76	21	Peptostreptococcus
20	254	68.6	182	18	Growth factor LHL
21	254	68.6	182	18	LHL growth factor
22	251.5	68.0	71	21	Peptostreptococcus
23	246	66.5	178	18	Growth factor LHL
24	246	66.5	178	18	Amino acid sequenc
25	246	66.5	198	18	Growth factor LHL
26	246	66.5	198	18	Amino acid sequenc
27	246	66.5	342	18	Growth factor TUHL
28	246	66.5	342	20	TUHL amino acid se
29	246	66.5	482	20	Amino acid sequenc
30	246	66.5	495	18	Growth factor CATA
31	246	66.5	495	20	CATAB-TEV aminoaci
32	69.5	18.8	2062	23	Herbicidally activ
33	68.5	18.5	1045	23	Herbicidally activ
34	67.5	18.2	368	22	Drosophila melanog
35	67.5	18.2	836	23	Modified ISPIA-1 p
36	67.5	18.2	871	23	Brevibacillus late
37	66.5	18.0	1032	23	Herbicidally activ
38	65	17.6	87	22	Human liver peptid
39	65	17.6	87	22	Peptide #4104 enco
40	65	17.6	87	22	Protein #3936 enco
41	65	17.6	87	22	Human brain expres
42	65	17.6	87	22	Human bone marrow
43	65	17.6	87	22	Peptide #4011 enco
44	65	17.6	87	23	Human peptide enco
45	65	17.6	156	20	Human secreted pro

ALIGNMENTS

RESULT 1
AA1982540
ID AA1982540 standard; Protein; 72 AA.

XX
AC AA1982540;

XX
DT 20-JUL-2000 (first entry)

XX
DE Peptostreptococcus strain 312 protein L domain B4 protein sequence.

XX
KW Immunoglobulin light chain binding protein; PpL; protein L;

XX
KW Peptostreptococcus; human immunoglobulin kappa chain;

XX
KW immunoaffinity chromatography.

XX
OS Peptostreptococcus sp.

XX
PN WO200015803-A1.

XX
PD 23-MAR-2000.

XX
PF 14-SEP-1999; 99WO-GB03048.

XX
PR 14-SEP-1998; 98GB-0019998.

XX
PR 26-APR-1999; 99GB-0009578.

XX
(ACTI-) ACTINOVA LTD.

XX
Gore MG, Beckingham JA, Roberts SE;

XX
WPI: 2000-271441/23.

XX
N-PSDB; AAA08429.

PT New modified immunoglobulin light chain binding protein, useful in
PT immunoaffinity chromatography, has a dissociation constant of 400 nM or
PT more at pH8 with respect to human immunoglobulin kappa-chain -
XX
XX
PS Disclosure; Page 44-45; 56pp; English.
XX
XX The present invention describes an immunoglobulin (Ig) light chain
CC binding protein (PI) which has been modified by one or more amino acid
CC substitutions such that the dissociation constant (Kd) of the protein
CC with respect to human Ig kappa-chain is 400 nM or more at pH8. PI is
CC useful in immunoaffinity chromatography. The present sequence is a
CC Peptostreptococcus protein L Ig light chain binding domain, which is
CC given in the disclosure of the present invention.
XX
XX Sequence 72 AA;
SQ
Query Match 100.0%; Score 370; DB 21; Length 72;
Best Local Similarity 100.0%; Pred. No. 6.9e-39;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KEKTPPEPKEEVTIKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGYTADLE 60
DB 1 KEKTPPEPKEEVTIKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGYTADLE 60
QY 61 DGGYTINIRFAG 72
DB 61 DGGYTINIRFAG 72
RESULT 2
AAR42993
ID AAR42993 standard; Protein; 305 AA.
XX
XX AAR42993;
DT 25-MAR-2003 (updated)
DT 16-MAY-1994 (first entry)
XX
XX Immunoglobulin light chain binding protein (Protein L).
DE
XX Immunoglobulin; light chain; binding; identification; purification;
KW separation.
KW
XX
XX E. coli LE392/pHDL, DSM 7054.
XX
XX Key Location/Qualifiers
FH 5..305
FT Domain /label= B1 immunoglobulin light chain binding
FT Domain 81..305
FT /label= B2 immunoglobulin light chain binding
FT Domain 153..305
FT /label= B3 immunoglobulin light chain binding
FT Domain 225..305
FT /label= B4 immunoglobulin light chain binding
FT Domain 297..305
FT /label= B5 immunoglobulin light chain binding
XX WO9322342-A1.
XX
XX 11-NOV-1993.
XX
XX 28-APR-1993; 93WO-SE00375.
XX
XX 28-APR-1992; 92SE-0001331.
XX
XX (HIGH-) HIGHTECH RECEPTOR AB.
XX
XX Bjoerck L, Sjoerbring U;

XX
DR WPI; 1993-368722/46.
DR N-PSDB; AAQ50452.
XX
XX New protein L binding light chains of all immunoglobulin classes
PT - for binding purifying and identifying immunoglobulin, also
PT related DNA, vectors and host cells
XX
XX Claim 1; Page 36; 71pp; English.
XX
XX The protein (Protein L) is capable of binding to immunoglobulin G
CC light chains. It is useful for binding, separating (purifying) and
CC identifying immunoglobulin and for removing immunoglobulin molecules
CC from serum. Hybrid proteins of the L protein can bind all human
CC immunoglobulin classes and many immunoglobulins from other species.
CC They are highly soluble and retain their binding activity at high
CC temperatures over a pH range of 3-10. They can be immobilised
CC without loss of activity.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 305 AA;
Query Match 100.0%; Score 370; DB 14; Length 305;
Best Local Similarity 100.0%; Pred. No. 4.8e-38;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KEKTPPEPKEEVTIKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGYTADLE 60
DB 225 KEKTPPEPKEEVTIKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGYTADLE 284
QY 61 DGGYTINIRFAG 72
DB 285 DGGYTINIRFAG 296
RESULT 3
AAR42994
ID AAR42994 standard; Protein; 434 AA.
XX
XX AAR42994;
DT 25-MAR-2003 (updated)
DT 16-MAY-1994 (first entry)
XX
XX Sequence encoding immunoglobulin light chain binding protein.
DE Immunoglobulin; light chain; binding; identification; purification;
KW separation; ss.
KW
XX
XX E. coli L392/pHDLG, DSM 7055.
XX
XX Key Location/Qualifiers
FH 5..305
FT Domain /label= B1 immunoglobulin light chain binding
FT Domain 81..305
FT /label= B2 immunoglobulin light chain binding
FT Domain 153..305
FT /label= B3 immunoglobulin light chain binding
FT Domain 225..305
FT /label= B4 immunoglobulin light chain binding
FT Domain 297..305
FT /label= B5 immunoglobulin light chain binding
FT Domain 309..434
FT /label= C1 immunoglobulin heavy chain binding
FT Domain 364..434
FT /label= D intermediate immunoglobulin heavy
FT chain binding domain.

PR 14-SEP-1998; 98GB-0019998.
 PR 26-APR-1999; 99GB-0009578.
 XX
 PA (ACTI-) ACTINOVA LTD.
 XX
 XX Gore MG, Beckingham JA, Roberts SE;
 PI
 XX WPI; 2000-271441/23.
 DR N-PSDB; AAA08428.
 DR
 XX New modified immunoglobulin light chain binding protein, useful in
 PT immunoaffinity chromatography, has a dissociation constant of 400 nM or
 PT more at pH8 with respect to human immunoglobulin kappa-chain -
 XX
 XX Disclosure; Page 43; 56pp; English.
 PS
 XX The present invention describes an immunoglobulin (Ig) light chain
 CC binding protein (Pl) which has been modified by one or more amino acid
 CC substitutions such that the dissociation constant (Kd) of the protein
 CC with respect to human Ig kappa-chain is 400 nM or more at pH8. Pl is
 CC useful in immunoaffinity chromatography. The present sequence is a
 CC Peptostreptococcus protein L Ig light chain binding domain, which is
 CC given in the disclosure of the present invention.
 XX
 XX Sequence 72 AA;
 SQ
 Query Match 91.6%; Score 339; DB 21; Length 72;
 Best Local Similarity 90.3%; Pred. NO. 5.5e-35;
 Matches 65; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 KEKTPPEKPEVTIKANLIYADGKTQTAEFGKGTAEATAEAYRYADLLAKENGKYTDLE 60
 DB 1 KEKTPPEKPEVTIKANLIYADGKTQTAEFGKGTAEATAEAYRYADLLAKENGKYTDVA 60
 QY 61 DGGYTINIRFAG 72
 DB 61 DKGYTINIRFAG 72
 RESULT 6
 AAY82544
 ID AAY82544 standard; Protein; 75 AA.
 XX
 AC AAY82544;
 XX
 DT 20-JUL-2000 (first entry)
 XX
 DE Peptostreptococcus strain 3316 protein L domain C4 protein sequence.
 XX
 KW Immunoglobulin light chain binding protein; PpL; protein L;
 KW Peptostreptococcus; human immunoglobulin kappa chain;
 KW immunoaffinity chromatography.
 XX
 OS Peptostreptococcus sp.
 XX
 PN WO200015803-A1.
 XX
 PD 23-MAR-2000.
 XX
 PF 14-SEP-1999; 99WO-GB03048.
 XX
 PR 14-SEP-1998; 98GB-0019998.
 PR 26-APR-1999; 99GB-0009578.
 XX
 PA (ACTI-) ACTINOVA LTD.
 XX
 XX Gore MG, Beckingham JA, Roberts SE;
 PI
 XX WPI; 2000-271441/23.
 DR N-PSDB; AAA08433.
 DR
 XX New modified immunoglobulin light chain binding protein, useful in
 PT immunoaffinity chromatography, has a dissociation constant of 400 nM or

PT more at pH8 with respect to human immunoglobulin kappa-chain -
 XX
 PS Disclosure; Page 49-50; 56pp; English.
 XX
 XX The present invention describes an immunoglobulin (Ig) light chain
 CC binding protein (Pl) which has been modified by one or more amino acid
 CC substitutions such that the dissociation constant (Kd) of the protein
 CC with respect to human Ig kappa-chain is 400 nM or more at pH8. Pl is
 CC useful in immunoaffinity chromatography. The present sequence is a
 CC Peptostreptococcus protein L Ig light chain binding domain, which is
 CC given in the disclosure of the present invention.
 XX
 XX Sequence 75 AA;
 SQ
 Query Match 88.9%; Score 329; DB 21; Length 75;
 Best Local Similarity 90.0%; Pred. NO. 1.1e-33;
 Matches 63; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 3 KTEPEKPEVTIKANLIYADGKTQTAEFGKGTAEATAEAYRYADLLAKENGKYTDLEDG 62
 DB 5 ETPEPKPEVTIKVNLIFADGKTQTAEFGKGTAEATAEAYRYADLLAKENGKYTDLEDG 64
 QY 63 GYTINIRFAG 72
 DB 65 GYTINIRFAG 74
 RESULT 7
 AAR42204
 ID AAR42204 standard; Protein; 291 AA.
 XX
 AC AAR42204;
 XX
 DT 25-MAR-2003 (updated)
 DT 18-MAY-1994 (first entry)
 XX
 DE Immunoglobulin binding protein derived from protein L.
 XX
 KW Peptide; immunoglobulin; binding; analysis; purification; ELISA;
 KW enzyme linked immunoabsorbant assay.
 XX
 OS Synthetic.
 XX
 PN WO9322439-A1.
 XX
 PD 11-NOV-1993.
 XX
 PF 07-MAY-1993; 93WO-GB00950.
 XX
 PR 07-MAY-1992; 92GB-0009804.
 PR 24-DEC-1992; 92GB-0026928.
 XX
 PA (PUBL-) PUBLIC HEALTH LAB SERVICE BOARD.
 XX
 XX Atkinson A, Duggieby CJ, Murphy JP, Trowern AR;
 XX
 XX WPI; 1993-368798/46.
 DR N-PSDB; AAQ50947.
 DR
 XX New immunoglobulin binding proteins derived from Protein L -
 PT which bind immunoglobulin kappa light chains but not albumin or
 PT cell walls
 XX
 PS Claim 12; Figure 2; 28pp; English.
 XX
 CC The synthetic immunoglobulin binding proteins derived from protein
 CC L comprise repeated sequences from protein L which bind
 CC immunoglobulin kappa light chains. They can be used in protein
 CC analysis, purification procedures and other biochemical processes e.
 CC g. ELISA. The synthetic molecules are of particular advantage if
 CC they are free of regions in protein L which exhibit albumin and cell
 CC wall binding.
 CC (Updated on 25-MAR-2003 to correct PN field.)

```

XX SQ Sequence 291 AA;
Query Match 88.9%; Score 329; DB 14; Length 291;
Best Local Similarity 90.0%; Pred. No. 6.5e-33;
Matches 63; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 3 KTPPEPKEEVTIKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDG 62
Db 221 ETPEPKEEVTIKVNLIFADGKTQTAEFKGTFAEATAEAYRYADLLAKVNGEYTDLEDG 280

Qy 63 GYTINIRFAG 72
Db 281 GYTINIRFAG 290

RESULT 8
AAR42203
ID AAR42203 standard; Protein: 1027 AA.
XX AC AAR42203;
XX DT 25-MAR-2003 (updated)
XX DT 18-MAY-1994 (first entry)
XX DE Protein L.
XX KW Peptide; immunoglobulin; binding; analysis; purification; ELISA;
XX KW enzyme linked immunoabsorbant assay.
XX OS Peptococcus magnus.
XX FH Key Location/Qualifiers
XX FT Peptide 36..59
XX FT /label= Signal sequence.
XX FT Protein 60..968
XX FT /label= Mature protein L.
XX PN W09322439-A1.
XX PD 11-NOV-1993.
XX PF 07-MAY-1993; 93WO-GB00950.
XX PR 07-MAY-1992; 92GB-0009804.
XX PR 24-DEC-1992; 92GB-0026928.
XX PA (PUBL-) PUBLIC HEALTH LAB SERVICE BOARD.
XX PI Atkinson A, Duggleby CJ, Murphy JP, Trowern AR;
XX DR WPI; 1993-368798/46.
XX DR N-PSDB; AAQ50946.
XX FT New immunoglobulin binding proteins derived from Protein L -
XX FT which bind immunoglobulin kappa light chains but not albumin or
XX FT cell walls
XX PS Disclosure; Figure 1; 28pp; English.
XX CC The synthetic immunoglobulin binding proteins derived from protein
XX CC L correspond to the repeated sequences in protein L which bind
XX CC immunoglobulin kappa light chains. They can be used in protein
XX CC analysis, purification procedures and other biochemical processes e.
XX CC g. ELISA. The synthetic molecules are of particular advantage if
XX CC they are free of regions in protein L which exhibit albumin and cell
XX CC wall binding.
XX CC (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 1027 AA;
Query Match 88.9%; Score 329; DB 14; Length 1027;
Best Local Similarity 90.0%; Pred. No. 3.6e-32;

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Matches 63; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 3 KTPPEPKEEVTIKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDG 62
Db 503 ETPEPKEEVTIKVNLIFADGKTQTAEFKGTFAEATAEAYRYADLLAKVNGEYTDLEDG 562

Qy 63 GYTINIRFAG 72
Db 563 GYTINIRFAG 572

RESULT 9
AAR43699
ID AAR43699 standard; Protein: 1027 AA.
XX AC AAR43699;
XX DT 25-MAR-2003 (updated)
XX DT 18-MAY-1994 (first entry)
XX DE Protein L.
XX KW Peptide; immunoglobulin; binding; immobilisation; light chains;
XX KW antibodies; diagnosis; pharmaceutical; ss.
XX OS Peptococcus magnus.
XX FH Key Location/Qualifiers
XX FT Peptide 36..59
XX FT /label= Signal sequence.
XX FT Protein 60..968
XX FT /label= Mature protein L.
XX PN W09322438-A1.
XX PD 11-NOV-1993.
XX PF 07-MAY-1993; 93WO-GB00949.
XX PR 07-MAY-1992; 92GB-0009804.
XX PA (PUBL-) PUBLIC HEALTH LAB SERVICE BOARD.
XX PI Atkinson A, Duggleby CJ, Murphy JP, Trowern AR;
XX DR WPI; 1993-368797/46.
XX DR P-PSDB; AAR43699.
XX FT Immunoglobulin binding polypeptide, protein L - used for prodn.
XX FT of pharmaceuticals and for immobilising antibodies e.g. on
XX FT columns, in diagnostic tests and in assays
XX PS Claim 4; Figure 1; 29pp; English.
XX CC Protein L forms a complex with immunoglobulin kappa light chain.
XX CC Purified protein can be used as a reagent for immobilising
XX CC antibodies e.g. on columns, in diagnostic tests and in assays. It
XX CC may also be used in the production of pharmaceuticals.
XX CC (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 1027 AA;
Query Match 88.9%; Score 329; DB 14; Length 1027;
Best Local Similarity 90.0%; Pred. No. 3.6e-32;
Matches 63; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 3 KTPPEPKEEVTIKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDG 62
Db 503 ETPEPKEEVTIKVNLIFADGKTQTAEFKGTFAEATAEAYRYADLLAKVNGEYTDLEDG 562

Qy 63 GYTINIRFAG 72
Db 563 GYTINIRFAG 572

```

```

RESULT 10
AAAY82538 standard; Protein: 72 AA.
XX AC AAY82538;
XX XX
DT 20-JUL-2000 (first entry)
XX DE
XX PEptostreptococcus strain 312 protein L domain B2 protein sequence.
XX KW Immuoglobulin light chain binding protein; Ppl; protein L;
KW Peptostreptococcus; human immunoglobulin kappa chain;
KW immunoaffinity chromatography.
XX OS
XX PEptostreptococcus sp.
XX WO200015803-A1.
XX PN
XX 23-MAR-2000.
XX PD
XX 14-SEP-1999; 99WO-GB03048.
XX PF
XX 14-SEP-1998; 98GB-0019998.
XX PR 26-APR-1999; 99GB-0009578.
XX PA (ACTI-) ACTINOVA LTD.
XX PI Gore MG, Beckingham JA, Roberts SE;
XX WPI; 2000-271441/23.
XX DR N-PSDB; AAA08427.
XX PT New modified immunoglobulin light chain binding protein, useful in
PT immunoaffinity chromatography, has a dissociation constant of 400 nM or
XX more at pH8 with respect to human immunoglobulin kappa-chain -
XX Disclosure; Page 42; 56pp; English.
XX CC The present invention describes an immunoglobulin (Ig) light chain
CC binding protein (Pi) which has been modified by one or more amino acid
CC substitutions such that the dissociation constant (Kd) of the protein
CC with respect to human Ig kappa-chain is 400 nM or more at pH8. Pi is
CC useful in immunoaffinity chromatography. The present sequence is a
CC Peptostreptococcus protein L Ig light chain binding domain, which is
CC given in the disclosure of the present invention.
XX SX Sequence 72 AA;
Query Match 87.0%; Score 322; DB 21; Length 72;
Best Local Similarity 84.7%; Pred. No. 7.6e-33;
Matches 61; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 1 KKTTPPKPEEVIKANLIYADGKTQTAEFGTFAETAARYADLLAKENGYKTADLE 60
Db 1 KKTTPPKPEEVIKANLIYADGKTQTAEFGTFAETAARYADLKKDNGEYTVDNA 60
QY 61 DGGYTINIRFAG 72
Db 61 DKGYTLNIRFAG 72
RESULT 11
AAB10432 standard; Protein: 367 AA.
XX ID
XX AC AAB10432;
XX XX
XX 01-DEC-2000 (first entry)
XX DE Expression vector pSEX11L4 protein.G.
XX
```


XX The present invention describes an immunoglobulin (Ig) light chain
CC binding protein (PI) which has been modified by one or more amino acid
CC substitutions such that the dissociation constant (Kd) of the protein
CC with respect to human Ig kappa-chain is 400 nM or more at pH8. PI is
CC useful in immunoaffinity chromatography. The present sequence
CC represents an Ig light chain binding PpL construct derived from
CC Peptostreptococcus sp. protein L.
XX
SQ Sequence 82 AA;

Query Match 82.2%; Score 304; DB 21; Length 82;
Best Local Similarity 84.3%; Pred. No. 1.7e-30;
Matches 59; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 3 KTEPEPKKEVTIKANLIYADGKTQTAEFGKGTAEATAEAYRYADLLAKENGKYTADLEDG 62
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
12 ETPEPKKEVTIKVNLIFADGKIQTAEFGKGTAEATAEAYRYADLLAKVNGEYTDLEDG 71

QY 63 GYTINIRFAG 72
Db | :||:|
72 GNHMIKIFAG 81

RESULT 15
AAI82545
ID AAY82545 standard; Protein; 82 AA.
XX
AC AAY82545;
XX
DT 20-JUL-2000 (first entry)
XX
DE PpL mutant protein sequence SEQ ID NO:19.
XX
KW Immunoglobulin light chain binding protein; PpL; protein L;
KW Peptostreptococcus; human immunoglobulin kappa chain; mutant;
KW immunoaffinity chromatography; site directed mutagenesis.
XX
OS Peptostreptococcus sp.
XX
PN WO200015803-A1.
XX
PD 23-MAR-2000.
XX
PF 14-SEP-1999; 99WO-GE03048.
XX
PR 14-SEP-1998; 98GB-0019998.
PR 26-APR-1999; 99GB-0009578.
XX
PA (ACTI-) ACTINOVA LTD.
XX
PI Gore MG, Beckingham JA, Roberts SE;
XX
DR WPI; 2000-271441/23.
DR N-PSDB; AAA08442.
XX
PT New modified immunoglobulin light chain binding protein, useful in
PT immunoaffinity chromatography, has a dissociation constant of 400 nM or
PT more at pH8 with respect to human immunoglobulin kappa-chain -
XX
PS Example 1; Page 50-51; 56pp; English.
XX
CC The present invention describes an immunoglobulin (Ig) light chain
CC binding protein (PI) which has been modified by one or more amino acid
CC substitutions such that the dissociation constant (Kd) of the protein
CC with respect to human Ig kappa-chain is 400 nM or more at pH8. PI is
CC useful in immunoaffinity chromatography. The present sequence is a
CC mutant Peptostreptococcus protein L, which is an Ig light chain binding
CC protein, from the present invention.
XX
SQ Sequence 82 AA;

Query Match 80.3%; Score 297; DB 21; Length 82;

Best Local Similarity 82.9%; Pred. No. 1.3e-29;
Matches 58; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 3 KTEPEPKKEVTIKANLIYADGKTQTAEFGKGTAEATAEAYRYADLLAKENGKYTADLEDG 62
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
12 ETPEPKKEVTIKVNLIFADGKIQTAEFGKGTAEATAEAYRYADLLAKVNGEYTDLEDG 71

QY 63 GYTINIRFAG 72
Db | :||:|
72 GNHMIKIFAG 81

Search completed: September 3, 2003, 11:19:19
Job time : 49.3288 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:16:02 ; Search time 15.7808 Seconds
(without alignments)
193.043 Million cell updates/sec

Title: US-08-325-278B-1_COPY_225_296

Perfect score: 370

Sequence: 1 KEKTEPEKKEVTVKANLIY.....GKYTADLEGGYTINIRFAG 72

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued_Patents_AA.*
- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pap.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pap.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pap.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pap.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pap.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	370	100.0	305	2	US-08-795-475-1
2	370	100.0	434	2	US-08-795-475-3
3	329	88.9	75	3	US-08-446-137B-8
4	329	88.9	291	3	US-08-446-137B-4
5	329	88.9	1027	3	US-08-446-137B-2
6	315.5	85.3	71	3	US-08-446-137B-6
7	306	82.7	74	3	US-08-446-137B-7
8	254	68.6	182	3	US-08-828-741B-2
9	254	68.6	182	4	US-09-160-567-2
10	254	68.6	182	4	US-09-710-299-2
11	250.5	67.7	71	3	US-08-446-137B-5
12	246	66.5	178	3	US-08-828-741B-13
13	246	66.5	178	4	US-09-160-567-13
14	246	66.5	178	4	US-09-710-299-13
15	246	66.5	198	3	US-08-828-741B-8
16	246	66.5	198	4	US-09-160-567-8
17	246	66.5	198	4	US-09-710-299-8
18	246	66.5	342	3	US-08-828-741B-6
19	246	66.5	342	4	US-09-160-567-6
20	246	66.5	342	4	US-09-710-299-6
21	246	66.5	495	3	US-08-828-741B-4
22	246	66.5	495	4	US-09-160-567-4
23	246	66.5	495	4	US-09-710-299-4
24	65	17.6	342	2	US-08-724-394A-6
25	65	17.6	540	2	US-08-724-394A-4
26	65	17.6	610	2	US-08-724-394A-5
27	64.5	17.4	279	4	US-09-314-701-60

28	62	16.8	490	4	US-09-252-149B-26	Sequence 26, Appl
29	62	16.8	544	1	US-08-387-156-10	Sequence 10, Appl
30	62	16.8	544	2	US-08-694-865-10	Sequence 10, Appl
31	62	16.8	544	2	US-08-878-748-10	Sequence 10, Appl
32	62	16.8	544	3	US-09-124-491-10	Sequence 10, Appl
33	62	16.8	544	4	US-09-383-912-10	Sequence 10, Appl
34	62	16.8	699	2	US-08-694-865-16	Sequence 16, Appl
35	62	16.8	699	3	US-09-124-491-16	Sequence 16, Appl
36	62	16.8	699	4	US-09-383-912-16	Sequence 16, Appl
37	62	16.8	770	4	US-09-252-991A-26865	Sequence 26865, A
38	62	16.8	924	3	US-08-619-812-8	Sequence 8, Appl
39	62	16.8	926	1	US-07-908-253-2	Sequence 2, Appl
40	62	16.8	926	1	US-08-455-970A-2	Sequence 2, Appl
41	62	16.8	926	1	US-08-387-156-6	Sequence 6, Appl
42	62	16.8	926	2	US-08-694-865-6	Sequence 6, Appl
43	62	16.8	926	2	US-08-878-748-6	Sequence 6, Appl
44	62	16.8	926	2	US-08-535-837-2	Sequence 2, Appl
45	62	16.8	926	3	US-09-124-491-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-795-475-1
; Sequence 1, Application US/08795475
; Patent No. 5965390
; GENERAL INFORMATION:
; APPLICANT: Bivick, Lars
; APPLICANT: Sjvdring, Ulf
; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,475
; FILING DATE: 11-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 100084.402D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 305 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli LE392/pHDL, DSM 7054
US-08-795-475-1

Query Match 100.0%; Score 370; DB 2; Length 305;
Best Local Similarity 100.0%; Pred. No. 5,1e-40;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEKTEPEKKEVTVKANLIYADGKQTAEFGTFAETAAYRAADLAKENGKKTADLE 60
|||||

Db 225 KETPEPEKVEVTKANLIYADGKTQTAEFGTFAEATAEAYRYADLLAKENGYTADLE 284

Qy 61 DGGYTINIRFAG 72

Db 285 DGGYTINIRFAG 296

RESULT 2

US-08-795-475-3

; Sequence 3, Application US/08795475

; Patent No. 5965390

; GENERAL INFORMATION:

; APPLICANT: Bjvick, Lars

; APPLICANT: Sjvbring, Ulf

; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SEED and BERRY LLP

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; CITY: Seattle

; STATE: Washington

; COUNTRY: USA

; ZIP: 98104-7092

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/795,475

; FILING DATE: 11-FEB-1997

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: McMasters, David D.

; REGISTRATION NUMBER: 33,963

; REFERENCE/DOCKET NUMBER: 100084.402D1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 622-4900

; TELEFAX: (206) 682-6031

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 434 amino acids

; TYPE: amino acid

; STRANDEDNESS: unknown

; TOPOLOGY: unknown

; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

; ORIGINAL SOURCE:

; ORGANISM: Escherichia coli LE392/pHDLG, DSM 7055

US-08-795-475-3

Query Match 100.0%; Score 370; DB 2; Length 434;

Best Local Similarity 100.0%; Pred. No. 8.3e-40;

Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KETPEPEKVEVTKANLIYADGKTQTAEFGTFAEATAEAYRYADLLAKENGYTADLE 60

Db 225 KETPEPEKVEVTKANLIYADGKTQTAEFGTFAEATAEAYRYADLLAKENGYTADLE 284

Qy 61 DGGYTINIRFAG 72

Db 285 DGGYTINIRFAG 296

RESULT 3

US-08-446-137B-8

; Sequence 8, Application US/08446137B

; Patent No. 6162903

; GENERAL INFORMATION:

; APPLICANT: Trowern, Angus R.

; APPLICANT: Atkinson, Anthony

; APPLICANT: Murphy, Jonathan P.

; APPLICANT: Laurence, Oliver S.

; APPLICANT: Duggleby, Clive J.

; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEINS DERIVED

; FROM L PROTEIN AND THEIR USES

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SEED and BERRY LLP

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; CITY: Seattle

; STATE: Washington

; COUNTRY: USA

; ZIP: 98104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/446,137B

; FILING DATE: 22-MAY-1995

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: McMasters, David D.

; REGISTRATION NUMBER: 33,963

; REFERENCE/DOCKET NUMBER: 100084.406

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 622-4900

; TELEFAX: (206) 682-6031

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 75 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

US-08-446-137B-8

Query Match 88.9%; Score 329; DB 3; Length 75;

Best Local Similarity 90.0%; Pred. No. 1.6e-35;

Matches 63; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 3 KTEPEPEKVEVTKANLIYADGKTQTAEFGTFAEATAEAYRYADLLAKENGYTADLE 62

Db 5 ETPEPEKVEVTKVNLIFADGKTQTAEFGTFAEATAEAYRYADLLAKENGYTADLE 64

Qy 63 GYTINIRFAG 72

Db 65 GYTINIRFAG 74

RESULT 4

US-08-446-137B-4

; Sequence 4, Application US/08446137B

; Patent No. 6162903

; GENERAL INFORMATION:

; APPLICANT: Trowern, Angus R.

; APPLICANT: Atkinson, Anthony

; APPLICANT: Murphy, Jonathan P.

; APPLICANT: Laurence, Oliver S.

; APPLICANT: Duggleby, Clive J.

; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEINS DERIVED

; FROM L PROTEIN AND THEIR USES

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SEED and BERRY LLP

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; CITY: Seattle

; STATE: Washington

; COUNTRY: USA

; ZIP: 98104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446.137B
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 100084.406
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 291 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-446-137B-4

Query Match      88.9%; Score 329; DB 3; Length 291;
Best Local Similarity 90.0%; Pred. No. 1e-34;
Matches 63; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      3 KTEPEPKEEVTIKANLIYADGKTQTAEFGKTFEAETAEAYRYADLLAKENGKYTADLEDG 62
Db      221 ETPEEPKEEVTIKVNLIFADGKTQTAEFGKTFEETAEAYRYADLLAKVNGEYTDLEDG 280

QY      63 GYTINIRFAG 72
Db      281 GYTINIKFAG 290

RESULT 5
US-08-446-137B-2
; Sequence 2, Application US/08446137B
; Patent No. 6162903
; GENERAL INFORMATION:
; APPLICANT: Trowern, Angus R.
; APPLICANT: Atkinson, Anthony
; APPLICANT: Murphy, Jonathan P.
; APPLICANT: Laurence, Oliver S.
; APPLICANT: Duggleby, Clive J.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEINS DERIVED
; FROM L PROTEIN AND THEIR USES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446.137B
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 100084.406
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-446-137B-2

Query Match      88.9%; Score 329; DB 3; Length 1027;
Best Local Similarity 90.0%; Pred. No. 5.7e-34;
Matches 63; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      3 KTEPEPKEEVTIKANLIYADGKTQTAEFGKTFEAETAEAYRYADLLAKENGKYTADLEDG 62
Db      503 ETPEEPKEEVTIKVNLIFADGKTQTAEFGKTFEETAEAYRYADLLAKVNGEYTDLEDG 562

QY      63 GYTINIRFAG 72
Db      563 GYTINIKFAG 572

RESULT 6
US-08-446-137B-6
; Sequence 6, Application US/08446137B
; Patent No. 6162903
; GENERAL INFORMATION:
; APPLICANT: Trowern, Angus R.
; APPLICANT: Atkinson, Anthony
; APPLICANT: Murphy, Jonathan P.
; APPLICANT: Laurence, Oliver S.
; APPLICANT: Duggleby, Clive J.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEINS DERIVED
; FROM L PROTEIN AND THEIR USES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446.137B
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 100084.406
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 71 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-446-137B-6

Query Match      85.3%; Score 315.5; DB 3; Length 71;
Best Local Similarity 87.5%; Pred. No. 8.5e-34;
Matches 63; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY      1 KEKTEPEPKEEVTIKANLIYADGKTQTAEFGKTFEAETAEAYRYADLLAKENGKYTADLE 60
Db      1 KEK-PEEPKEEVTIKVNLIFADGKTQTAEFGKTFEETAEAYRYADLLAKENGKYTADLE 59

QY      61 DGGYTINIRFAG 72
Db      60 DGGNTINIKFAG 71
```

RESULT 7
US-08-446-137B-7
; Sequence 7, Application US/08446137B
; Patent No. 6162903
; GENERAL INFORMATION:
; APPLICANT: Townen, Angus R.
; APPLICANT: Atkinson, Anthony
; APPLICANT: Murphy, Jonathan P.
; APPLICANT: Laurence, Oliver S.
; APPLICANT: Dugleby, Clive J.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEINS DERIVED
; FROM L PROTEIN AND THEIR USES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,137B
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McWaters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 100084.406
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 74 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-446-137B-7

Query Match 82.7%; Score 306; DB 3; Length 74;
Best Local Similarity 84.3%; Pred. No. 1.5e-32;
Matches 59; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
QY 3 KTEPEEKEVTIKANLIYADGKTQAEFGKTFEATAEAYRYADLLAKENGKYTDLEDG 62
; :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 5 ETEPEEKEVTIKNLIFADCKIQTAEFKGTFEATAEAYRYADLLAKENGKYTDLEDG 64
; :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 63 GYTINIRFAG 72
; :|||||:|||||
Db 65 GNTINIKFAG 74
; :|||||:|||||

RESULT 8
US-08-828-741B-2
; Sequence 2, Application US/08828741B
; Patent No. 6043069
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
; TITLE OF INVENTION: PRODUCING SAME
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City

; STATE: New York
; COUNTRY: United States of America
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,741B
; FILING DATE: 26-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10591
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 182 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-828-741B-2
Query Match 68.6%; Score 254; DB 3; Length 182;
Best Local Similarity 66.2%; Pred. No. 3e-25;
Matches 47; Conservative 12; Mismatches 12; Indels 0; Gaps 0;
QY 2 EKTPEEKEVTIKANLIYADGKTQAEFGKTFEATAEAYRYADLLAKENGKYTDLED 61
; :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 QAAPKQNTTEVTIKANLIFANGSTQAEFGKTFEATSEAYAYADTLKKDNGEYTVADV 79
; :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 62 GYTINIRFAG 72
; :|||||:|||||
Db 80 KGYTLNIRFAG 90
; :|||||:|||||
RESULT 9
US-09-160-567-2
; Sequence 2, Application US/09160567
; Patent No. 6326179
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
; TITLE OF INVENTION: PRODUCING SAME
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/160,567
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,741
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

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; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-710-299-2

Query Match          68.6%; Score 254; DB 4; Length 182;
Best Local Similarity 66.2%; Pred.No. 3e-25;
Matches 47; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY 2 EKTPEPKERTVIKANLIYADGKQTAEFGTFAEATAEAAYRYADLLAKENGKYTDADLED 61
   :  ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |
Db 20 GAAPKDNTTEVTIKANLIFANGSTQTAEPFKGTFEKATSEAYAYADTLKKDNGEYTVDVAD 79
   :  ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |

QY 62 QGYTINIRFAG 72
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Db 80 KGYTLNKFAG 90

RESULT 11
US-08-446-137B-5
; Sequence 5, Application US/08446137B
; Patent No. 6162903
; GENERAL INFORMATION:
; APPLICANT: Trowern, Angus R.
; APPLICANT: Atkinson, Anthony
; APPLICANT: Murphy, Jonathan P.
; APPLICANT: Laurence, Oliver S.
; APPLICANT: Dugleby, Clive J.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEINS DERIVED
; TITLE OF INVENTION: FROM L PROTEIN AND THEIR USES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,137B
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 100084.406
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 71 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-446-137B-5

Query Match          67.7%; Score 250.5; DB 3; Length 71;
Best Local Similarity 68.6%; Pred.No. 2.4e-25;
Matches 48; Conservative 11; Mismatches 10; Indels 1; Gaps 1;

QY 3 KTEPPEKEVTIKANLIYADGKQTAEFGTFAEATAEAAYRYADLLAKENGKYTDADLEDG 62
   :  ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |
Db 2 ETP-EPEEVTIKANLIFADGSTQNAEFGTKFAKAVSDAYAYADALKDNGEYTVDVADK 60
   :  ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |

QY 63 GYTINIRFAG 72
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Db 61 GLTNKIFAG 70
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RESULT 12
US-08-828-741B-13
; Sequence 13, Application US/08828741B
; Patent No. 6043069
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlington, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
; TITLE OF INVENTION: PRODUCING SAME
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,741B
; FILING DATE: 26-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10591
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-828-741B-13

Query Match 66.5%; Score 246; DB 3; Length 178;
Best Local Similarity 73.0%; Pred. No. 3.2e-24;
Matches 46; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 10 EEVTKANLIYDGKQTQAEFGKTFAEATAYRYADLLAKENGKYTADLEDGGYTINIR 69
Db 12 EEVTKANLIIFANGSTQAEFGKTFEKAISEAYAYADTLKKDNGEYTVDVADKGYTLNIK 71
QY 70 FAG 72
Db 72 FAG 74

RESULT 13
US-09-160-567-13
; Sequence 13, Application US/09160567
; Patent No. 6326179
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlington, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
; TITLE OF INVENTION: PRODUCING SAME
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City

STATE: New York
COUNTRY: United States of America
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,567
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,741
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 178 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-160-567-13
Query Match 66.5%; Score 246; DB 4; Length 178;
Best Local Similarity 73.0%; Pred. No. 3.2e-24;
Matches 46; Conservative 9; Mismatches 8; Indels 0; Gaps 0;
QY 10 EEVTKANLIYDGKQTQAEFGKTFAEATAYRYADLLAKENGKYTADLEDGGYTINIR 69
Db 12 EEVTKANLIIFANGSTQAEFGKTFEKAISEAYAYADTLKKDNGEYTVDVADKGYTLNIK 71
QY 70 FAG 72
Db 72 FAG 74
RESULT 14
US-09-710-299-13
; Sequence 13, Application US/09710299
; Patent No. 6521741
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlington, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
; TITLE OF INVENTION: PRODUCING SAME
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/710,299
; FILING DATE: 09-NOV-6521741-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: 08/828,741
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10591
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-710-299-13

Query Match          66.5%; Score 246; DB 4; Length 178;
Best Local Similarity 73.0%; Pred. No. 3.2e-24;
Matches 46; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 10 EEVTKANLIYADGKTQTAEFKGTFAETAAYRYADLLAKENGYTADLEGGYTINIR 69
Db 12 EEVTKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKONGEYTVDVADKGYTLNIK 71
QY 70 FAG 72
Db 72 FAG 74

RESULT 15
US-08-828-741B-8
; Sequence 8, Application US/08828741B
; Patent No. 6043069
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlington, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
; TITLE OF INVENTION: PRODUCING SAME
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,741B
; FILING DATE: 26-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10591
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 198 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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; MOLECULE TYPE: protein
US-08-828-741B-8

Query Match          66.5%; Score 246; DB 3; Length 198;
Best Local Similarity 73.0%; Pred. No. 3.7e-24;
Matches 46; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 10 EEVTKANLIYADGKTQTAEFKGTFAETAAYRYADLLAKENGYTADLEGGYTINIR 69
Db 32 EEVTKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKONGEYTVDVADKGYTLNIK 91
QY 70 FAG 72
Db 92 FAG 94

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:23:22; Search time 26.6301 Seconds
(without alignments)
371.228 Million cell updates/sec

Title: US-08-325-278B-1_COPY_225_296

Perfect score: 370

Sequence: 1 KKTPEPKKEVTIKANLIY.....GKYTADLEGGYTINIRFAG 72

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Gapop 10.0 , Gapext 0.5

Searched: 513375 seqs, 137303645 residues

Total number of hits satisfying chosen parameters: 513375

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	370	100.0	72	10	US-09-808-212A-10
2	370	100.0	305	8	US-08-325-278-1
3	370	100.0	434	8	US-08-325-278-3
4	339	91.6	72	10	US-09-808-212A-8
5	329	88.9	75	10	US-09-808-212A-18
6	322	87.0	72	10	US-09-808-212A-6
7	315.5	85.3	71	10	US-09-808-212A-14
8	306	82.7	74	10	US-09-808-212A-16
9	304	82.2	82	10	US-09-808-212A-2
10	269	72.7	76	10	US-09-808-212A-4
11	254	68.0	182	12	US-10-345-618-2
12	251.5	68.0	71	10	US-09-808-212A-12
13	246	66.5	178	12	US-10-345-618-13
14	246	66.5	198	12	US-10-345-618-8
15	246	66.5	342	12	US-10-345-618-6

16	246	66.5	482	12	US-10-345-618-16
17	246	66.5	495	12	US-10-345-618-4
18	246	66.5	836	10	US-09-858-525A-10
19	67.5	18.2	871	10	US-09-858-525A-2
20	65	17.6	87	9	US-09-864-761-37235
21	65	17.6	155	15	US-10-097-065-456
22	65	17.6	156	15	US-10-097-065-251
23	65	17.6	263	10	US-09-955-866-11
24	65	17.6	263	10	US-09-896-738-17
25	65	17.6	319	10	US-09-910-174A-12
26	65	17.6	319	15	US-10-156-424A-12
27	65	17.6	334	11	US-09-746-783-134
28	65	17.6	334	15	US-10-097-065-161
29	65	17.6	357	10	US-09-910-174A-14
30	65	17.6	359	15	US-10-156-424A-11
31	65	17.6	513	10	US-09-910-174A-18
32	65	17.6	584	10	US-09-910-174A-16
33	65	17.6	584	10	US-09-955-866-12
34	65	17.6	584	10	US-09-896-738-18
35	64.5	17.4	279	14	US-10-059-964-60
36	64.5	17.4	279	15	US-10-314-639-60
37	62.5	16.9	485	10	US-09-934-868-80
38	62	16.8	695	11	US-09-305-924-13
39	62	16.8	953	11	US-09-884-696-3
40	62	16.8	1741	10	US-09-971-536-68
41	60.5	16.4	1179	15	US-10-156-761-13670
42	60	16.2	841	9	US-09-815-242-5779
43	60	16.2	841	9	US-09-815-242-12751
44	59.5	16.1	414	9	US-09-039-927A-4
45	58.5	15.8	261	10	US-09-245-764-7

ALIGNMENTS

RESULT 1

US-09-808-212A-10
; Sequence 10, Application US/09808212A
; Patent No. US20020137918A1
; GENERAL INFORMATION:
; APPLICANT: Gore, Michael Graham
; APPLICANT: Beckingham, Jennifer Ann
; APPLICANT: Roberts, Iman Eleri
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN
; FILE REFERENCE: 100084.414US
; CURRENT APPLICATION NUMBER: US/09/808.212A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Peptostreptococcus sp.
US-09-808-212A-10

Query Match 100.0%; Score 370; DB 10; Length 72;
Best Local Similarity 100.0%; Pred. No. 1.9e-36;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	KKTPEPKKEVTIKANLIYADGKTQTAEFGKGTAEATAEAYRYADLLAKENGYTADLE	60
Db	1	KKTPEPKKEVTIKANLIYADGKTQTAEFGKGTAEATAEAYRYADLLAKENGYTADLE	60
Qy	61	DGGYTNIRFAG	72
Db	61	DGGYTNIRFAG	72

RESULT 2

US-08-325-278-1
; Sequence 1, Application US/08325278
; Publication No. US2003002728A1
; GENERAL INFORMATION:

```
; APPLICANT: Bjvrck, Lars
; APPLICANT: Sjvbrng, Ulf
; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,278
; FILING DATE: 26-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 450023.401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 305 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli LE392/pHDL, DSM 7054
;
US-08-325-278-1

Query Match 100.0%; Score 370; DB 8; Length 305;
Best Local Similarity 100.0%; Pred. No. 1.2e-35;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKTPEEPKEEVTKANLIYADGKTQTAEFGTFAEATAEAYRYADLLAKENGYTADLE 60
Db 225 KKTPEEPKEEVTKANLIYADGKTQTAEFGTFAEATAEAYRYADLLAKENGYTADLE 60

QY 61 DGGYTINIRFAG 72
Db 285 DGGYTINIRFAG 296

RESULT 3
US-08-325-278-3
; Sequence 3, Application US/08325278
; Publication No. US20030027283A1
; GENERAL INFORMATION:
; APPLICANT: Bjvrck, Lars
; APPLICANT: Sjvbrng, Ulf
; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,278
; FILING DATE: 26-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 450023.401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 434 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli LE392/pHDLG, DSM 7055
;
US-08-325-278-3

Query Match 100.0%; Score 370; DB 8; Length 434;
Best Local Similarity 100.0%; Pred. No. 1.8e-35;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 225 KKTPEEPKEEVTKANLIYADGKTQTAEFGTFAEATAEAYRYADLLAKENGYTADLE 60

QY 61 DGGYTINIRFAG 72
Db 285 DGGYTINIRFAG 296

RESULT 4
US-08-808-212A-8
; Sequence 8, Application US/09808212A
; Patent No. US20020137918A1
; GENERAL INFORMATION:
; APPLICANT: Gore, Michael Graham
; APPLICANT: Beckingham, Jennifer Ann
; APPLICANT: Robertts, Sian Eleiri
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN
; FILE REFERENCE: 100084.414US
; CURRENT APPLICATION NUMBER: US/09/808,212A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Peptostreptococcus sp.
;
US-08-808-212A-8

Query Match 91.6%; Score 339; DB 10; Length 72;
Best Local Similarity 90.3%; Pred. No. 8.4e-33;
Matches 65; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 KKTPEEPKEEVTKANLIYADGKTQTAEFGTFAEATAEAYRYADLLAKENGYTADLE 60
Db 1 KKTPEEPKEEVTKANLIYADGKTQTAEFGTFAEATAEAYRYADLLAKENGYTADLE 60

QY 61 DGGYTINIRFAG 72
Db 61 DGGYTINIRFAG 72

RESULT 5
US-08-808-212A-18
; Sequence 18, Application US/09808212A
; Patent No. US20020137918A1
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; GENERAL INFORMATION:
; APPLICANT: Gore, Michael Graham
; APPLICANT: Beckingham, Jennifer Ann
; APPLICANT: Roberts, Sian Eleri
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN
; FILE REFERENCE: 100084.414US
; CURRENT APPLICATION NUMBER: US/09/808,212A
; CURRENT FILING DATE: 2001-03-13
; SOFTWARE: FastSEQ for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 18
; TYPE: PRT
; LENGTH: 75
; ORGANISM: Peptostreptococcus sp.
US-09-808-212A-18

Query Match      88.9%; Score 329; DB 10; Length 75;
Best Local Similarity 90.0%; Pred. No. 1.3e-31;
Matches 63; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 3 KTEPEEKKEVTIKANLIYADGKTQTAEFGKTFEATAEAYRYADLLAKENGYTADLE 62
Db 5 ETPEEKKEVTIKVNLIFADGKTQTAEFGKTFEATAEAYRYADLLAKVNGEYTDLE 64

Qy 63 GYTINIRFAG 72
Db 65 GYTINIRFAG 74

RESULT 6
US-09-808-212A-6
; Sequence 6, Application US/09808212A
; Patent No. US20020137918A1
; GENERAL INFORMATION:
; APPLICANT: Gore, Michael Graham
; APPLICANT: Beckingham, Jennifer Ann
; APPLICANT: Roberts, Sian Eleri
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN
; FILE REFERENCE: 100084.414US
; CURRENT APPLICATION NUMBER: US/09/808,212A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Peptostreptococcus sp.
US-09-808-212A-6

Query Match      87.0%; Score 322; DB 10; Length 72;
Best Local Similarity 84.7%; Pred. No. 8.5e-31;
Matches 61; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KTEPEEKKEVTIKANLIYADGKTQTAEFGKTFEATAEAYRYADLLAKENGYTADLE 60
Db 1 KTEPEEKKEVTIKANLIYADGKTQTAEFGKTFEATAEAYRYADLLAKVNGEYTDVA 60

Qy 61 DGGYTINIRFAG 72
Db 61 DGGYTINIRFAG 72

RESULT 7
US-09-808-212A-14
; Sequence 14, Application US/09808212A
; Patent No. US20020137918A1
; GENERAL INFORMATION:
; APPLICANT: Gore, Michael Graham
; APPLICANT: Beckingham, Jennifer Ann
; APPLICANT: Roberts, Sian Eleri
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN
; FILE REFERENCE: 100084.414US
; CURRENT APPLICATION NUMBER: US/09/808,212A
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; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Peptostreptococcus sp.
US-09-808-212A-14

Query Match      85.3%; Score 315.5; DB 10; Length 71;
Best Local Similarity 87.5%; Pred. No. 4.8e-30;
Matches 63; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

Qy 1 KTEPEEKKEVTIKANLIYADGKTQTAEFGKTFEATAEAYRYADLLAKENGYTADLE 60
Db 1 KEK-PEEPKEEVIKVNLIFFADGKTQTAEFGKTFEATAKAYAYADLLAKENGEYTDLE 59

Qy 61 DGGYTINIRFAG 72
Db 60 DGGTINIRFAG 71

RESULT 8
US-09-808-212A-16
; Sequence 16, Application US/09808212A
; Patent No. US20020137918A1
; GENERAL INFORMATION:
; APPLICANT: Gore, Michael Graham
; APPLICANT: Beckingham, Jennifer Ann
; APPLICANT: Roberts, Sian Eleri
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN
; FILE REFERENCE: 100084.414US
; CURRENT APPLICATION NUMBER: US/09/808,212A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Peptostreptococcus sp.
US-09-808-212A-16

Query Match      82.7%; Score 306; DB 10; Length 74;
Best Local Similarity 84.3%; Pred. No. 6.7e-29;
Matches 59; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 3 KTEPEEKKEVTIKANLIYADGKTQTAEFGKTFEATAEAYRYADLLAKENGYTADLE 62
Db 5 ETPEEKKEVTIKVNLIFADGKTQTAEFGKTFEATAKAYAYANLLAKENGEYTDLE 64

Qy 63 GYTINIRFAG 72
Db 65 GNTINIRFAG 74

RESULT 9
US-09-808-212A-2
; Sequence 2, Application US/09808212A
; Patent No. US20020137918A1
; GENERAL INFORMATION:
; APPLICANT: Gore, Michael Graham
; APPLICANT: Beckingham, Jennifer Ann
; APPLICANT: Roberts, Sian Eleri
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN
; FILE REFERENCE: 100084.414US
; CURRENT APPLICATION NUMBER: US/09/808,212A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Peptostreptococcus sp.
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US-09-808-212A-2

Query Match 82.2%; Score 304; DB 10; Length 82;
Best Local Similarity 84.3%; Pred. No. 1.3e-28;
Matches 59; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 3 KTEPEPKEVITKANLIYADGKTQTAEFGTFAEATAEAYRYADLLAKENGKYTADLEDG 62
DB 12 ETPEPKEVITKANLIYADGKTQTAEFGTFAEATAEAYRYADLLAKENGKYTADLEDG 71
QY 63 GYTINIRFAG 72
DB 72 GNHNIKIFAG 81

RESULT 10

US-09-808-212A-4
; Sequence 4, Application US/09808212A
; Patent No. US20020137918A1
; GENERAL INFORMATION:
; APPLICANT: Gore, Michael Graham
; APPLICANT: Beckingham, Jennifer Ann
; APPLICANT: Roberts, Sian Eleri
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN
; FILE REFERENCE: 100084.414US
; CURRENT APPLICATION NUMBER: US/09/808,212A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Peptostreptococcus sp.
US-09-808-212A-4

Query Match 72.7%; Score 269; DB 10; Length 76;
Best Local Similarity 68.4%; Pred. No. 1.6e-24;
Matches 52; Conservative 11; Mismatches 9; Indels 4; Gaps 1;
QY 1 KEKTPPEP-----KEEVITKANLIYADGKTQTAEFGTFAEATAEAYRYADLLAKENGKYT 56
DB 1 KEETPETDSEEEVITKANLIYADGKTQTAEFGTFAEATAEAYRYADLLAKENGKYT 60
QY 57 ADLEDGGYTINIRFAG 72
DB 61 VDVAADRGYTINIRFAG 76

RESULT 11

US-10-345-618-2
; Sequence 2, Application US/10345618
; Publication No. US2003014848A1
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF PRODUCING SAME
; FILE REFERENCE: 13474
; CURRENT APPLICATION NUMBER: US/10/345,618
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US/09/509,031
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:LHL protein
; OTHER INFORMATION: sequence
US-10-345-618-2

Query Match 68.6%; Score 254; DB 12; Length 182;
Best Local Similarity 66.2%; Pred. No. 2.9e-22;
Matches 47; Conservative 12; Mismatches 12; Indels 0; Gaps 0;
QY 2 EKTPEPKEEVITKANLIYADGKTQTAEFGTFAEATAEAYRYADLLAKENGKYTADLED 61
DB 20 QAAPKNDTEEVITKANLIYADGKTQTAEFGTFAEATAEAYRYADLLAKENGKYTADLED 79
QY 62 GYTINIRFAG 72
DB 80 KGYTLNIRFAG 90

RESULT 12

US-09-808-212A-12
; Sequence 12, Application US/09808212A
; Patent No. US20020137918A1
; GENERAL INFORMATION:
; APPLICANT: Gore, Michael Graham
; APPLICANT: Beckingham, Jennifer Ann
; APPLICANT: Roberts, Sian Eleri
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN
; FILE REFERENCE: 100084.414US
; CURRENT APPLICATION NUMBER: US/09/808,212A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Peptostreptococcus sp.
US-09-808-212A-12

Query Match 68.0%; Score 251.5; DB 10; Length 71;
Best Local Similarity 67.6%; Pred. No. 1.7e-22;
Matches 48; Conservative 12; Mismatches 10; Indels 1; Gaps 1;
QY 2 EKTPEPKEEVITKANLIYADGKTQTAEFGTFAEATAEAYRYADLLAKENGKYTADLED 61
DB 1 KETP-EPEEVITKANLIYADGKTQTAEFGTFAEATAEAYRYADLLAKENGKYTADLED 59
QY 62 GYTINIRFAG 72
DB 60 KGLTLNIRFAG 70

RESULT 13

US-10-345-618-13
; Sequence 13, Application US/10345618
; Publication No. US2003014848A1
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF PRODUCING SAME
; FILE REFERENCE: 13474
; CURRENT APPLICATION NUMBER: US/10/345,618
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US/09/509,031
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:LHL-omp
; OTHER INFORMATION: protein sequence
US-10-345-618-13

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OM protein - protein search, using sw model

Run on: September 3, 2003, 10:59:36 ; Search time 16.4438 Seconds
(without alignments)
1116.704 Million cell updates/sec

Title: US-08-325-278B-3

Perfect score: 2235

Sequence: 1 AVENKETPTPTDSEEV.....GVDGWTVDATKFTVTM 434

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2_5/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PTCUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2235	100.0	434	2	US-08-795-475-3
2	1565	70.0	305	2	US-08-795-475-1
3	1263.5	56.5	1027	3	US-08-446-137B-2
4	1216	54.4	291	3	US-08-446-137B-4
5	706.5	31.6	664	3	US-08-669-408B-2
6	622.5	27.9	502	1	US-08-378-761A-25
7	622.5	27.9	502	1	US-08-485-286-25
8	622	27.8	493	1	US-08-378-761A-23
9	622	27.8	493	1	US-08-485-286-23
10	618	27.7	342	3	US-08-828-741B-6
11	618	27.7	342	4	US-09-160-567-6
12	618	27.7	342	4	US-09-710-299-6
13	618	27.7	489	1	US-08-378-761A-19
14	618	27.7	489	1	US-08-485-286-19
15	615	27.5	178	3	US-08-828-741B-13
16	615	27.5	178	4	US-09-160-567-13
17	615	27.5	178	4	US-09-710-299-13
18	615	27.5	198	3	US-08-828-741B-8
19	615	27.5	198	4	US-09-160-567-8
20	615	27.5	198	4	US-09-710-299-8
21	614	27.5	495	3	US-08-828-741B-4
22	614	27.5	495	4	US-09-160-567-4
23	614	27.5	495	4	US-09-710-299-4
24	613	27.4	182	3	US-08-828-741B-2
25	613	27.4	182	4	US-09-160-567-2
26	613	27.4	182	4	US-09-710-299-2
27	404	18.1	413	3	US-08-669-408B-10

28	369.5	16.5	402	1	US-08-378-761A-17	Sequence 17, Appl
29	369.5	16.5	402	1	US-08-485-286-17	Sequence 8, Appl
30	334	14.9	75	3	US-08-446-137B-8	Sequence 6, Appl
31	315.5	14.1	71	3	US-08-446-137B-6	Sequence 7, Appl
32	306	13.7	74	3	US-08-446-137B-7	Sequence 5, Appl
33	303	13.6	71	3	US-08-446-137B-5	Sequence 2, Appl
34	293	13.1	57	3	US-09-117-233-16	Sequence 12, Appl
35	292	13.1	57	3	US-09-117-233-2	Sequence 38, Appl
36	292	13.1	60	3	US-09-117-233-12	Sequence 10, Appl
37	287	12.8	56	3	US-09-058-459-38	Sequence 6, Appl
38	287	12.8	56	3	US-09-127-926-38	Sequence 4, Appl
39	286	12.8	57	3	US-09-117-233-8	Sequence 68, Appl
40	286	12.8	58	3	US-09-117-233-10	Sequence 58, Appl
41	286	12.8	58	3	US-09-444-305A-1	
42	286	12.8	60	3	US-09-117-233-6	
43	285	12.8	60	3	US-09-117-233-4	
44	283	12.7	56	3	US-09-058-459-68	
45	283	12.7	56	3	US-09-127-926-68	

ALIGNMENTS

RESULT 1
US-08-795-475-3
; Sequence 3, Application US/08795475
; Patent No. 5965390
; GENERAL INFORMATION:
; APPLICANT: Bjvrck, Lars
; APPLICANT: Sjvbring, Ulf
; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,475
; FILING DATE: 11-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 100084.402D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 434 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli LE392/pHDLG, DSM 7055
US-08-795-475-3

Query Match 100.0%; Score 2235; DB 2; Length 434;
Best Local Similarity 100.0%; Pred. No. 6.2e-170;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVENKETPTPTDSEEVITKANLIFANGSTQAEKGTFFKATSEAYADTLKKDN 60
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Db 1 AVENKEETPETDSEEVITKANLIFANGSTQTAFFKGTPEKATSEAYAYADTLKKN 60
QY 61 GEYTVADVADKGYTLNIFKAGKEKTPPEPKEEVTIKANLIYADGKTQTAFFKGTPEEATAE 120
Db 61 GEYTVADVADKGYTLNIFKAGKEKTPPEPKEEVTIKANLIYADGKTQTAFFKGTPEEATAE 120
QY 121 AVYADALKDNGEYTVADVADKGYTLNIFKAGKEKTPPEPKEEVTIKANLIYADGKTQTA 180
Db 121 AVYADALKDNGEYTVADVADKGYTLNIFKAGKEKTPPEPKEEVTIKANLIYADGKTQTA 180
QY 181 EFKGTFEEATAEAYRYADLLAKENGKGYTVADVADKGYTLNIFKAGKEKTPPEPKEEVTIKA 240
Db 181 EFKGTFEEATAEAYRYADLLAKENGKGYTVADVADKGYTLNIFKAGKEKTPPEPKEEVTIKA 240
QY 241 NLIYADGKTQTAFFKGTPEEATAEAYRYADLLAKENGKGYTVADVADKGYTLNIFKAGKEKTPPEPKEEVTIKA 300
Db 241 NLIYADGKTQTAFFKGTPEEATAEAYRYADLLAKENGKGYTVADVADKGYTLNIFKAGKEKTPPEPKEEVTIKA 300
QY 301 EKPEEPMDYKLLNGKTLKGETTTEAVDAATAEAKVFKOYANDNGVDGWTYDDATKTFT 360
Db 301 EKPEEPMDYKLLNGKTLKGETTTEAVDAATAEAKVFKOYANDNGVDGWTYDDATKTFT 360
QY 361 VTEKPEVIDASELTAVTYTKLVINGKTLKGETTTKAVDAETAETAEAKVFKOYANDNGVDGW 420
Db 361 VTEKPEVIDASELTAVTYTKLVINGKTLKGETTTKAVDAETAETAEAKVFKOYANDNGVDGW 420
QY 421 TYDDATKTFTVTTEM 434
Db 421 TYDDATKTFTVTTEM 434

RESULT 2

US-08-795-475-1
; Sequence 1, Application US/08795475
; Patent No. 5965390
; GENERAL INFORMATION:
; APPLICANT: Bjvrck, Lars
; APPLICANT: Sjvbring, Ulf
; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,475
; FILING DATE: 11-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 100084.402D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 305 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli LE392/pHDL, DSM 7054

US-08-795-475-1

Query Match 70.0%; Score 1565; DB 2; Length 305;
Best Local Similarity 100.0%; Pred. No. 6.9e-117;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVENKEETPETDSEEVITKANLIFANGSTQTAFFKGTPEKATSEAYAYADTLKKN 60
Db 1 AVENKEETPETDSEEVITKANLIFANGSTQTAFFKGTPEKATSEAYAYADTLKKN 60
QY 61 GEYTVADVADKGYTLNIFKAGKEKTPPEPKEEVTIKANLIYADGKTQTAFFKGTPEEATAE 120
Db 61 GEYTVADVADKGYTLNIFKAGKEKTPPEPKEEVTIKANLIYADGKTQTAFFKGTPEEATAE 120
QY 121 AVYADALKDNGEYTVADVADKGYTLNIFKAGKEKTPPEPKEEVTIKANLIYADGKTQTA 180
Db 121 AVYADALKDNGEYTVADVADKGYTLNIFKAGKEKTPPEPKEEVTIKANLIYADGKTQTA 180
QY 181 EFKGTFEEATAEAYRYADLLAKENGKGYTVADVADKGYTLNIFKAGKEKTPPEPKEEVTIKA 240
Db 181 EFKGTFEEATAEAYRYADLLAKENGKGYTVADVADKGYTLNIFKAGKEKTPPEPKEEVTIKA 240
QY 241 NLIYADGKTQTAFFKGTPEEATAEAYRYADLLAKENGKGYTVADVADKGYTLNIFKAGKEKTPPEPKEEVTIKA 300
Db 241 NLIYADGKTQTAFFKGTPEEATAEAYRYADLLAKENGKGYTVADVADKGYTLNIFKAGKEKTPPEPKEEVTIKA 300
QY 301 EKPEE 305
Db 301 EKPEE 305

RESULT 3

US-08-446-137B-2
; Sequence 2, Application US/08446137B
; Patent No. 6162903
; GENERAL INFORMATION:
; APPLICANT: Townen, Angus R.
; APPLICANT: Atkinson, Anthony
; APPLICANT: Murphy, Jonathan P.
; APPLICANT: Laurence, Oliver S.
; APPLICANT: Duggleby, Clive J.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEINS DERIVED
; FROM L PROTEIN AND THEIR USES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,137B
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 100084.406
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein


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; REFERENCE/DOCKET NUMBER: 61743/102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 664 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-669-408B-2

Query Match 31.6%; Score 706.5; DB 3; Length 664;
Best Local Similarity 43.9%; Pred. No. 3.6e-48;
Matches 192; Conservative 51; Mismatches 143; Indels 51; Gaps 17;

QY 24 ANLIIFANGSTQTAEPKGFEEKATSEAYAYADTLK-KDNGEYTVDVADKGYTL--NIKFA- 79
Db 148 ANEIVNNSDAYTAESIQPLKINDAY---DVLESKDYSKY--DSODKVNNLADQLRDVA 202
QY 80 -----GKEKTPPEEKVEETIKANLIYADGKTQTAEFGKGTFEATAEA--YRYA 125
Db 203 QAVOLEAPTVIDAPELTPALTYTKLVKGNTP--SGEITK-----AIDTATAEKEFKQYA 256
QY 126 DALKDNGEYTVDVADKGYTLNIKFA---GKEKTPPEEKVEETIKANLIYADGKTQTAEF 182
Db 257 TANNVD--GWSYDDATKTFTVTEKPAVIDAPELTPALTYTKLVKGNTP--SGEITK--- 310
QY 183 KGTFEATAEAYRYADLLAKENGYTVDVADKGYTLNIKFA--GKEKTPPEEKVEETIK 239
Db 311 KAVDAETAETAKFKQYATANNVDGWSYDDATKTFTVTEKPAVIDAPELTPALTYTKLVK 370
QY 240 ANLIYADGKTQTAEFGKGTFAEATAEAYRYADLLAKENGYTADLEDGGYTYINIRFAGKV 299
Db 371 GNTP--SGEITTKAIDATAEAEKFKQYATANGV--DGWSYDDATKTFTVTEKPA--V 422
QY 300 DEKPE--EPMQDYKLIILNGKTLKGETTTEAVDAATAEAKVKFOYANDNGVDGWTYDDATK 357
Db 423 IDAPELTPALTYTKLVKGNTPSGEITTKAVDAETAETAKFKQYANENGWYGSYDDATK 482
QY 358 TTTVTTEKPEVIDASELTPAVTYTKLVINGKTLKGETTTTKAVDAETAETAKFKQYANDNGVD 417
Db 483 TTTVTTEKPAVIDAPELTPALTYTKLVINGKTLKGETTTTKAVDAETAETAKFKQYANENGVD 542
QY 418 GWTYDDATKTFTVTEM 434
Db 543 GWTYDDATKTFTVTEM 559

RESULT 6
US-08-378-761A-25
; Sequence 25, Application US/08378761A
; Patent No. 5635384
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; TITLE OF INVENTION: USING
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,761A
; FILING DATE: 26-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 38272B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-378-761A-25

Query Match 27.9%; Score 622.5; DB 1; Length 502;
Best Local Similarity 41.1%; Pred. No. 1.2e-41;
Matches 178; Conservative 36; Mismatches 136; Indels 83; Gaps 16;

QY 37 EFKGTF-----EKATSEAYAYADTLKKDNGEYTVDV-ADKGYTLNIKFAKKEKTPPEPK 89
Db 38 DHKGFQPVLPPEKVPKPELWFYTE--LKTSTSSITLAIMDNLVLFGRPPG----- 87
QY 90 EEVTIKANLIYADGKTQTAEFGKGTFEATAEAYRYADALKDNGEYTVDVADKGYTLNIK 149
Db 88 -----GWWEFGKDGTHLLGDNPRLWLGFGGRYQD-LIGNKGLSETVTMGRAE MTRAVN 139
QY 150 FAGKEKTPPEEKVEETIKANLIYADGKTQTAEFGKGTFEATAEAYRYADLLAKENGYTV 209
Db 140 DLAKKKKAADPQ-----ADTKSLVK-----LVVMVCEGLRFNTV-----SRTV 178
QY 210 DV---ADKGYTLNIKFAKKEKTPPEKVEETIKANLIYADGKTQT-ABFKGTFAEATAEA 265
Db 179 DAGFNSHQGVTLTVT-QGK----QVQKWDRIKSAFAEADHPTAVIPDMQKLGKDKNEA 233
QY 266 YRYADLLAKENGYTADLEDGGYTYINIRFAGKVDKPE-----EPMQDYKLIILNGK 317
Db 234 ARIVALV--KNOTTAATAAGTAGSCARVRRSSCGVD-KPEVIDASELTPAVTYTKLVINGK 290
QY 318 TLKGETTTEAVDAATAEAKVKFOYANDNGVDGWTYDDATKTFTVTE----- 363
Db 291 TLKGETTTEAVDAATAEAKVKFOYANDNGVDGWTYDDATKTFTVTEKPEVIDASELTPAV 350
QY 364 ---KPEVIDASELTPAVTYTKLVINGKTLKGETTTTKAVDAETAETAKFKQYANDNGVDGYW 420
Db 351 TRSKPEVIDASELTPAVTYTKLVINGKTLKGETTTEAVDAATAEAKVKFOYANDNGVDGYW 410
QY 421 TYDDATKTFTVTE 433
Db 411 TYDDATKTFTVTE 423

RESULT 7
US-08-485-286-25
; Sequence 25, Application US/08485286
; Patent No. 5646026
; Patent No. 5646026
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; TITLE OF INVENTION: USING
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
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US-08-485-286-23
; Sequence 23, Application US/08485286
; Patent No. 5646026
; Patent No. 5646026 5646119
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; TITLE OF INVENTION: USING
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,286
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/378761
; FILING DATE: 26-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 38272B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 493 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-485-286-23

Query Match 27.8%; Score 622; DB 1; Length 493;
Best Local Similarity 40.6%; Pred. NO. 1.2e-41;
Matches 176; Conservative 38; Mismatches 127; Indels 92; Gaps 17;

QY 37 EFKGTF-----EKATSEAYADTLKKDNGEYTDV-ADKGYTLNFKAGKEKTPPEPK 89
DB 38 DHKGFQVLPPEKKVPPELWYTE-LKTRTSITLAIRMDNLVLVGFRTPG-----87

QY 90 BEVTIKANLIYADGKTQTAEFGTFEEATAEAYRYADALKKDNGETYVDVADKGYTLNFK 149
DB 88 -----GVWFEKDGTHLLGDNPRLWFGGRVQD-LIGNKGLGYTMGRAETRAVN 139

QY 150 FAGKEKTPPEKPEVTIKANLIYADGKTQTAEFGTFEEATAEAYRYADLLAKENGKTV 209
DB 140 DLAKKKAADPQ-----ADTKSLVK-----LVVMVCEGLRFNTV-----SRTV 178

QY 210 DV---ADKGYTLNFKAGKEKTPPEKPEVTIKANLIYADGKTQT-APFKGTFEATAEA 265
DB 179 DAGNSQHGVTLTVT-QGK-----QVQKWDRIKSKAAFEWADHPTAIPDMQKLGDKRNEA 233

QY 266 YRYADLLAKENGKTTADLDGGYTLNIRFACKGVDEKPE-----EPMDYTKLILNGK 317
DB 234 ARIVALVKNQT---TAAATAG-SVNV-----DKPEVIDASELTPAVTYKLIVNGK 281

QY 318 TLKGETTTEAYDAATAEKVFKQYANDNGVDGWTYDDATKTTFTVTE-----363
DB 282 TLKGETTTEAYDAATAEKVFKQYANDNGVDGWTYDDATKTTFTVTEKPEVIDASELTPAV 341

QY 364 ---KPEVIDASELTPAVTYKLIVNGKTLKGETTTKAVDAETAETAKAFKQYANDNGVDGW 420
DB 342 TRSKPEVIDASELTPAVTYKLIVNGKTLKGETTTEAYDAATAEKVFKQYANDNGVDGEW 401

QY 421 TYDDATKTTFTVTE 433
DB 402 TYDDATKTTFTVTE 414

RESULT 10
US-08-828-741B-6
; Sequence 6, Application US/08828741B
; Patent No. 6043069
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Sues, Gabriele M.
; APPLICANT: Tarlington, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
; TITLE OF INVENTION: PRODUCING SAME
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,741B
; FILING DATE: 26-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10591
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 342 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-828-741B-6

Query Match 27.7%; Score 618; DB 3; Length 342;
Best Local Similarity 75.9%; Pred. NO. 1.5e-41;
Matches 126; Conservative 5; Mismatches 15; Indels 20; Gaps 1;

QY 16 SEEVTKANLIIFANGSTQTAEFGTFEKATSEAYAYADTLKKONGEYTVDVADKGYTLN 75
DB 174 SAEVTKANLIIFANGSTQTAEFGTFEKATSEAYAYADTLKKONGEYTVDVADKGYTLN 233

QY 76 IKFAGKEKTPPE-----PKPEVTIKANLIYADGKTQTAEFGTFE 115
DB 234 IKFAGKEATNRTDGTGYILQINSRMGGLTSAEVTIKANLIIFANGSTQTAEFGTFE 293

QY 116 EATAEAYRYADALKKDNGETYVDVADKGYTLNIRFAGKEKTPPEPK 161
DB 294 KATSEAYAYADTLKKDNGETYVDVADKGYTLNIRFAGKESAWRHQ 339

RESULT 11
US-09-160-567-6
; Sequence 6, Application US/09160567

Patent No. 6326179
GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,567
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,741
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 342 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-160-567-6

Query Match 27.7%; Score 618; DB 4; Length 342;
Best Local Similarity 75.9%; Pred. No. 1.5e-41;
Matches 126; Conservative 5; Mismatches 15; Indels 20; Gaps 1;

QY 16 S E E V T I K A N L I F A N G S T O T A E P K G T F E K A T S E A Y A D T L K K D N G E Y T V D V A D K G Y T L N 75
Db 174 S A E E V T I K A N L I F A N G S T O T A E P K G T F E K A T S E A Y A D T L K K D N G E Y T V D V A D K G Y T L N 233

QY 76 I R F A G K E K T P E E -----P K E E V T I K A N L I Y A D G K T Q T A E F K G T F E 115
Db 234 I F A G K E A T N R N T D G S T D Y G I L Q I N S R W G L T S A E E V T I K A N L I F A N G S T O T A E F K G T F E 293

QY 116 E A T A E A Y R A D A L K K D N G E Y T V D V A D K G Y T L N I K F A G K E K T P E E P K 161
Db 294 K A T S E A Y A D T L K K D N G E Y T V D V A D K G Y T L N I K F A G K E S A W R H P Q 339

RESULT 12
US-09-710-299-6
Sequence 6, Application US/09710299
Patent No. 6521741
GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
Suess, Gabriele M.
Tarlinton, David M.
Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
PRODUCING SAME
NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/710,299
FILING DATE: 09-No. 6521741-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,741
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 342 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-710-299-6

Query Match 27.7%; Score 618; DB 4; Length 342;
Best Local Similarity 75.9%; Pred. No. 1.5e-41;
Matches 126; Conservative 5; Mismatches 15; Indels 20; Gaps 1;

QY 16 S E E V T I K A N L I F A N G S T O T A E P K G T F E K A T S E A Y A D T L K K D N G E Y T V D V A D K G Y T L N 75
Db 174 S A E E V T I K A N L I F A N G S T O T A E P K G T F E K A T S E A Y A D T L K K D N G E Y T V D V A D K G Y T L N 233

QY 76 I R F A G K E K T P E E -----P K E E V T I K A N L I Y A D G K T Q T A E F K G T F E 115
Db 234 I F A G K E A T N R N T D G S T D Y G I L Q I N S R W G L T S A E E V T I K A N L I F A N G S T O T A E F K G T F E 293

QY 116 E A T A E A Y R A D A L K K D N G E Y T V D V A D K G Y T L N I K F A G K E K T P E E P K 161
Db 294 K A T S E A Y A D T L K K D N G E Y T V D V A D K G Y T L N I K F A G K E S A W R H P Q 339

RESULT 13
US-08-378-761A-19
Sequence 19, Application US/08378761A
Patent No. 5635384
GENERAL INFORMATION:
APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D
APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
PRECUSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
TITLE OF INVENTION: USING
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:

ADDRESSEE: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: US
ZIP: 46268

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,286

FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/378761
FILING DATE: 26-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 38272B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 489 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-286-19

[illegible]

Query Match	27.7%	Score	618;	DB	1;	Length	489;	
Best Local Similarity	40.9%;	Pred.	No. 2.5e-41;					
Matches	175;	Conservative	35;	Mismatches	131;	Indels	88; Gaps	16;
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Db	38	DHKGIFQPVLPEKKVPDELWFYTE-LKTRTSSITLAIMDNLYLVGFTPG-----	87					
QY	90	EEVTIKANLIYADGKTKQTAEFKGTFEATAEAARYADALKKDNGEYTVDVADKYTYTNLIK	149					
Db	88	-----GVWMEFGDGDDTHLLGNPNRWLGFGGRYQD-LIGNKLETVTMGRAEMTRAVN	139					
QY	150	FAGKEKTPPEPKBEVTIKANLIYADGKTQTAEFKGTFEATAEAARYADLLAKENGKTV	209					
Db	140	DLAKKKAADPQ-----ADTKSKLVK---LVVMVEGLRNTV-----SFTV	178					
QY	210	DV---ADKGVTNLNKFAGKEKTPPEPKBEVTIKANLIYADGKTKQT-AEFKGTFAEATAEA	265					
Db	179	DAGFNSQHGWTKLTVT-QGK---QVOKWDRIKAAFEWAHDPTAVIPDMQKLGIKDKNEA	233					
QY	266	YRYADILLAKENGKVTADLEDGGVTINIRFAGKK--VDEKPEEP-MDTYKILANGKTLKG	321					
Db	234	ARIVALVKNOT-----TAAATAGSRPEVIDASELTPAVTTYKLVINGKTLKG	281					
QY	322	ETTTEAADAATAEKVFQKYANDNGVDGEWTYYDDATKTTFTVE-----K	364					
Db	282	ETTTEAADAATAEKVFQKYANDNGVDGEWTYYDDATKTTFTVEKPEVIDASELTPAVTRSK	341					
QY	365	PEVIDASELTPAVTTYKLVINGKTLKETTTKAVDAETAEKAFQKYANDNGVDGWYYDD	424					
Db	342	PEVIDASELTPAVTTYKLVINGKTLGETTEAVDAATAEKVFQKYANDNGVDGEYDD	401					
QY	425	ATKTFVTTE	433					
Db	402	ATKTFVTTE	410					

RESULT 15
US-08-828-741B-13
; Sequence 13, Application US/08828741B
; Patent No. 6043069

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Job time : 17.4438 secs

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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:03:32 ; Search time 45.2206 Seconds
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Title: US-08-325-278B-3

Perfect score: 2235

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Searched: 513375 seqs, 137303645 residues

Total number of hits satisfying chosen parameters: 513375

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1585	70.0	305	8	US-08-325-278-1
3	697.5	31.2	669	9	US-09-878-756-4
4	618	27.7	342	12	US-10-345-618-6
5	615	27.5	178	12	US-10-345-618-13
6	615	27.5	198	12	US-10-345-618-8
7	614	27.5	495	12	US-10-345-618-4
8	613	27.4	182	12	US-10-345-618-2
9	608	27.2	482	12	US-10-345-618-16
10	389	17.4	76	10	US-09-808-212A-4
11	371	16.6	72	10	US-09-808-212A-6
12	370	16.6	72	10	US-09-808-212A-10
13	369	16.5	72	10	US-09-808-212A-8
14	341	15.3	82	10	US-09-808-212A-2
15	336	15.0	166	12	US-10-338-411-21

Sequence 18, Appl
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Sequence 16, Appl
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Sequence 56, Appl
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Sequence 68, Appl
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Sequence 33, Appl
Sequence 118, Appl
Sequence 16, Appl
Sequence 56, Appl
Sequence 58, Appl
Sequence 14, Appl
Sequence 35, Appl
Sequence 10, Appl
Sequence 6, Appl
Sequence 7, Appl
Sequence 184, Appl
Sequence 5, Appl
Sequence 383, Appl
Sequence 2, Appl
Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-08-325-278-3
; Sequence 3, Application US/08325278
; Publication No. US20030027283A1
; GENERAL INFORMATION:
; APPLICANT: Bjvrck, Lars
; APPLICANT: Sjbvring, Ulf
; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,278
; FILING DATE: 26-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMaisters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 450023.401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 434 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown

```

; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli LE392/pHDLG, DSM 7055
US-08-325-278-3

Query Match      100.08; Score 2235; DB 8; Length 434;
Best Local Similarity 100.08; Pred. No. 5.7e-158;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY      1 AVENEKEETPEPTDSEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAVADTLKKDN 60
        |||||||
Db      1 AVENEKEETPEPTDSEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAVADTLKKDN 60
        |||||||

QY      61 GEYTVDVADKGYTLNIFAGKEKTPPEPKKEVTIKANLIYADGKTQTAEFKGTFEETAAE 120
        |||||||
Db      61 GEYTVDVADKGYTLNIFAGKEKTPPEPKKEVTIKANLIYADGKTQTAEFKGTFEETAAE 120
        |||||||

QY      121 ATRYADALKKONGEYTVDVADKGYTLNIFAGKEKTPPEPKKEVTIKANLIYADGKTQTAE 180
        |||||||
Db      121 ATRYADALKKONGEYTVDVADKGYTLNIFAGKEKTPPEPKKEVTIKANLIYADGKTQTAE 180
        |||||||

QY      181 EFKGTFEEATAEAYRYADLLAKENGKTYTVDVADKGYTLNIFAGKEKTPPEPKKEEVTIKA 240
        |||||||
Db      181 EFKGTFEEATAEAYRYADLLAKENGKTYTVDVADKGYTLNIFAGKEKTPPEPKKEEVTIKA 240
        |||||||

QY      241 NLIYADGKTQTAEAFKGTFAEATAEAYRYADLLAKENGKTYTADLEDGGYTNIRFAGKKYD 300
        |||||||
Db      241 NLIYADGKTQTAEAFKGTFAEATAEAYRYADLLAKENGKTYTADLEDGGYTNIRFAGKKYD 300
        |||||||

QY      301 EKPEEPMDTYKLIILNGKTLKGETTTEAVDAATAEKVFKQYANDNGVDGWTYDDATKTKFT 360
        |||||||
Db      301 EKPEEPMDTYKLIILNGKTLKGETTTEAVDAATAEKVFKQYANDNGVDGWTYDDATKTKFT 360
        |||||||

QY      361 VPEKEVIDASBELTPAVTYYKLVIINGKTLKGETTTTAVDAETAETAKAFKQYANDNGVDGW 420
        |||||||
Db      361 VPEKEVIDASBELTPAVTYYKLVIINGKTLKGETTTTAVDAETAETAKAFKQYANDNGVDGW 420
        |||||||

QY      421 TYDDATKTKFTVTTEM 434
        |||||||
Db      421 TYDDATKTKFTVTTEM 434
        |||||||

```

```

RESULT 2
US-08-325-278-1
: Sequence 1, Application US/08325278
: Publication No. US20030027283A1
: GENERAL INFORMATION:
: APPLICANT: Bjvrck, Lars
: APPLICANT: Sjvbring, Olf
: TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SEED and BERRY LLP
: STREET: 6300 Columbia Center, 701 Fifth Avenue
: CITY: Seattle
: STATE: Washington
: COUNTRY: USA
: ZIP: 98104-7092
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/325,278
: FILING DATE: 26-OCT-1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Mcmasters, David D.
: REGISTRATION NUMBER: 33,963
: REFERENCE/DOCKET NUMBER: 450023.401
: TELECOMMUNICATION INFORMATION:

```

```

; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 305 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli LE392/pHDL, DSM 7054
; US-08-325-278-1

Query Match 70.0%; Score 1565; DB 8; Length 305;
Best Local Similarity 100.0%; Pred. No. 1.7e-108;
Matches 305; Conservative 0; Mismatches 0; Indels 0;

Qy 1 AVENKEETPTPTDSEEEVTIKANLIIFANGSTQTAEFKGTPEKATSEAYAYAD
Db 1 AVENKEETPTPTDSEEEVTIKANLIIFANGSTQTAEFKGTPEKATSEAYAYAD
Qy 61 GEYTVVDADKGYTLNKFAGKEKTPPEPKEEVTIKANLIYADGKTQTAEFKGTF
Db 61 GEYTVVDADKGYTLNKFAGKEKTPPEPKEEVTIKANLIYADGKTQTAEFKGTF
Qy 121 AYRYADALKKDNGEYTVVDADKGYTLNKFAGKEKTPPEPKEEVTIKANLIYAD
Db 121 AYRYADALKKDNGEYTVVDADKGYTLNKFAGKEKTPPEPKEEVTIKANLIYAD
Qy 181 EFKGTPEEATAEAYRYADLLAKENGKYYTVVDADKGYTLNKFAGKEKTPPEPKEE
Db 181 EFKGTPEEATAEAYRYADLLAKENGKYYTVVDADKGYTLNKFAGKEKTPPEPKEE
Qy 241 NLIYADGKTQTAEFKGTFEATAEAYRYADLLAKENGKYTADLEDGYYTINIRF
Db 241 NLIYADGKTQTAEFKGTFEATAEAYRYADLLAKENGKYTADLEDGYYTINIRF
Qy 301 EKPEE 305
Db 301 EKPEE 305

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RESULT 3
US-09-878-756-4
; Sequence 4, Application US/09878756
; Patent No. US20020025322A1
; GENERAL INFORMATION:
; APPLICANT: Potter, Andrew A.
; APPLICANT: Bolton, Alexandra J.
; APPLICANT: Song, Xin Ming
; TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH MIG PROTEIN
; FILE REFERENCE: 9000-0056
; CURRENT APPLICATION NUMBER: US/09/878,756
; CURRENT FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 669
; TYPE: PRT
; ORGANISM: Streptococcus dysgalactiae
US-09-878-756-4

Query Match          31.2%; Score 697.5; DB 9; Length 669;
Best Local Similarity 43.3%; Pred. No. 1e-43;
Matches 190; Conservative 49; Mismatches 147; Indels 51;

QY      24  ANLIFANGSTQTAEFKGTTEKATSEAYAYADTLK-KDNGEYTVDVADKGYTL--
      ||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      148  ANEIVNSDAYTAEISTQSIYKLINDAY----DVLESKDYSK--DSQDKVNNLAD
      ||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      80  -----GKEKTPEEPKEEVTEIKANLIYADKTKTQTAFFKGTFFEEATAEA
      ||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | |

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Db 203 QAVOLEAPTVIDAPALTPALTYKLVKGNF--SGETTK----AIDTAKEFKQYA 256
Qy 126 DALKKDNGEYTVADVADKGYTLNKAFA--GKEKTPPEPKBEVTIKANLIYADGKTQAEF 182
Db 257 TANVVD--GWSYDDATKTFVTEKPAVIDALELTPALTYKLVKGNF--SGETTKAI 313
Qy 183 KGTFEATAYRAYADLLAKENGKYTVDVADKGYTLNKAFA--GKEKTPPEPKBEVTIK 239
Db 314 DAATAEKEFKQYATAN--NVDGWSYDYATKTFVTEKPAVIDAPELTPALTYKLVK 370
Qy 240 ANLIYADGKTQAEFKTFAEATAEAYRYADLLAKENKTYADLEGGYTLNIRFAGKKV 299
Db 371 GNTF--SGETTKAIDATAEKEFKQYATAN--NVDGWSYDDATKTFVTEKPA---V 422
Qy 300 DEKPE--EPMDTYKLIILNGTKLGETTTEAVDAATAEKFQYANDKNGVDGYTDATK 357
Db 423 IDAPELTPALTYKLVKGNFSGETTKAVDAETAFAKQYATANNVDSYDDATK 482
Qy 358 TFWTEKPEVIDASELTPAVTYKLVINGKTLGKETTAKVDAETAFAKQYANDNGVD 417
Db 483 TFWTEKPAVIDAPELTPALTYKLVINGKTLGKETTAKVADVETAFAKQYANDGVD 542
Qy 418 GVWYDDATKTFVTTEM 434
Db 543 GVWYDDATKTFVTTEM 559

RESULT 4
US-10-345-618-6
; Sequence 6, Application US/10345618
; Publication No. US20030148484A1
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBOIDS AND A METHOD OF PRODUCING SAME
; FILE REFERENCE: 13474
; CURRENT APPLICATION NUMBER: US/10/345,618
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US/09/509,031
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TLHL protein
; OTHER INFORMATION: sequence
US-10-345-618-6

Query Match 27.7%; Score 618; DB 12; Length 342;
Best Local Similarity 75.9%; Pred. No. 3.3e-38;
Matches 126; Conservative 5; Mismatches 15; Indels 20; Gaps 1;

Qy 16 SEEVTIKANLIFANGSTQTAEFKGTSEAYAYADTLKKDNGEYTVDVADKGYTLN 75
Db 174 SAEVTIKANLIFANGSTQTAEFKGTSEAYAYADTLKKDNGEYTVDVADKGYTLN 233
Qy 76 IKFAGKEKTPPE-----PKEEVTIKANLIYADGKTQTAEFKGTPE 115
Db 234 IKFAGKEATNRNTDGSYDGIQINSRWGLTSAEVTIKANLIFANGSTQTAEFKGTPE 293
Qy 116 EATAEAYRYADLKKDNGEYTVDVADKGYTLNKFAGKEKTPPEPK 161
Db 294 KATSEAYAYADTLKKDNGEYTVDVADKGYTLNKFAGKESAWRHPQ 339

RESULT 5
US-10-345-618-13
; Sequence 13, Application US/10345618
```

```
; Publication No. US20030148484A1
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBOIDS AND A METHOD OF PRODUCING SAME
; FILE REFERENCE: 13474
; CURRENT APPLICATION NUMBER: US/10/345,618
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US/09/509,031
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LHL-omp
; OTHER INFORMATION: protein sequence
US-10-345-618-13

Query Match 27.5%; Score 615; DB 12; Length 178;
Best Local Similarity 76.2%; Pred. No. 2.3e-38;
Matches 125; Conservative 5; Mismatches 14; Indels 20; Gaps 1;

Qy 18 EEVTIKANLIFANGSTQTAEFKGTSEAYAYADTLKKDNGEYTVDVADKGYTLN 77
Db 12 EEVTIKANLIFANGSTQTAEFKGTSEAYAYADTLKKDNGEYTVDVADKGYTLN 71
Qy 78 FAGKEKTPPE-----PKEEVTIKANLIYADGKTQTAEFKGTPEEA 117
Db 72 FAGKEATNRNTDGSYDGIQINSRWGLTSAEVTIKANLIFANGSTQTAEFKGTPEKA 131
Qy 118 TAEAYRYADLKKDNGEYTVDVADKGYTLNKFAGKEKTPPEPK 161
Db 132 TSEAYAYADTLKKDNGEYTVDVADKGYTLNKFAGKESAWRHPQ 175

RESULT 6
US-10-345-618-8
; Sequence 8, Application US/10345618
; Publication No. US20030148484A1
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBOIDS AND A METHOD OF PRODUCING SAME
; FILE REFERENCE: 13474
; CURRENT APPLICATION NUMBER: US/10/345,618
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US/09/509,031
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LHL.seq
; OTHER INFORMATION: protein sequence
US-10-345-618-8

Query Match 27.5%; Score 615; DB 12; Length 198;
Best Local Similarity 76.2%; Pred. No. 2.6e-38;
Matches 125; Conservative 5; Mismatches 14; Indels 20; Gaps 1;

Qy 18 EEVTIKANLIFANGSTQTAEFKGTSEAYAYADTLKKDNGEYTVDVADKGYTLN 77
Db 32 EEVTIKANLIFANGSTQTAEFKGTSEAYAYADTLKKDNGEYTVDVADKGYTLN 91
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QY 78 FAGKEKTPPE-----PKEEVTIKANLIYADGKTQTAEFGTFEFA 117
| | | | |
DB 92 FAGKEATNRTDGDYGIQINSRWGGLTSAEEVTIKANLIIFANGSTQTAEFGTFEFA 151
| | | | |
QY 118 TAEAYRYADALKKNGEYTVDVADKGYTLNIFAGKEKTPPEPK 161
| | | | |
DB 152 TSEAYAYADTLKKNGEYTVDVADKGYTLNIFAGKESAWRHQP 195
| | | | |

RESULT 7
US-10-345-618-4
; Sequence 4, Application US/10345618
; Publication No. US20030148484A1
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING SAME
; FILE REFERENCE: 13474
; CURRENT APPLICATION NUMBER: US/10/345,618
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US/09/509,031
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:CATAB-TEV
; OTHER INFORMATION: protein sequence
US-10-345-618-4

Query Match 27.5%; Score 614; DB 12; Length 495;
Best Local Similarity 78.6%; Pred. No. 1.1e-37;
Matches 125; Conservative 4; Mismatches 10; Indels 20; Gaps 1;
QY 16 SEEEVTIKANLIIFANGSTQTAEFGTFEKAATSEAYAYADTLKKNGEYTVDVADKGYTLN 75
| | | | |
DB 174 SAEVETIKANLIIFANGSTQTAEFGTFEKAATSEAYAYADTLKKNGEYTVDVADKGYTLN 233
| | | | |
QY 76 IKFAGKEKTPPE-----PKEEVTIKANLIYADGKTQTAEFGTFE 115
| | | | |
DB 234 IKFAGKEATNRTDGDYGIQINSRWGGLTSAEEVTIKANLIIFANGSTQTAEFGTFE 293
| | | | |
QY 116 EATAEAYRYADALKKNGEYTVDVADKGYTLNIFAGKE 154
| | | | |
DB 294 KATSEAYAYADTLKKNGEYTVDVADKGYTLNIFAGKE 332
| | | | |

RESULT 8
US-10-345-618-2
; Sequence 2, Application US/10345618
; Publication No. US20030148484A1
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING SAME
; FILE REFERENCE: 13474
; CURRENT APPLICATION NUMBER: US/10/345,618
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US/09/509,031
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 182
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:LHL protein
; OTHER INFORMATION: sequence
US-10-345-618-2
Query Match 27.4%; Score 613; DB 12; Length 182;
Best Local Similarity 78.5%; Pred. No. 3.3e-38;
Matches 124; Conservative 5; Mismatches 9; Indels 20; Gaps 1;
QY 15 DSEEEVTIKANLIIFANGSTQTAEFGTFEKAATSEAYAYADTLKKNGEYTVDVADKGYTLN 74
| | | | |
DB 25 DNTFEVTIKANLIIFANGSTQTAEFGTFEKAATSEAYAYADTLKKNGEYTVDVADKGYTLN 84
| | | | |
QY 75 NIKFAGKEKTPPE-----KEEVTIKANLIYADGKTQTAEFGTFE 114
| | | | |
DB 85 NIKFAGKEATNRTDGDYGIQINSRWGGLTSAEEVTIKANLIIFANGSTQTAEFGTFE 144
| | | | |
QY 115 EATAEAYRYADALKKNGEYTVDVADKGYTLNIFAG 152
| | | | |
DB 145 EKATSEAYAYADTLKKNGEYTVDVADKGYTLNIFAG 182
| | | | |
RESULT 9
US-10-345-618-16
; Sequence 16, Application US/10345618
; Publication No. US20030148484A1
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING SAME
; FILE REFERENCE: 13474
; CURRENT APPLICATION NUMBER: US/10/345,618
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US/09/509,031
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 16
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:comTLgL protein
; OTHER INFORMATION: sequence
US-10-345-618-16

Query Match 27.2%; Score 608; DB 12; Length 482;
Best Local Similarity 80.0%; Pred. No. 2.9e-37;
Matches 124; Conservative 5; Mismatches 10; Indels 16; Gaps 1;
QY 16 SEEEVTIKANLIIFANGSTQTAEFGTFEKAATSEAYAYADTLKKNGEYTVDVADKGYTLN 75
| | | | |
DB 321 SAEVETIKANLIIFANGSTQTAEFGTFEKAATSEAYAYADTLKKNGEYTVDVADKGYTLN 380
| | | | |
QY 76 IKFAGKEKTPPE-----PEEPKEEVTIKANLIYADGKTQTAEFGTFEATA 119
| | | | |
DB 381 IKFAGKEASGGGGGGGGGGGGGGGGGGSAEEVTIKANLIIFANGSTQTAEFGTFEKAAT 440
| | | | |
QY 120 EAYRYADALKKNGEYTVDVADKGYTLNIFAGKE 154
| | | | |
DB 441 EAYAYADTLKKNGEYTVDVADKGYTLNIFAGKE 475
| | | | |

RESULT 10
US-09-808-212A-4
; Sequence 4, Application US/09808212A
; Patent No. US20020137918A1
; GENERAL INFORMATION:
; APPLICANT: Gore, Michael Graham
; APPLICANT: Beckingham, Jennifer Ann

; APPLICANT: Roberts, Sian Eleri
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN
; FILE REFERENCE: 100084.414US
; CURRENT APPLICATION NUMBER: US/09/808,212A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Peptostreptococcus sp.
US-09-808-212A-4

Query Match 17.4%; Score 389; DB 10; Length 76;
Best Local Similarity 100.0%; Pred. No. 4.1e-22;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 KEETPTPTDSEEVYTIKANLIFANGSTQTAEFKGTFAEATAYAYADTLKKNGEY 64
DB 1 KEETPTPTDSEEVYTIKANLIFANGSTQTAEFKGTFAEATAYAYADTLKKNGEY 60
QY 65 VDVAADKGYTLNKFAG 80
DB 61 VDVAADKGYTLNKFAG 76

RESULT 11
US-09-808-212A-6
; Sequence 6, Application US/09808212A
; Patent No. US20020137918A1
; GENERAL INFORMATION:
; APPLICANT: Gore, Michael Graham
; APPLICANT: Beckingham, Jennifer Ann
; APPLICANT: Roberts, Sian Eleri
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN
; FILE REFERENCE: 100084.414US
; CURRENT APPLICATION NUMBER: US/09/808,212A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Peptostreptococcus sp.
US-09-808-212A-6

Query Match 16.6%; Score 371; DB 10; Length 72;
Best Local Similarity 100.0%; Pred. No. 8.2e-21;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 81 KEETPEEPKEEVYTIKANLIYADGKTQTAEFKGTFAEATAYADALKKDNGEYTDVA 140
DB 1 KEETPEEPKEEVYTIKANLIYADGKTQTAEFKGTFAEATAYADALKKDNGEYTDVA 60
QY 141 DKGYTLNKFAG 152
DB 61 DKGYTLNKFAG 72

RESULT 12
US-09-808-212A-10
; Sequence 10, Application US/09808212A
; Patent No. US20020137918A1
; GENERAL INFORMATION:
; APPLICANT: Gore, Michael Graham
; APPLICANT: Beckingham, Jennifer Ann
; APPLICANT: Roberts, Sian Eleri
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN
; FILE REFERENCE: 100084.414US
; CURRENT APPLICATION NUMBER: US/09/808,212A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 10
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Peptostreptococcus sp.
US-09-808-212A-10

Query Match 16.6%; Score 370; DB 10; Length 72;
Best Local Similarity 100.0%; Pred. No. 9.7e-21;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 225 KEETPEEPKEEVYTIKANLIYADGKTQTAEFKGTFAEATAYADLLAKENGYTDADLE 284
DB 1 KEETPEEPKEEVYTIKANLIYADGKTQTAEFKGTFAEATAYADLLAKENGYTDADLE 60
QY 285 DGGYTNIRFAG 296
DB 61 DGGYTNIRFAG 72

RESULT 13
US-09-808-212A-8
; Sequence 8, Application US/09808212A
; Patent No. US20020137918A1
; GENERAL INFORMATION:
; APPLICANT: Gore, Michael Graham
; APPLICANT: Beckingham, Jennifer Ann
; APPLICANT: Roberts, Sian Eleri
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN
; FILE REFERENCE: 100084.414US
; CURRENT APPLICATION NUMBER: US/09/808,212A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Peptostreptococcus sp.
US-09-808-212A-8

Query Match 16.5%; Score 369; DB 10; Length 72;
Best Local Similarity 100.0%; Pred. No. 1.1e-20;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 153 KEETPEEPKEEVYTIKANLIYADGKTQTAEFKGTFAEATAYADLLAKENGYTDVA 212
DB 1 KEETPEEPKEEVYTIKANLIYADGKTQTAEFKGTFAEATAYADLLAKENGYTDVA 60
QY 213 DKGYTLNKFAG 224
DB 61 DKGYTLNKFAG 72

RESULT 14
US-09-808-212A-2
; Sequence 2, Application US/09808212A
; Patent No. US20020137918A1
; GENERAL INFORMATION:
; APPLICANT: Gore, Michael Graham
; APPLICANT: Beckingham, Jennifer Ann
; APPLICANT: Roberts, Sian Eleri
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN
; FILE REFERENCE: 100084.414US
; CURRENT APPLICATION NUMBER: US/09/808,212A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Peptostreptococcus sp.
US-09-808-212A-2

Query Match 15.3%; Score 341; DB 10; Length 82;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:01:51 ; Search time 317.131 Seconds
(without alignments)
1191.101 Million cell updates/sec

Title: US-08-325-278B-3
Perfect score: 2235
Sequence: 1 AVENKEPPEPTDSEEV.....GVDGWVYDDATKFTVTM 434

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 5580241 seqs, 870357830 residues

Total number of hits satisfying chosen parameters: 5580241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_AA_Main:*

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2:	/cgn2_6/ptodata/1/paa/US06_COMB.pep.*
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25:	/cgn2_6/ptodata/1/paa/US099B_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2235	100.0	434	7	US-08-325-278A-3 Sequence 3, Appli

3	2235	100.0	434	7	US-08-325-278B-3 Sequence 3, Appli
4	1587.5	71.0	719	22	US-09-791-537-10210 Sequence 10210, A
5	1587.5	71.0	719	22	US-09-791-537-96101 Sequence 96101, A
6	1565	70.0	305	7	US-08-325-278-1 Sequence 1, Appli
7	1565	70.0	305	7	US-08-325-278A-1 Sequence 1, Appli
8	1565	70.0	305	7	US-08-325-278B-1 Sequence 1, Appli
9	1372	69.4	467	25	US-09-880-469-12 Sequence 12, Appli
10	1372	69.4	467	25	US-09-889-182A-4 Sequence 4, Appli
11	1263.5	56.5	992	22	US-09-791-537-88366 Sequence 88366, A
12	1263.5	56.5	1027	7	US-08-331-637-2 Sequence 2, Appli
13	1263.5	56.5	1027	8	US-08-446-137A-2 Sequence 2, Appli
14	1263.5	56.5	1027	15	US-09-187-295-2 Sequence 2, Appli
15	1216	54.4	291	8	US-08-446-137A-4 Sequence 4, Appli
16	708	31.7	593	22	US-09-791-537-86905 Sequence 86905, A
17	706.5	31.6	664	10	US-08-669-408-2 Sequence 2, Appli
18	706.5	31.6	664	10	US-08-669-408A-2 Sequence 2, Appli
19	697.5	31.2	669	23	US-09-878-756-4 Sequence 4, Appli
20	692.5	31.0	480	22	US-09-791-537-79119 Sequence 79119, A
21	683	30.6	448	22	US-09-791-537-86901 Sequence 86901, A
22	683	30.6	448	31	US-60-388-059-5 Sequence 5, Appli
23	670	30.0	185	17	US-09-315-208-2 Sequence 2, Appli
24	670	30.0	185	22	US-09-791-537-5341 Sequence 5341, Ap
25	634.5	28.4	228	23	US-09-889-182A-2 Sequence 2, Appli
26	627	28.1	250	23	US-09-889-182A-6 Sequence 6, Appli
27	625	28.0	208	5	US-08-110-653-11 Sequence 11, Appli
28	622.5	27.9	502	7	US-08-378-761-25 Sequence 25, Appli
29	622	27.8	493	7	US-08-378-761-23 Sequence 23, Appli
30	618	27.7	342	19	US-09-509-031-6 Sequence 6, Appli
31	618	27.7	342	23	US-09-820-048A-6 Sequence 6, Appli
32	618	27.7	489	7	US-08-378-761-19 Sequence 19, Appli
33	615	27.5	178	19	US-09-509-031-13 Sequence 13, Appli
34	615	27.5	178	23	US-09-820-048A-13 Sequence 13, Appli
35	615	27.5	198	23	US-09-509-031-8 Sequence 8, Appli
36	615	27.5	198	23	US-09-820-048A-8 Sequence 8, Appli
37	614	27.5	495	19	US-09-509-031-4 Sequence 4, Appli
38	614	27.5	495	23	US-09-820-048A-4 Sequence 4, Appli
39	613	27.4	182	19	US-09-509-031-2 Sequence 2, Appli
40	613	27.4	182	23	US-09-820-048A-2 Sequence 2, Appli
41	608	27.2	482	19	US-09-509-031-16 Sequence 16, Appli
42	481	21.5	429	22	US-09-791-537-146174 Sequence 146174, A
43	404	18.1	413	10	US-08-669-408-10 Sequence 10, Appli
44	404	18.1	413	10	US-08-669-408A-10 Sequence 10, Appli
45	404	18.1	413	22	US-09-791-537-131407 Sequence 131407, A

ALIGNMENTS

RESULT 1
US-08-325-278-3
; Sequence 3, Application US/08325278
; GENERAL INFORMATION:
; APPLICANT: Bjvrck, Lars
; APPLICANT: Sjvbring, Ulf
; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,278
; FILING DATE: 26-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

```

; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 450023.401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 434 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli LE392/pHDLG, DSM 7055
; US-08-325-278-3

Query Match 100.0%; Score 2235; DB 7; Length 434;
Best Local Similarity 100.0%; Pred. No. 7.5e-162;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVENKEETPETDSEEVTIKANLIIFANGSTQTAFFKGTSEAYAYADTLKKDN 60
DB 1 AVENKEETPETDSEEVTIKANLIIFANGSTQTAFFKGTSEAYAYADTLKKDN 60
QY 61 GEYTVADVADKGYTLNIFAGKEKTPPEPKKEEVTIKANLIYADGKTQTAEFKGTPEEATAE 120
DB 61 GEYTVADVADKGYTLNIFAGKEKTPPEPKKEEVTIKANLIYADGKTQTAEFKGTPEEATAE 120
QY 121 AYRYADALKKONGEYTVADVADKGYTLNIFAGKEKTPPEPKKEEVTIKANLIYADGKTQTA 180
DB 121 AYRYADALKKONGEYTVADVADKGYTLNIFAGKEKTPPEPKKEEVTIKANLIYADGKTQTA 180
QY 181 EFKGTFEATAEAYRYADLLAKENGYTVADVADKGYTLNIFAGKEKTPPEPKKEEVTIKA 240
DB 181 EFKGTFEATAEAYRYADLLAKENGYTVADVADKGYTLNIFAGKEKTPPEPKKEEVTIKA 240
QY 241 NLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGYTADLEGGYTTINIRFAGKVD 300
DB 241 NLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGYTADLEGGYTTINIRFAGKVD 300
QY 301 EKPEPMDTYKLIILNGKTLKGTTTAEVDAATAEAKVFKQYANDNGVDGWTYDDATKTFT 360
DB 301 EKPEPMDTYKLIILNGKTLKGTTTAEVDAATAEAKVFKQYANDNGVDGWTYDDATKTFT 360
QY 361 VTEKPEVIDASELTPAVTTYKLIVNGKTLKGTTTAKVDAETAFAKAFQYANDNGVDGVM 420
DB 361 VTEKPEVIDASELTPAVTTYKLIVNGKTLKGTTTAKVDAETAFAKAFQYANDNGVDGVM 420
QY 421 TYDDATKTFTVTTEM 434
DB 421 TYDDATKTFTVTTEM 434

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RESULT 2

US-08-325-278A-3

; Sequence 3, Application US/08325278A

; GENERAL INFORMATION:

; APPLICANT: Björck, Lars

; Sjöbring, Ulf

; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Seed IP Law Group

; STREET: 701 Fifth Avenue Suite 6300

; CITY: Seattle

; STATE: Washington

; COUNTRY: USA

; ZIP: 98104-7092

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

RESULT 3

US-08-325-278B-3

; Sequence 3, Application US/08325278B

; GENERAL INFORMATION:

; APPLICANT: Björck, Lars

; Sjöbring, Ulf

; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Seed IP Law Group

US-09-791-537-96101

Query Match 71.0%; Score 1587.5; DB 22; Length 719;
Best Local Similarity 76.3%; Pred. No. 4.6e-112;
Matches 334; Conservative 13; Mismatches 56; Indels 35; Gaps 6;

QY 2 VENKEETPETDSEETIKANLIFANGSTQTAETFEKGTSEAYAYADTLKKDNG 61
DB 95 VENKEETPETDSEETIKANLIFANGSTQTAETFEKGTSEAYAYADTLKKDNG 154

QY 62 EYTVADVADGKYLNIKFAKKEKTPPEPKKEVTIKANLIYADGKTQTAETFEATAEA 121
DB 155 EYTVADVADGKYLNIKFAKKEKTPPEPKKEVTIKANLIYADGKTQTAETFEATAEA 214

QY 122 YRYADALKDNGEYTVADVADGKYLNIKFAKKEKTPPEPKKEVTIKANLIYADGKTQTAET 181
DB 215 YRYADALKDNGEYTVADVADGKYLNIKFAKKEKTPPEPKKEVTIKANLIYADGKTQTAET 274

QY 182 FKGTPEATAEAYRYADLLAKENGYTVADVADGKYLNIKFAKKEKTPPEPKKEVTIKAN 241
DB 275 FKGTPEATAEAYRYADLLAKENGYTVADVADGKYLNIKFAKKEKTPPEPKKEVTIKAN 334

QY 242 LIYADGKTQTAETFEKGTSEAYAYADLLAKENGYTVADVADGKYLNIKFAKKEKTPPEPK 301
DB 335 LIYADGKTQTAETFEKGTSEAYAYADLLAKENGYTVADVADGKYLNIKFAKKEKTPPEPK 394

QY 302 KPEPMD-TYK--LILNGKTLKGETTEAVDAATAEKYQVANDNGVD--GEWYDDATK 357
DB 395 KPEKQVTKENIYEPEDGVQTATPKGTFAEATAEAY--RYADLLSKHEKGYTADLDG 452

QY 358 TETVT-----EKPEVIDASELTPATVTVKLVINGKTLGETTTRAVDAETAE 404
DB 453 GYTNIRFAGKEPETPEKPEVQ-----GYASYEAEAAKALKND 496

QY 405 KAFQYANDNGVDGVWY 422
DB 497 DVNKSYYTIRQAGDGRYY 514

RESULT 6

US-08-325-278-1
; Sequence 1, Application US/08325278
; GENERAL INFORMATION:
; APPLICANT: Bjvrck, Lars
; APPLICANT: Sjobring, Ulf
; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,278
; FILING DATE: 26-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMASTERS, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 450023.401
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 305 amino acids

RESULT 7

US-08-325-278A-1
; Sequence 1, Application US/08325278A
; GENERAL INFORMATION:
; APPLICANT: Bjorck, Lars
; APPLICANT: Sjobring, Ulf
; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed IP Law Group
; STREET: 701 Fifth Avenue Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,278A
; FILING DATE: 26-Oct-1994
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 100084.402
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 305 amino acids
; TYPE: amino acid

; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli LE392/pHDL, DSM 7054
; US-08-325-278-1

Query Match 70.0%; Score 1565; DB 7; Length 305;
Best Local Similarity 100.0%; Pred. No. 6.7e-111;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVENKEETPETDSEETIKANLIFANGSTQTAETFEKGTSEAYAYADTLKKD 60
DB 1 AVENKEETPETDSEETIKANLIFANGSTQTAETFEKGTSEAYAYADTLKKD 60

QY 61 GEYTVADVADGKYLNIKFAKKEKTPPEPKKEVTIKANLIYADGKTQTAETFEATAE 120
DB 61 GEYTVADVADGKYLNIKFAKKEKTPPEPKKEVTIKANLIYADGKTQTAETFEATAE 120

QY 121 AYRYADALKDNGEYTVADVADGKYLNIKFAKKEKTPPEPKKEVTIKANLIYADGKTQTA 180
DB 121 AYRYADALKDNGEYTVADVADGKYLNIKFAKKEKTPPEPKKEVTIKANLIYADGKTQTA 180

QY 181 EKFGTPEATAEAYRYADLLAKENGYTVADVADGKYLNIKFAKKEKTPPEPKKEVTIKA 240
DB 181 EKFGTPEATAEAYRYADLLAKENGYTVADVADGKYLNIKFAKKEKTPPEPKKEVTIKA 240

QY 241 NLIYADGKTQTAETFEKGTSEAYAYADLLAKENGYTVADVADGKYLNIKFAKKEKTPPEPK 300
DB 241 NLIYADGKTQTAETFEKGTSEAYAYADLLAKENGYTVADVADGKYLNIKFAKKEKTPPEPK 300

QY 301 EKPEE 305
DB 301 EKPEE 305

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;
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli LE392/pHDL, DSM 7054
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-08-325-278A-1

Query Match      70.0%; Score 1565; DB 7; Length 305;
Best Local Similarity 100.0%; Pred. No. 6.7e-111;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVENKEETPETPTDSEEEVTKANLIFANGSTQTAFFKGTPEKATSEAYAYADTLKKDN 60
Db 1 AVENKEETPETPTDSEEEVTKANLIFANGSTQTAFFKGTPEKATSEAYAYADTLKKDN 60
QY 61 GEYTVADVADKGYTLNKFAGKEKTPPEPKKEEVTIKANLIYADGKTQTAEFGTFFEEATAE 120
Db 61 GEYTVADVADKGYTLNKFAGKEKTPPEPKKEEVTIKANLIYADGKTQTAEFGTFFEEATAE 120
QY 121 AYRYADALKKDNGEYTVADVADKGYTLNKFAGKEKTPPEPKKEEVTIKANLIYADGKTQTA 180
Db 121 AYRYADALKKDNGEYTVADVADKGYTLNKFAGKEKTPPEPKKEEVTIKANLIYADGKTQTA 180
QY 181 EFKGTFFEEATAEAYRYADLLAKENGKGYTVADVADKGYTLNKFAGKEKTPPEPKKEEVTIKA 240
Db 181 EFKGTFFEEATAEAYRYADLLAKENGKGYTVADVADKGYTLNKFAGKEKTPPEPKKEEVTIKA 240
QY 241 NLIYADGKTQTAEFGKTFEATAEAYRYADLLAKENGKGYTVADVADKGYTLNKFAGKEKTPPEPKKEEVTIKANLIYADGKTQTAEFGKTFEATAE 300
Db 241 NLIYADGKTQTAEFGKTFEATAEAYRYADLLAKENGKGYTVADVADKGYTLNKFAGKEKTPPEPKKEEVTIKANLIYADGKTQTAEFGKTFEATAE 300
QY 301 EKPEE 305
Db 301 EKPEE 305

RESULT 8
US-08-325-278B-1
; Sequence 1, Application US/08325278B
; GENERAL INFORMATION:
; APPLICANT: Bjorck, Lars
; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed IP Law Group
; STREET: 701 Fifth Avenue Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,278B
; FILING DATE: 26-Oct-1994
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 100084.402
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 305 amino acids
; TYPE: amino acid
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;
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli LE392/pHDL, DSM 7054
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-08-325-278B-1

Query Match      70.0%; Score 1565; DB 7; Length 305;
Best Local Similarity 100.0%; Pred. No. 6.7e-111;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVENKEETPETPTDSEEEVTKANLIFANGSTQTAFFKGTFFKATSEAYAYADTLKKDN 60
Db 1 AVENKEETPETPTDSEEEVTKANLIFANGSTQTAFFKGTFFKATSEAYAYADTLKKDN 60
QY 61 GEYTVADVADKGYTLNKFAGKEKTPPEPKKEEVTIKANLIYADGKTQTAEFGTFFEEATAE 120
Db 61 GEYTVADVADKGYTLNKFAGKEKTPPEPKKEEVTIKANLIYADGKTQTAEFGTFFEEATAE 120
QY 121 AYRYADALKKDNGEYTVADVADKGYTLNKFAGKEKTPPEPKKEEVTIKANLIYADGKTQTA 180
Db 121 AYRYADALKKDNGEYTVADVADKGYTLNKFAGKEKTPPEPKKEEVTIKANLIYADGKTQTA 180
QY 181 EFKGTFFEEATAEAYRYADLLAKENGKGYTVADVADKGYTLNKFAGKEKTPPEPKKEEVTIKA 240
Db 181 EFKGTFFEEATAEAYRYADLLAKENGKGYTVADVADKGYTLNKFAGKEKTPPEPKKEEVTIKA 240
QY 241 NLIYADGKTQTAEFGKTFEATAEAYRYADLLAKENGKGYTVADVADKGYTLNKFAGKEKTPPEPKKEEVTIKANLIYADGKTQTAEFGKTFEATAE 300
Db 241 NLIYADGKTQTAEFGKTFEATAEAYRYADLLAKENGKGYTVADVADKGYTLNKFAGKEKTPPEPKKEEVTIKANLIYADGKTQTAEFGKTFEATAE 300
QY 301 EKPEE 305
Db 301 EKPEE 305

RESULT 9
US-09-980-469-12
; Sequence 12, Application US/09980469
; GENERAL INFORMATION:
; APPLICANT: Shiv , Shani
; TITLE OF INVENTION: PROCESS OF EXPRESSING AND ISOLATING RECOMBINANT PROTEINS AND R
; FILE OF INVENTION: PROTEIN PRODUCTS FROM PLANTS, PLANT DERIVED TISSUES OR CULTUR
; FILE REFERENCE: 01/22924
; CURRENT APPLICATION NUMBER: US/09/980,469
; CURRENT FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: pUC19-cell-protL-cekNG-HDEL fusion encoded product
US-09-980-469-12

Query Match      69.4%; Score 1550; DB 25; Length 467;
Best Local Similarity 79.2%; Pred. No. 1.8e-109;
Matches 328; Conservative 3; Mismatches 43; Indels 40; Gaps 7;

QY 1 AVENKEETPETPTDSEEEVTKANLIFANGSTQTAFFKGTFFKATSEAYAYADTLKKDN 60
Db 40 AVENKEETPETPTDSEEEVTKANLIFANGSTQTAFFKGTFFKATSEAYAYADTLKKDN 99
QY 61 GEYTVADVADKGYTLNKFAGKEKTPPEPKKEEVTIKANLIYADGKTQTAEFGTFFEEATAE 120
Db 100 GEYTVADVADKGYTLNKFAGKEKTPPEPKKEEVTIKANLIYADGKTQTAEFGTFFEEATAE 159
QY 121 AYRYADALKKDNGEYTVADVADKGYTLNKFAGKEKTPPEPKKEEVTIKANLIYADGKTQTA 180
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Db 160 AYRYADALKNDNGEYTVDVADKGYTLNIRKFAKKEKTPPEPKKEEVTIKANLIYADGKTQTA 219
QY 181 EFKGTGFEATAEAYRYADLL-ARENGKYTVDVADKGYTLNIRKFAKKEKTPPEPKKEEVTIK 239
Db 220 EFKGTGFEATAEAYRYADLLAAKENGKYTVDVADKGYTLNIRKFAKKEKTPPEPKKEEVTIK 279
QY 240 ANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTDADLEGGYTNIRFAGKVV 299
Db 280 ANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTDADLEGGYTNIRFAGKVV 339
QY 300 DEKPEPMDYKLLNGKTLKGTTTTEAYDAA-----TAEKVFQYANDN 344
Db 340 DEKPEGIPT-----PTPSASGPACCVLGNQWNTGFTAQVTVKN-TGSA 386
QY 345 GVDGEWYDDAKYTFVTTEKPEVIDASELT-----PAVTYKLVINGKTLKGET 393
Db 387 PVDG-WTL-----TFSFPGQQVQTQAWSSTVTSQSGSAVTVRNAPWNGNPAGGT 434

RESULT 10
US-09-889-182A-4
; Sequence 4, Application US/09889182A
; GENERAL INFORMATION:
; APPLICANT: Breitling, Frank
; TITLE OF INVENTION: SELECTION OF MONOCLONAL ANTIBODIES
; FILE REFERENCE: 4121-126
; CURRENT APPLICATION NUMBER: US/09/889,182A
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: pct/de00/00079
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-889-182A-4

Query Match 61.4%; Score 1372; DB 23; Length 367;
Best Local Similarity 82.4%; Pred. No. 4.9e-96;
Matches 271; Conservative 19; Mismatches 29; Indels 10; Gaps 3;

QY 5 KEETPTPTDSEEEVTIKANLIFANGSTQTAEFKGTTFEKATSEAYAYADTLKKDNGEYT 64
Db 25 KEKTPPEP---KEEVTIKANLIYADGKTQTAEFKGTTFEATAEAYRYADALKNDNGEYT 80
QY 65 VDVADKGYTLNIRKFAKKEKTPPEPKKEEVTIKANLIYADGKTQTAEFKGTTFEATAEAYRY 124
Db 81 VDVADKGYTLNIRKFAKKEKTPPEPKKEEVTIKANLIYADGKTQTAEFKGTTFEATAEAYRY 140
QY 125 ADALKNDNGEYTVDVADKGYTLNIRKFAKKEKTPPEPKKEEVTIKANLIYADGKTQTAEPKG 184
Db 141 ADALKNDNGEYTVDVADKGYTLNIRKFAKKEKTPPEPKKEEVTIKANLIYADGKTQTAEPKG 200
QY 185 TFEATAEAYRYADLLAKENGKYTVDVADKGYTLNIRKFAKKEKTPPEPKKEEVTIKANLIY 244
Db 201 TFEATAEAYRYADALKNDNGEYTVDVADKGYTLNIRKFAKKEKTPPEPKKEEVTIKANLIY 260
QY 245 ADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTDADLEGGYTNIRFAGKVKVDEKPE 304
Db 261 ADGKTQTAEFKGTFAEATAEAYRYADALKNDNGEYTVDVADKGYTLNIRKFAKKEKTPPEPK 320
QY 305 EPMDYKLLNGKTLKGTTTTEAVDAATA 333
Db 321 SEED-----LNG-AVDGQNDTSTSPSA 343

RESULT 11
US-09-791-537-88366
; Sequence 88366, Application US/09791537
; GENERAL INFORMATION:
```

```
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 88366
; LENGTH: 992
; TYPE: PRT
; ORGANISM: Peptostreptococcus magnus
US-09-791-537-88366

Query Match 56.5%; Score 1263.5; DB 22; Length 992;
Best Local Similarity 58.8%; Pred. No. 4.2e-87;
Matches 281; Conservative 36; Mismatches 90; Indels 71; Gaps 12;

QY 2 VENKEETPTPTDSEEEVTIKANLIFANGSTQTAEFKGTTFEKATSEAYAYADTLKKDNG 61
Db 241 MERKLEKETPE--PEEVTIKANLIFADGSTQNAEFKGTFAKAVSDAYADALKDNG 298
QY 62 EYTVDVADKGYTLNIRKFAKKEKTPPEPKKEEVTIKANLIYADGKTQTAEPKGFEEATAEA 121
Db 299 EYTVDVADKGLTLNIRKFAKKEKTPPEPKKEEVTIKVNLIFADGKTQTAEPKGFEEATAKA 358
QY 122 YRYADALKNDNGEYTVDVADKGYTLNIRKFAKKE--KTPPEPKKEEVTIKANLIYADGKTQT 179
Db 359 YAYADLLAKENGKYTDADLEGGYTNIRKFAKKEKTPPEPKKEEVTIKVNLIFADGKIQT 418
QY 180 AEFKGTGFEATAEAYRYADLLAKENGKYTVDVADKGYTLNIRKFAKKE--KTPPEPKKEEVT 237
Db 419 AEFKGTGFEATAKAYAYANLLAKENGKYTDADLEGGYTNIRKFAKKEKTPPEPKKEEVT 478
QY 238 IKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTDADLEGGYTNIRFAGK 297
Db 479 IKVNLIFADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTDADLEGGYTNIRFAGK 538
QY 298 K-----VDE-----KPEEPM-----DTY-KLILNGKTLKG----- 321
Db 539 EQGENPGITIDWLLKNAKEAIEKELKEAGITSDLYFSLINKAKTVEGVEALKNELKA 598
QY 322 ----ET-----TTEAVDAATAEAKVFOYAND-----NGVDGEWYDDATFTFTVTEK 364
Db 599 HAGEETPELKDGYATYEEAEAAKALKNDVDNNAYEIVQGDGRYYY--VLKIEVADEE 656
QY 365 PEVIDASELTPAVTVTKLVINGKTLKGFTTKAVDAETAEKAPKQYANDNGVDGVWY 422
Db 657 EPGEDTPEVOEGYATYE-----EAEAAKAEALKEKEDKVNNAVYEVQGDGRYYY 704

RESULT 12
US-08-331-637-2
; Sequence 2, Application US/08331637
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROTEIN L AND PROCESS FOR ITS PREPARATION BY
; TITLE OF INVENTION: RECOMBINANT DNA TECHNOLOGY
; NUMBER OF SEQUENCES: 23
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,637
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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Query Match 56.58; Score 1263.5; DB 8; Length 1027;

RESULT 14
US-09-187

	Query Match	56.5%	Score 1263.5;	DB 15;	Length 1027;
	Best Local Similarity	58.8%;	Pred. No. 4.4e-87;		
	Matches 281; Conservative	36;	Mismatches 90;	Indels 71;	Gaps 12;
QY	2 VENKEETPETDSEEVITKANLIFANGSTQTAEFGKTFEKATSEAYAVADTLKKDNG	61	:		: : :
Dd	276 MERKLSEKETPE--PEEEVITKANLIADFAGSGTQAEEFKGTFAKVSAYADALKKDNG	333	:		: : :
QY	62 EYTVDVADKYLTINLIKPFAGKEKTPEEPKEEVTKANLIYADGGTKQTAAEFKGTFFEATAEA	121	:		: : :

Db 334 EYTDVADKGLTLNIFAGKKEPEPEKEVTIKVNLIFADGKTQTAEFKGTPEEATAKA 393
QY 122 YRYADALKDNGEYTVDVADKGYTLNIFAGKE--KTPPEPKEEVTIKANLIYADGKTQT 179
Db 394 YAYADLLAKENGEYTDGNGTINIFAGKETPETPEPKEEVTIKVNLIFADGKIQT 453
QY 180 AEFKGTPEEATAEAYRYADLLAKENGYTVDVADKGYTLNIFAGKE--KTPPEPKEEVT 237
Db 454 AEFKGTPEEATAEAYRYADLLAKENGEYTDGNGTINIFAGKETPETPEPKEEVT 513
QY 238 IKANLIYADGKTQTAEFKGTPEEATAEAYRYADLLAKENGYTDGNGTINIFAGKE 297
Db 514 IKVNLIFADGKTQTAEFKGTPEEATAEAYRYADLLAKENGEYTDGNGTINIFAGKE 573
QY 298 K-----VDE-----KPEEPM-----DTY-KLILNGKTLKG----- 321
Db 574 EQPGENPGITIDEWLLKNAKEAIELKEAGITSDLYFSLINKAKTVESVEALKNEILKA 633
QY 322 -----ET-----TTEAVDAATAEKVKFYAND-----NGVDGEWTVDDATKTFVTVEK 364
Db 634 HAGEETPELKGYATYEAEAAAKEALKNDVNNAYEIVQGADGRYYY--VLKIEVADDE 691
QY 365 PEVIDASLTPAVTYKLVINGTKLGETTTKAVDAETAETAEKAFKOYANDNGVDGVWY 422
Db 692 EPGEDTPEVQEGYATYE-----EAEAAAKEALKEDKVNNAEYEVVQADGRYYY 739

RESULT 15

US-08-446-137A-4

; Sequence 4, Application US/08446137A

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEINS DERIVED

; FROM PROTEIN L AND THEIR USES

; NUMBER OF SEQUENCES: 4

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/446,137A

; FILING DATE: 22-05-1995

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: MITCHARD, LEONARD C.

; REGISTRATION NUMBER: 29,009

; REFERENCE/DOCKET NUMBER: 1418-9

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 816-4000

; TELEFAX: (703) 816-4100

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 291 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-446-137A-4

Query Match

Best Local Similarity 54.4%; Score 1216; DB 8; Length 291;

Matches 241; Conservative 20; Mismatches 25; Indels 6; Gaps 3;

QY 10 EPTDSEEEVTIKANLIFANGSTQAEFKGTPEEATAEAYRYADALK 129
Db 2 ETPE--PEEVTIKANLIFADGSTQAEFKGTFAKAVSDAYAYADALKDNGEYTVDVAD 59
QY 70 KGYTLNIFAGKETPEEKEVTIKANLIYADGKTQTAEFKGTPEEATAEAYRYADALK 129
Db 60 KGLTLNIFAGKETPEEKEVTIKVNLIFADGKTQTAEFKGTPEEATAEAYRYADALK 119
QY 130 KNGEYTVDVADKGYTLNIFAGKE--KTPPEPKEEVTIKANLIYADGKTQTAEFKGTPE 187

Db 120 KENGEYTDGNGTINIFAGKETPETPEPKEEVTIKVNLIFADGKIQTAEFKGTPE 179
QY 188 EATAEAYRYADLLAKENGYTVDVADKGYTLNIFAGKE--KTPPEPKEEVTIKANLIYA 245
Db 180 EATAKAYAYANLLAKENGEYTDGNGTINIFAGKETPETPEPKEEVTIKVNLIFA 239
QY 246 DGKTQTAEFKGTFAEATAEAYRYADLLAKENGYTDGNGTINIFAGK 297
Db 240 DGKTQTAEFKGTFAEATAEAYRYADLLAKVNGEYTDGNGTINIFAGK 291

Search completed: September 3, 2003, 11:13:54
Job time : 318.131 secs

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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:02:46 ; Search time 17.6184 Seconds
(without alignments)
773.734 Million cell updates/sec

Title: US-08-325-278B-3
Perfect score: 2235
Sequence: 1 AVENKEETPETDSEEV.....GVDGWTYYDATKFTVTTEM 434

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 148256 seqs, 31410045 residues

Total number of hits satisfying chosen parameters: 148256

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New.*
1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	683	30.6	448	6	US-10-460-524-5
2	287	12.8	55	1	PCT-US03-21559-3
3	287	12.8	55	1	PCT-US03-21559-5
4	286	12.8	58	6	US-10-458-297-4
5	285	12.8	60	6	US-10-458-297-2
6	284	12.7	55	1	PCT-US03-21559-4
7	281.5	12.6	58	6	US-10-458-297-1
8	170.5	7.6	1849	6	US-10-637-544-2
9	160	7.2	2705	1	PCT-US03-21510-97
10	160	7.2	2705	6	US-10-408-765A-2039
11	160	7.2	2705	6	US-10-089-320B-44
12	157.5	7.0	1166	5	US-09-200-650E-7
13	156	7.0	916	6	US-10-408-765A-1222
14	156	7.0	916	7	US-60-490-890-475
15	155.5	7.0	770	5	US-09-897-516A-4453
16	153.5	6.9	701	6	US-10-333-120A-7
17	148.5	6.6	2647	1	PCT-US03-21510-95
18	147	6.6	521	6	US-10-430-752A-5
19	145.5	6.5	2315	6	US-10-603-114-5434
20	144	6.4	728	6	US-10-467-534-81
21	140	6.3	693	6	US-10-333-120A-10
22	140	6.3	901	6	PCT-US03-21510-96
23	136.5	6.1	2602	1	US-10-603-113-14747
24	136	6.1	630	6	US-10-603-113-20275
25	134.5	6.0	1262	6	US-10-617-320-5067
26	133	6.0	458	6	US-10-467-421-37

27	133	6.0	1742	6	US-10-615-383-4	Sequence 4, Appli
28	132.5	5.9	2060	6	US-10-381-596A-2	Sequence 2, Appli
29	132	5.9	487	5	US-09-897-516A-5285	Sequence 5285, Ap
30	131	5.9	6669	1	PCT-US03-21379-80	Sequence 80, Appl
31	131	5.8	930	5	US-09-200-650E-3	Sequence 3, Appli
32	130	5.8	1277	6	US-10-326-956-665	Sequence 665, App
33	130	5.8	1965	6	US-10-640-833-3829	Sequence 3829, Ap
34	130	5.8	1972	6	US-10-617-320-3251	Sequence 3251, Ap
35	129.5	5.8	1204	6	US-10-640-833-4083	Sequence 4083, Ap
36	128	5.7	718	6	US-10-603-108-2753	Sequence 2753, Ap
37	126	5.6	542	5	US-09-820-843B-4	Sequence 4, Appli
38	125.5	5.6	1315	5	US-09-200-650E-5	Sequence 5, Appli
39	124	5.5	1899	6	US-10-631-467-919	Sequence 919, App
40	124	5.5	3063	6	US-10-631-467-919	Sequence 918, App
41	123.5	5.5	1359	6	US-10-326-956-1053	Sequence 1053, Ap
42	121.5	5.4	2142	6	US-10-603-108-3459	Sequence 3459, Ap
43	121	5.4	1531	1	PCT-US02-37235-44	Sequence 44, Appl
44	120.5	5.4	818	5	US-09-897-516A-5123	Sequence 5123, Ap
45	120.5	5.4	1939	6	US-10-408-765A-2188	Sequence 2188, Ap

ALIGNMENTS

RESULT 1
US-10-460-524-5
; Sequence 5, Application US/10460524
; GENERAL INFORMATION:
; APPLICANT: Hernan, Ronald A
; APPLICANT: Mehig, Richard J
; APPLICANT: Brookie, Ian
; APPLICANT: Jenkins, Elizabeth
; TITLE OF INVENTION: Affinity Peptides and Method for Purification of Recombinant P
; FILE REFERENCE: SGM 7047.1
; CURRENT APPLICATION NUMBER: US/10/460,524
; CURRENT FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: US 60/388,059
; PRIOR FILING DATE: 2002-06-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Streptococcus
US-10-460-524-5

Query Match	30.6%	Score	683	DB	6	Length	448
Best Local Similarity	53.2%	Pred. No.	4e-38				
Matches	176	Conservative	15	Mismatches	92	Indels	48
Gaps	9						
QY	130	KDNGEYTVDAVKGYTLNFKFAGKEKTPPEPEEVIKANLIYAD-GKQTAEFKGTTEE	188				
DB	45	RNGELT-----NLLGNSETTLALRNEESATADLTAAAVADTVAAAAAENAGA	92				
QY	189	ATAEAYRYADLIA-----KENGKYTVDAVKGYTLNFKFAGKEKTPPEPEEVIKAN	241				
DB	93	AAWEAAAAADALAKAKADALKEFNKYGVSDYKYNLNNAKTVEGIDKLAQVVSAAKAR	152				
QY	242	LIYA-DG-----KTQTAEFKGTFAEATAEAYRYAD---LLAKENGKYTADLEDGGYTI	292				
DB	153	ISEATDGLSDFLKSOTP-----AEDTVKSIELAEAKVLANRELDKYGV----SDYHK	202				
QY	293	RFAGKVDKPE-----BPMDTYKLILNGKTLKGETTEAVDAATAEKFVKQYAND	343				
DB	203	INNAKTVEGVKELIDELIALLPKTDYTKLILNGKTLKGETTEAVDAATAEKFVKQYAND	262				
QY	344	NGVDGEWYDDATKFTTVEKPEVIDASSELTPAVTYYKLIVNGKTLKGETTTKAVDAETA	403				
DB	263	NGVDGEWYDDATKFTTVEKPEVIDASSELTPAVTYYKLIVNGKTLKGETTTKAVDAETA	322				
QY	404	EKAFKQYANDNGVDGWTYYDDATKFTTTEM	434				
DB	323	EKAFKQYANDNGVDGWTYYDDATKFTTTEM	353				

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RESULT 2
PCT-US03-21559-3
; Sequence 3, Application PC/TUS0321559
; GENERAL INFORMATION:
; APPLICANT: President Biosystems
; TITLE OF INVENTION: PROTEIN CHIPS
; FILE REFERENCE: 13744-002W01
; CURRENT APPLICATION NUMBER: PCT/US03/21559
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: US 10/193,377
; PRIOR FILING DATE: 2002-07-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-21559-3

Query Match 12.8%; Score 287; DB 1; Length 55;
Best Local Similarity 100.0%; Pred. No. 4.3e-13;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 309 TYKLINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDGWTYDDATKTFVTVE 363
Db 1 TYKLINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDGWTYDDATKTFVTVE 55

RESULT 3
PCT-US03-21559-5
; Sequence 5, Application PC/TUS0321559
; GENERAL INFORMATION:
; APPLICANT: President Biosystems
; TITLE OF INVENTION: PROTEIN CHIPS
; FILE REFERENCE: 13744-002W01
; CURRENT APPLICATION NUMBER: PCT/US03/21559
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: US 10/193,377
; PRIOR FILING DATE: 2002-07-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-21559-5

Query Match 12.8%; Score 287; DB 1; Length 55;
Best Local Similarity 100.0%; Pred. No. 4.3e-13;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 379 TYKLINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDGWTYDDATKTFVTVE 433
Db 1 TYKLINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDGWTYDDATKTFVTVE 55

RESULT 4
US-10-458-297-4
; Sequence 4, Application US/10458297
; GENERAL INFORMATION:
; APPLICANT: Eiichi Ogino
; APPLICANT: Michio Nomura
; APPLICANT: Takashi Asahi
; APPLICANT: Shuichi Kaneko
; APPLICANT: Akito Sakai
; TITLE OF INVENTION: ADSORBENT FOR ELIMINATING HEPATITIS C VIRUS, ADSORBENT, AND ADSOR
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/458,297
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: US/09/380,644C
; PRIOR FILING DATE: 2002-07-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
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; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: JP 09/71483
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: word
; SEQ ID NO 4
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: lgg - binding peptide
US-10-458-297-4
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```
Query Match 12.8%; Score 286; DB 6; Length 58;
Best Local Similarity 96.5%; Pred. No. 5.4e-13;
Matches 55; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY 377 VTTYKLINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDGWTYDDATKTFVTVE 433
Db 1 MTTYKLINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDGWTYDDATKTFVTVE 57
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RESULT 5
```

```
US-10-458-297-2
```

```
; Sequence 2, Application US/10458297
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Eiichi Ogino
```

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; APPLICANT: Michio Nomura
```

```
; APPLICANT: Takashi Asahi
```

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; APPLICANT: Shuichi Kaneko
```

```
; APPLICANT: Akito Sakai
```

```
; TITLE OF INVENTION: ADSORBENT FOR ELIMINATING HEPATITIS C VIRUS, ADSORBENT, AND ADS
```

```
; FILE REFERENCE:
```

```
; CURRENT APPLICATION NUMBER: US/10/458,297
```

```
; CURRENT FILING DATE: 2003-06-11
```

```
; PRIOR APPLICATION NUMBER: US/09/380,644C
```

```
; PRIOR FILING DATE: 1999-11-09
```

```
; PRIOR APPLICATION NUMBER: JP 09/71483
```

```
; PRIOR FILING DATE: 1997-03-25
```

```
; NUMBER OF SEQ ID NOS: 5
```

```
; SOFTWARE: word
```

```
; SEQ ID NO 2
```

```
; LENGTH: 60
```

```
; TYPE: PRT
```

```
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
```

```
; OTHER INFORMATION: lgg - binding peptide
```

```
US-10-458-297-2
```

```
Query Match 12.8%; Score 285; DB 6; Length 60;
```

```
Best Local Similarity 98.2%; Pred. No. 6.5e-13;
```

```
Matches 55; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 378 TTYKLINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDGWTYDDATKTFVTVE 433
Db 5 TTYKLINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDGWTYDDATKTFVTVE 60
```

```
RESULT 6
```

```
PCT-US03-21559-4
```

```
; Sequence 4, Application PC/TUS0321559
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: President Biosystems
```

```
; TITLE OF INVENTION: PROTEIN CHIPS
```

```
; FILE REFERENCE: 13744-002W01
```

```
; CURRENT APPLICATION NUMBER: PCT/US03/21559
```

```
; CURRENT FILING DATE: 2003-07-10
```

```
; PRIOR APPLICATION NUMBER: US 10/193,377
```

```
; PRIOR FILING DATE: 2002-07-11
```

```
; NUMBER OF SEQ ID NOS: 11
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 4
```



```

; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-21559-4

Query Match      12.7%; Score 284; DB 1; Length 55;
Best Local Similarity 96.4%; Pred. No. 6.8e-13;
Matches 53; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 309 TYKLINGKTLKGETTTTAVDAATAEKVFKQYANDNGVDGWTYDDATKFTVTTE 363
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 TYKLIVNGKTLKGETTTTAVDAATAEKVFKQYANDNGVDGWTYDDATKFTVTTE 55
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
US-10-458-297-1
; Sequence 1, Application US/10458297
; GENERAL INFORMATION:
; APPLICANT: Elji Ogino
; APPLICANT: Michio Nomura
; APPLICANT: Takashi Asahi
; APPLICANT: Shuichi Kaneko
; APPLICANT: Akito Sakai
; TITLE OF INVENTION: ADSORBENT FOR ELIMINATING HEPATITIS C VIRUS, ADSORBENT, AND ADSORBENT METHOD
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/458,297
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: US/09/380,644C
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: JP 09/71483
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: word
; SEQ ID NO 1
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: lgg - binding domain of protein G
US-10-458-297-1

Query Match      12.6%; Score 281.5; DB 6; Length 58;
Best Local Similarity 98.2%; Pred. No. 1.1e-12;
Matches 56; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 378 TTYKLIVNGKTLKGETTTKAVD-AETAFAKQYANDNGVDGWTYDDATKFTVTTE 433
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 2 TTYKLIVNGKTLKGETTTKAVDAAETAFAKQYANDNGVDGWTYDDATKFTVTTE 58
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 8
US-10-637-544-2
; Sequence 2, Application US/10637544
; GENERAL INFORMATION:
; APPLICANT: Chr. Hansen A/S
; TITLE OF INVENTION: Peptides with anti-hypertensive properties
; FILE REFERENCE: P1032U501
; CURRENT APPLICATION NUMBER: US/10/637,544
; CURRENT FILING DATE: 2003-08-11
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1849
; TYPE: PRT
; ORGANISM: Lactobacillus helveticus
US-10-637-544-2

Query Match      7.6%; Score 170.5; DB 6; Length 1849;
Best Local Similarity 25.9%; Pred. No. 0.0012;
Matches 117; Conservative 44; Mismatches 165; Indels 125; Gaps 25;

QY 73 TLNIRFAGKEKTEPEEKVEITKANLIYADGKTQTAEFKGTPEETAFAA--YRYADALKK 130
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1415 TLNL---DSENTVYTNKDKFTI-SGTISDDYKFYDLSINGNDVETSWSAVDYHSKEGIRK 1470
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 131 DNGEYTVADVADKGYTLNIRK-----FAGREKTEPEEKKE--VTIKANLIYA 173
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1471 -NFKHEVDLKKGKNTFNKVTDIQNSSSSQALVVYVEPAKTLAEFSVDKLLTKTANLQLL 1529
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 174 DGKTQTAEFK-----GTPEETAFAAYRYADLLAKENGKYTVADVADKGY-----TL 218
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1530 KATTDSEAKVYVSLDNGKTFNDVPADGFK-----VTENGTVQFKAVDK-YGNESKVKSV 1583
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 219 NIKFAGKEKTEPEEKVEITKANL-----IYADGKTQ-----TAEFKGTFAETAFAAYRADL 271
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1584 EIKGLNKENQPSDELAKAKENLQAKVDAGEKKDLDKYTADSKDKFDNALAKA---KDV 1640
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 272 LAKENGKYTADLEDDGGYTINIRFAGKVKDEKPEEPMYKLLIL-NGKTLKGETTTEAVDA 330
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1641 LADKNAK-LADLODAKALD--KAEQALTEKPAEP--TIPLLOGNNAVSNINTSSDNQV 1695
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 331 ATAFAKQYANDN-----GVDGWTY-----DDATKFTT-----VTEKP--- 365
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1696 AAPVHAEKDTKNDKNTTTEEGKDTKVMFKSVLYTKDLKKTRSTAQAAYSLSKLVTEKGLK 1755
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 366 -----EVIDASELTPA--VTYKLVYI-----NGKTL-----KGETTTKAV 398
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1756 VYTFKGVHYFKVDRNAVYVRNVGTGATLKRNFSVYQSNKGKASRKLKKGTTTIVYG 1815
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 399 DAETAFAKQYK-----NDNGVD 417
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1816 DQYKALKHYKYAIRIGEGRYIKSVNVRVD 1846
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

PCT-US03-21510-97
; Sequence 97, Application PC/TUS0321510
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: MP21S AS MODIFIERS OF THE p21 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX03-046C-PC
; CURRENT APPLICATION NUMBER: PCT/US03/21510
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US 60/394,795
; PRIOR FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US 60/401,739
; PRIOR FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US 60/411,010
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 60/437,158
; PRIOR FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 97
; LENGTH: 2705
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-21510-97

Query Match      7.2%; Score 160; DB 1; Length 2705;
Best Local Similarity 22.2%; Pred. No. 0.0095;
Matches 114; Conservative 60; Mismatches 187; Indels 152; Gaps 25;

QY 47 SEAYAYADTLKKDNGEYTVADVADK-----YTLAIKFAKGE--KTPEPEKEVITKANLIYA 101
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 793 AEADIDFDLIKNDNTFTVKYTPPGAGRYTIMVLFANQEIIPASPFHIKVDPSHDASKVKA 852
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 102 DGK-----TQTA-----EFKGTPEETAFAAYRADALKKNGEY 136
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 853 EGPLNRTGVEVGKPTHTFTVLTKGAGKAKLDVQFAGT-----AKGEVVRDFEIDNHDYSY 909
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 137 VD---VADKGYTLNIRFAGKEKTEPEE-----KEEVTIKR 168
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 910 VKYTAQQGNMAVTVTYGG-DVPKSPFVNVNAPPLDLSKIKVQGLNSKAVGQEQAFSV 968
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

QY 169 NLIYADGKTQTAEFKGTTEE-----ATAEAYRYADLLAKENGKTYVDVADKG 215
DB 969 NTRGAGGQGO-LDVRMTSPSRPIPCCKLEPGGAEAAQAVRY---MPPEEGPYKVDITVDG 1024
QY 216 YTL-NIKFAGKEKTEPEEKVEVT-----YADGKTQTAEFKGTFAEATAE 264
DB 1025 HPVPGSPFAVEGLPDPSPSKVCAYPGLKGLGVTPAPFSDTKAGTGGGLGTLVEGPCE 1084
QY 265 AYRYADLLAKENGKTYADL-----EDGGYTNIRFAGKKVDEKP-----EEDMDTYKLIL 314
DB 1085 ----AKIECDQNGDSCAVSYLPTPEGTYTNILFAEAHIPGSPFKATIRPVDFDPSKVRA 1140
QY 315 NGKTLK-----GETTTEAVDAATAEK-----VFKQYANDNGVDGEW--TYDDA- 355
DB 1141 SGPGLERKGVGEAATFTVDCSEAGEAELTIELSDAGVKAELVIHNNADGTYHITYSPAF 1200
QY 356 TKTFVTVEK-----PEVIDASELTPAVTYYKLVINGK-----TLKGETTTKAVDAET- 402
DB 1201 PGTYYTITIKYGGHPVPKFPFTRVHVQPAVDTSQVKVSGPVEPHGVLRVTTFTTVDARSL 1260
QY 403 -----AEKAFQYANDNGVDGVW 420
DB 1261 TATGNNHVTARVLNPSGAKTDTYVTDNG-DGTY 1292

RESULT 10

US-10-408-765A-2039
; Sequence 2039, Application US/10408765A
; GENERAL INFORMATION:

; APPLICANT: Fahy, Soumitra S.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2039
; LENGTH: 2705
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2039

Query Match 7.2%; Score 160; DB 6; Length 2705;
Best Local Similarity 22.2%; Pred. No. 0.0095;
Matches 114; Conservative 60; Mismatches 187; Indels 152; Gaps 25;

QY 47 SEAYAYADTLKKDNGEYTVDVADKG---YTLNKFAGKE--KTPEEPKEEYTIKANLIYA 101
DB 793 READIDFDLIKNDNDFVTKVTPPGAGRYTINVLFANQEIAPSPFIKVDPSHDSKVA 852
QY 102 DGK-----TQTA-----EFGKTFEEATAEAYRYADALKDNGEY 136
DB 853 EGPGLNRTGVEYKPTHTFVLTKGAGKAKLDVQFAGT---AKGEVVRDFEIIDNHDSYT 909
QY 137 VD---VADKGYTLNKFAGKEKTPPEP-----KEEVTIKA 168
DB 910 VKYTAVOQGNMAVTYTG- -DPVPKSPFVNVNAPPDLDSKIKVOGLNSKVAVGQOAFSV 968
QY 169 NLIYADGKTQTAEFKGTTEE-----ATAEAYRYADLLAKENGKTYVDVADKG 215
DB 969 NTRGAGGQGO-LDVRMTSPSRPIPCCKLEPGGAEAAQAVRY---MPPEEGPYKVDITVDG 1024
QY 216 YTL-NIKFAGKEKTEPEEKVEVT-----YADGKTQTAEFKGTFAEATAE 264
DB 1025 HPVPGSPFAVEGLPDPSPSKVCAYPGLKGLGVTPAPFSDTKAGTGGGLGTLVEGPCE 1084

QY 265 AYRYADLLAKENGKTYADL-----EDGGYTNIRFAGKKVDEKP-----EEDMDTYKLIL 314
DB 1085 ----AKIECDQNGDSCAVSYLPTPEGTYTNILFAEAHIPGSPFKATIRPVDFDPSKVRA 1140
QY 315 NGKTLK-----GETTTEAVDAATAEK-----VFKQYANDNGVDGEW--TYDDA- 355
DB 1141 SGPGLERKGVGEAATFTVDCSEAGEAELTIELSDAGVKAELVIHNNADGTYHITYSPAF 1200
QY 356 TKTFVTVEK-----PEVIDASELTPAVTYYKLVINGK-----TLKGETTTKAVDAET- 402
DB 1201 PGTYYTITIKYGGHPVPKFPFTRVHVQPAVDTSQVKVSGPVEPHGVLRVTTFTTVDARSL 1260
QY 403 -----AEKAFQYANDNGVDGVW 420
DB 1261 TATGNNHVTARVLNPSGAKTDTYVTDNG-DGTY 1292

RESULT 11

US-10-089-320B-44
; Sequence 44, Application US/10089320B
; GENERAL INFORMATION:

; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
; TITLE OF INVENTION: Shear Stress-Responsive Genes
; FILE REFERENCE: 1241.22
; CURRENT APPLICATION NUMBER: US/10/089,320B
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: JP 1999-280976
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
; LENGTH: 2705
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-089-320B-44

Query Match 7.2%; Score 160; DB 6; Length 2705;

Best Local Similarity 22.2%; Pred. No. 0.0095;
Matches 114; Conservative 60; Mismatches 187; Indels 152; Gaps 25;

QY 47 SEAYAYADTLKKDNGEYTVDVADKG---YTLNKFAGKE--KTPEEPKEEYTIKANLIYA 101
DB 793 READIDFDLIKNDNDFVTKVTPPGAGRYTINVLFANQEIAPSPFIKVDPSHDSKVA 852
QY 102 DGK-----TQTA-----EFGKTFEEATAEAYRYADALKDNGEY 136
DB 853 EGPGLNRTGVEYKPTHTFVLTKGAGKAKLDVQFAGT---AKGEVVRDFEIIDNHDSYT 909
QY 137 VD---VADKGYTLNKFAGKEKTPPEP-----KEEVTIKA 168
DB 910 VKYTAVOQGNMAVTYTG- -DPVPKSPFVNVNAPPDLDSKIKVOGLNSKVAVGQOAFSV 968
QY 169 NLIYADGKTQTAEFKGTTEE-----ATAEAYRYADLLAKENGKTYVDVADKG 215
DB 969 NTRGAGGQGO-LDVRMTSPSRPIPCCKLEPGGAEAAQAVRY---MPPEEGPYKVDITVDG 1024
QY 216 YTL-NIKFAGKEKTEPEEKVEVT-----YADGKTQTAEFKGTFAEATAE 264
DB 1025 HPVPGSPFAVEGLPDPSPSKVCAYPGLKGLGVTPAPFSDTKAGTGGGLGTLVEGPCE 1084
QY 265 AYRYADLLAKENGKTYADL-----EDGGYTNIRFAGKKVDEKP-----EEDMDTYKLIL 314
DB 1085 ----AKIECDQNGDSCAVSYLPTPEGTYTNILFAEAHIPGSPFKATIRPVDFDPSKVRA 1140
QY 315 NGKTLK-----GETTTEAVDAATAEK-----VFKQYANDNGVDGEW--TYDDA- 355
DB 1141 SGPGLERKGVGEAATFTVDCSEAGEAELTIELSDAGVKAELVIHNNADGTYHITYSPAF 1200
QY 356 TKTFVTVEK-----PEVIDASELTPAVTYYKLVINGK-----TLKGETTTKAVDAET- 402
DB 1201 PGTYYTITIKYGGHPVPKFPFTRVHVQPAVDTSQVKVSGPVEPHGVLRVTTFTTVDARSL 1260
QY 403 -----AEKAFQYANDNGVDGVW 420

Db 1261 TATGGNHVHTARVLPNSGAKTDTYVTDNG-DGT 1292

RESULT 12

US-09-200-650E-7

; Sequence 7, Application US/09200650E

; GENERAL INFORMATION:

; APPLICANT: Patti, Joseph M.

; APPLICANT: Foster, Timothy J.

; APPLICANT: Hook, Magnus A.O.

; APPLICANT: Eldhinn, Deirdre Ni

; APPLICANT: Perkins, Samuel L.

; TITLE OF INVENTION: Extracellular Matrix-Binding Proteins from Staphylococcus aureus

; FILE REFERENCE: P06283US2/BAS

; CURRENT APPLICATION NUMBER: US/09/200,650E

; CURRENT FILING DATE: 1998-11-25

; PRIOR APPLICATION NUMBER: 60/066,815

; PRIOR FILING DATE: 1997-11-26

; PRIOR APPLICATION NUMBER: 60/098,427

; PRIOR FILING DATE: 1998-08-31

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 7

; LENGTH: 1166

; TYPE: PRT

; ORGANISM: Staphylococcus aureus

US-09-200-650E-7

Query Match 7.0%; Score 157.5; DB 5; Length 1166;

Best Local Similarity 21.6%; Pred. No. 0.0052;

Matches 126; Conservative 74; Mismatches 192; Indels 191; Gaps 32;

```
QY 2 VENKEETPETDSEEVITKANLIFANGSTQAE-----FKGTPEKATSE--AYAYAD 54
Db 317 IDNKVKKGMTINYNKVN-IPSDLTDKNDPIDITDPSGEVIAGFDKATKQITYTFTD 375
QY 55 TLKKNDEYTVDVADK-----GY-----TLNKFAGKEKTPPEPKKEVTI--KANL 98
Db 376 YVDKYE-----DIKSLTLYSYDKKTPVPNETSILNLTFAFAGK---ETSONVTVDYQDPM 427
QY 99 IYADGKTQTAEEFGTPEEATAEAYRVADALKKNGEYTVDA-----DKGYTNIRKPAK 153
Db 428 VHGSNIQSITFLDDEKDQIEQIYVNPPLKKSATNTKVDIAGSQVDYDG---NIKL-GN 483
QY 154 EKTPEEPKEEVTI-----KANLIY-----172
Db 484 GSTIIDQNTKIKYKVNSDQQLPQSNRIYDFSOYDVTQFDNKKFSNNVATLDFGDIN 543
QY 173 -----ADGKTQTAEFKGTPEEATAEAYRYADLLAKEN-----GKYT 208
Db 544 SAYIIVKVSRYTPTSDGELDIAQ--GT-SMRTTDKGYNYAGYSNFIIVTSNDTGGGDGT 600
QY 209 VDVAADGYTL-----NIKFAGKEKTPPEPKKEEVTIKANLIYADGKTQTA-----EF 254
Db 601 VKPEEKLYKGDYVWEDVDKDGQVQGTDSKEKPMANVLVTIYDPGTTKSVRTDANGHYEF 660
QY 255 KG-----TFABATAEAYRYADLLAKENGYTADLEDGGYTNIRPAGKKVDEKPEPM 307
Db 661 GGLKDGETYIVKFEPTPGY---LPTKVNCTDGEKDSNGSSYTV-----KINGKODMSL 711
QY 308 DT-----YKLILNGKTLKGETTTEAVDAATAEKVPKQYANNGV--DGEWTVDDATKTF 359
Db 712 DTGFYKRPKNL---GDYVWEDTNKQGI-----QDANEPGINKDVKVTLKDSGKV 758
QY 360 ---TVTEKPEVIDASEL-----TPA---VTYKVLINGKTLKGETT---KAVDA 400
Db 759 IGTFTTDSKGYKFTDLONGNYVEFETPAGYTPTVKNTTADKDSNGLTFTTGVIKQADN 818
QY 401 ETAEAKFYQYANDNGVGVWYTD-----DAT-----KTFTVT 432
Db 819 MTLDRGFYKTPKISLGDYVW-YDSNKDGKQDSTEKGIKQVTVT 860
```

RESULT 13

US-10-408-765A-1222

; Sequence 1222, Application US/10408765A

; GENERAL INFORMATION:

; APPLICANT: Ghosh, Soumitra S.

; APPLICANT: Fahy, Eoin D.

; APPLICANT: Zhang, Bing

; APPLICANT: Gibson, Bradford W.

; APPLICANT: Taylor, Steven W.

; APPLICANT: Glenn, Gary M.

; APPLICANT: Warnock, Dale E.

; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION

; FILE REFERENCE: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME

; CURRENT APPLICATION NUMBER: 660088.465

; CURRENT FILING DATE: 2003-04-04

; NUMBER OF SEQ ID NOS: 3077

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1222

; LENGTH: 916

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-408-765A-1222

Query Match 7.0%; Score 156; DB 6; Length 916;

Best Local Similarity 23.5%; Pred. No. 0.005;

Matches 117; Conservative 56; Mismatches 153; Indels 172; Gaps 26;

```
QY 1 AVENKEETPETDSEEVITKANLIFANGSTQTAEFKGTFFKATSEAYAYADTLKDN 60
Db 491 AAEKEEPEA-----EEEVAAKKSPVKAT-APEVKEEG--EKEEEGQFEED--BEDE 541
QY 61 GEYTVADVADGYTLNIRKFAKKEKTPPEPKKEEVTIKANLIYADGKTQTAEFKGTPEEATAE 120
Db 542 GAKS-DAEGS-----GSEKGSSEKEEGE-----QEEGETE-AEAEAG--EEAEAK 583
QY 121 AYRYADALKKNGEYTVDVADKGYTLNIRKFAKKEKTPPEPKKEEVTIKANLIYADGKTQTA 180
Db 584 -----BEKKVEEKSEEVATKEELV-ADAKVEKP 610
QY 181 E-FKGTPEEATAEAYRYADLLAKENGYTV---DVADKGYT---LNIKFAGKEKTPPEP 232
Db 611 EKAKSPVKSPVE-----EKGKSPVKSPVEEKGKSPVKSPVEEKGKSPVKSPVKSP 660
QY 233 KEEVTIKANLIYADGKTQTAEF-----KGTFEATAEAYRYADLLAKENGYTA 281
Db 661 VEE-----GKSPVSKSPVEEAKKSPVKSPVEEAKSKA-----EVGKEQ 701
QY 282 DLEDGGYTNIRPAGK--KYDEKPEEPMDTYKLLINGKTLKGETTTEAVDAATAEKYF-- 337
Db 702 KEEB---EKEVKEAPKEEKEKPKDVPKKAESPVKEEAEVAEAVVTTTKSVKHLE 758
QY 338 -----KQYANDNG-----VDGEWTVDDATK- 357
Db 759 KETKEEGKLOQKEKEKAGGEGSEEGSDKGAGSKRKEEDIAVNGEVEKEEVEQETKE 818
QY 358 --TFTVTEKPEVIDASELTTPAVTITKLVINGKTLKGETTTEAVDAATAEAKAFKQYANDNG 415
Db 819 KSGREEEKGVVINGLDLSPA-----DEKKGGDSSEKVVVTKTVEK-----ITSEG 865
QY 416 VDGWTVDDATKTFVTTE 433
Db 866 GDGATKY--ITKSVTVTQ 881
```

RESULT 14

US-60-490-890-475

; Sequence 475, Application US/60490890

; GENERAL INFORMATION:

; APPLICANT: Li, Martha

; APPLICANT: Rupnow, Brent A.

; APPLICANT: Webster, Kevin R.

```
; APPLICANT: Jackson, Donald
; APPLICANT: Wong, Tai W.
; TITLE OF INVENTION: BIOMARKERS OF CYCLIN-DEPENDENT KINASE MODULATION
; FILE REFERENCE: D0310 PSP
; CURRENT APPLICATION NUMBER: US/60/490,890
; CURRENT FILING DATE: 2003-07-29
; NUMBER OF SEQ ID NOS: 2779
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 475
; LENGTH: 916
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-490-890-475

Query Match
Best Local Similarity 7.0%; Score 156; DB 7; Length 916;
Matches 117; Conservative 56; Mismatches 153; Indels 172; Gaps 26;

QY 1 AVENKEETPETDSEEEVTTKANLIFANGSTQTAFFKGTPEKATSEAYAYADTLKKN 60
Db 491 AAEKEEPEA-----EEEEAAKSPVKAT-APEVKEEG--EKEEEGQEEEE--EED 541
QY 61 GEYTVADKGYTLNIFKAGKEKTPPEPKEEVTIKANLIYADGKTQTAFFKGTPEEATAE 120
Db 542 GAKS-DQAEAG-----GSEKESSEKEGE-----QEGETE-AEAG--EEAEAK 583
QY 121 AYADALKKNGEYTVADKGYTLNIFKAGKEKTPPEPKEEVTIKANLIYADGKTQTA 180
Db 584 -----EKKVEEKSEEVATKEELV-ADAKVEKP 610
QY 181 E-FKGTPEEATAEAYRYADLLAKENGKTYV---DVADKGYT---LNIFKAGKEKTPPEP 232
Db 611 ERAKSPVPSPE-----ERKSPVPSPEEKGKSPVPSPEEKGKSPVPSKP 660
QY 233 KEEVTIKANLIYADGKTQTAFF-----KGTFAEATAEAYRYADLLAKENGKTYTA 281
Db 661 VEE-----KGKSPVPSPEEAKSPVPSPEEAKSKA-----EYVGKSEQ 701
QY 282 DLEDGTYTNIRPAGK--KVDEKPEPMDTYKLINGKTLKGETTTTTEAVDAATAEKFV-- 337
Db 702 KEEE--EKVEKPEEKEEKEKPKDVPPEKKAEKSPVKEEVAEAVVITKSKVHLE 758
QY 338 -----KOYANDNG-----VDGWTYDDATK- 357
Db 759 KETKEGKPLQKEKEKAGGEGSEEGSDGKAGSRKEDIANGVEGKKEVEQETKE 818
QY 358 --TFTVTEKPEVIDASELTTPAVTTYKLIVNGKTLKGETTTTAVDAEATAEKFQYANDNG 415
Db 819 KSGGREEEKGVVTNGLDLSPA-----DEKKGDKSEKVVVTKTVEK-----ITSEG 865
QY 416 VDGWYTYDDATKTFVTTE 433
Db 866 GDGATKY--ITKSVTVTQ 881

RESULT 15
US-09-897-516A-4453
; GENERAL INFORMATION:
; SEQUENCE 4453, Application US/09897516A
; APPLICANT: Corbin, David R.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Huesing, Joseph E.
; APPLICANT: Malvar, Thomas M.
; APPLICANT: Krasomil-Osterfeld, Karina C.
; APPLICANT: Slater, Steven C.
; APPLICANT: Spiridonov, Sergei
; TITLE OF INVENTION: Xenorhabdus sp. Genome Sequences And Uses Thereof
; CURRENT APPLICATION NUMBER: US/09/897,516A
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,161
; PRIOR FILING DATE: 2000-06-30
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; NUMBER OF SEQ ID NOS: 8415
; SEQ ID NO 4453
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Xenorhabdus sp.
US-09-897-516A-4453

Query Match
Best Local Similarity 7.0%; Score 155.5; DB 5; Length 770;
Matches 97; Conservative 65; Mismatches 186; Indels 81; Gaps 18;

QY 5 KEETPETPETDSEEE---EVTIKANLIFANGSTQTAFFKGTPEKATSEAYAYADTLKKN 61
Db 210 KKWVPLTRKINHKELVNDINLNAADVAYNKTTETDALIPIQODIAQAMKLADTANO-NA 268
QY 62 EYTVADKGYTLNIFKAGKEKTPPEPKEEVTIKANLIYADGKTQTAFFKGTPEEATAE 121
Db 269 TSAINNAENKVPTRKINDKELV-----NDIRLIAADVAYNKTTETDALIPIQODIAQ 323
QY 122 YRYADALKKNGEYTVADKGYTLNIFKAGKEKTPPEPKEEVTIKANLIYADGKTQTA 181
Db 324 MKLADTANO-NATSAINNAENKVPTRKINDKELV-----NDINLNAADVAYNKTTESDA 377
QY 182 FKGTPEEATAEAYRYADLLAKENGKTYVDVADKGYTLNIFKAGKEKTPPEPKEEVTIKAN 241
Db 378 LIPIQODVQAQMRQADTAIKE-----AESKVPLTRKINHKELV-----SDINLNA 424
QY 242 LIYADGKTQTAFFKGTFAEATAEAYRYADLLAKENGKTYADLEDGTYTNIRFAGKKVDE 301
Db 425 DVDAYNRTETDALIPIQODIAQAMKLAD-TANQNGA-TA-----IRDAASKV-- 470
QY 302 KPEEPMDTYKLINGKTLKGETTTEA--VDAATAEKFVKQYANDNGVDGEWYDDATKTF 359
Db 471 ----PLTRR---INGKELVNDIKLIASDVNAVYDKKEI-----DQLIDGVKELANAANN- 516
QY 360 TVTEKPEVIDASELTTPAVTTYKLIVNGKTLKGETTTTKAVDAEATAEK-----AFKOYA 411
Db 517 -----NADSKVPVFR-----INNKALLDIMLNASDVTIYAKGEIDQOINSVRKLA 563
QY 412 ND--NGVDG 418
Db 564 NDANNVNG 572

Search completed: September 3, 2003, 11:14:32
Job time : 19.6184 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2003, 10:59:36 ; Search time 11.5562 Seconds
(without alignments)
1116.704 Million cell updates/sec

Title: US-08-325-278B-1
Perfect score: 1565
Sequence: 1 AVENKBPETPTDSEEV.....GGYTINIRPAKKVDEKPEE 305

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A-COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B-COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A-COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B-COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTCTUS-COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1565	100.0	305	2	US-08-795-475-1
2	1565	100.0	434	2	US-08-795-475-3
3	1226.5	78.4	1027	3	US-08-446-137B-2
4	1216	77.7	291	3	US-08-446-137B-4
5	618	39.5	342	3	US-08-828-741B-6
6	618	39.5	342	4	US-09-160-567-6
7	618	39.5	342	4	US-09-710-299-6
8	615	39.3	178	3	US-08-828-741B-13
9	615	39.3	178	4	US-09-160-567-13
10	615	39.3	178	4	US-09-710-299-13
11	615	39.3	198	3	US-08-828-741B-8
12	615	39.3	198	4	US-09-160-567-8
13	615	39.3	198	4	US-09-710-299-8
14	614	39.2	495	3	US-08-828-741B-4
15	614	39.2	495	4	US-09-160-567-4
16	614	39.2	495	4	US-09-710-299-4
17	613	39.2	182	3	US-08-828-741B-2
18	613	39.2	182	4	US-09-160-567-2
19	613	39.2	182	4	US-09-710-299-2
20	334	21.3	75	3	US-08-446-137B-8
21	315.5	20.2	71	3	US-08-446-137B-6
22	306	19.6	74	3	US-08-446-137B-7
23	303	19.4	71	3	US-08-446-137B-5
24	167	10.7	664	3	US-08-669-408B-2
25	151.5	9.7	1183	2	US-08-447-031A-2
26	141.5	9.0	1638	4	US-09-071-035-258
27	141.5	9.0	1638	4	US-09-071-035-262

28	141.5	9.0	1638	4	US-09-071-035-266	Sequence 266, App
29	131.5	8.4	414	4	US-09-286-981B-16	Sequence 16, Appl
30	130.5	8.3	414	4	US-09-286-981B-10	Sequence 10, Appl
31	129	8.2	558	4	US-09-071-035-268	Sequence 268, App
32	128.5	8.2	564	3	US-09-308-022-6	Sequence 6, Appli
33	127.5	8.1	631	3	US-08-847-065-25	Sequence 25, Appl
34	124.5	8.0	669	4	US-09-071-035-264	Sequence 264, App
35	123.5	7.9	952	4	US-09-107-532A-4706	Sequence 4706, Ap
36	123	7.9	936	5	PCT-US93-05944-2	Sequence 2, Appli
37	123	7.9	1008	4	US-09-308-453-2	Sequence 2, Appli
38	122.5	7.8	471	4	US-09-107-532A-5705	Sequence 5705, Ap
39	121.5	7.8	522	3	US-08-961-083-120	Sequence 120, App
40	121.5	7.8	522	4	US-09-536-784-120	Sequence 120, App
41	121.5	7.8	1040	3	US-08-961-083-118	Sequence 118, App
42	121.5	7.8	1040	4	US-09-536-784-118	Sequence 118, App
43	116.5	7.4	734	4	US-09-328-352-4412	Sequence 4412, Ap
44	116.5	7.4	1912	1	US-08-409-995-4	Sequence 4, Appli
45	116.5	7.4	1912	3	US-08-685-467-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-795-475-1
; Sequence 1, Application US/08795475
; Patent No. 5965390
; GENERAL INFORMATION:
; APPLICANT: Bjvrock, Lars
; APPLICANT: Sjvbring, Ulf
; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,475
; FILING DATE: 11-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 100084.402D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 305 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli LE392/pHDL, DSM 7054

Query Match 100.0%; Score 1565; DB 2; Length 305;
Best Local Similarity 100.0%; Pred. No. 5e-126;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVENKBPETPTDSEEVTKANLIPANGSTQPAEFGTFEKATSBAYADTLKKDN 60
|||||

Db 1 AVENKEETPETDSEBEVTIKANLIIFANGSTQTAEPKGTPEKATSEAYAYADTLKKDN 60
QY 61 GEYTVVDVADKGYTLNIFAGKEKTPPEPKBEVTIKANLIYADGKTQTAEPKGTPEEATAE 120
Db 61 GEYTVVDVADKGYTLNIFAGKEKTPPEPKBEVTIKANLIYADGKTQTAEPKGTPEEATAE 120
QY 121 AYRADALKDNGEYTVVDVADKGYTLNIFAGKEKTPPEPKBEVTIKANLIYADGKTQTA 180
Db 121 AYRADALKDNGEYTVVDVADKGYTLNIFAGKEKTPPEPKBEVTIKANLIYADGKTQTA 180
QY 181 EFKGTPEEATAEAYRYADLLAKENGKYTVVDVADKGYTLNIFAGKEKTPPEPKBEVTIKA 240
Db 181 EFKGTPEEATAEAYRYADLLAKENGKYTVVDVADKGYTLNIFAGKEKTPPEPKBEVTIKA 240
QY 241 NLIYADGKTQTAEPKGTPEEATAEAYRYADLLAKENGKYTDLEDGGYTNIRFAGKVD 300
Db 241 NLIYADGKTQTAEPKGTPEEATAEAYRYADLLAKENGKYTDLEDGGYTNIRFAGKVD 300
QY 301 EKPEE 305
Db 301 EKPEE 305

RESULT 2

US-08-795-475-3
; Sequence 3, Application US/08795475
; Patent No. 5965390
; GENERAL INFORMATION:
; APPLICANT: Bjvick, Lars
; APPLICANT: Sjvick, Ulf
; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,475
; FILING DATE: 11-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 100084.402D1
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 434 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli LE392/pHDLG, DSM 7055
US-08-795-475-3

Query Match 100.0%; Score 1565; DB 2; Length 434;
Best Local Similarity 100.0%; Pred. No. 8.1e-126;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVENKEETPETDSEBEVTIKANLIIFANGSTQTAEPKGTPEKATSEAYAYADTLKKDN 60
:|||||

Db 1 AVENKEETPETDSEBEVTIKANLIIFANGSTQTAEPKGTPEKATSEAYAYADTLKKDN 60
QY 61 GEYTVVDVADKGYTLNIFAGKEKTPPEPKBEVTIKANLIYADGKTQTAEPKGTPEEATAE 120
Db 61 GEYTVVDVADKGYTLNIFAGKEKTPPEPKBEVTIKANLIYADGKTQTAEPKGTPEEATAE 120
QY 121 AYRADALKDNGEYTVVDVADKGYTLNIFAGKEKTPPEPKBEVTIKANLIYADGKTQTA 180
Db 121 AYRADALKDNGEYTVVDVADKGYTLNIFAGKEKTPPEPKBEVTIKANLIYADGKTQTA 180
QY 181 EFKGTPEEATAEAYRYADLLAKENGKYTVVDVADKGYTLNIFAGKEKTPPEPKBEVTIKA 240
Db 181 EFKGTPEEATAEAYRYADLLAKENGKYTVVDVADKGYTLNIFAGKEKTPPEPKBEVTIKA 240
QY 241 NLIYADGKTQTAEPKGTPEEATAEAYRYADLLAKENGKYTDLEDGGYTNIRFAGKVD 300
Db 241 NLIYADGKTQTAEPKGTPEEATAEAYRYADLLAKENGKYTDLEDGGYTNIRFAGKVD 300
QY 301 EKPEE 305
Db 301 EKPEE 305

RESULT 3

US-08-446-137B-2
; Sequence 2, Application US/08446137B
; Patent No. 6162903
; GENERAL INFORMATION:
; APPLICANT: Trowern, Angus R.
; APPLICANT: Atkinson, Anthony
; APPLICANT: Murphy, Jonathan P.
; APPLICANT: Laurence, Oliver S.
; APPLICANT: Duggleby, Clive J.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEINS DERIVED
; TITLE OF INVENTION: FROM L PROTEIN AND THEIR USES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,137B
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 100084.406
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-446-137B-2

Query Match 78.4%; Score 1226.5; DB 3; Length 1027;
Best Local Similarity 79.9%; Pred. No. 2e-96;
Matches 246; Conservative 22; Mismatches 31; Indels 9; Gaps 4;

QY 2 VENKEETPETDSEBEVTIKANLIIFANGSTQTAEPKGTPEKATSEAYAYADTLKKONG 61
:|||||

Db 276 MERKLESEKTEP--PEEVTIKANLIFADGSTONAEFKGTFAKAVSDAYAYADALKKONG 333
QY 62 EYTVADKGYTINIKFAGKKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEATABA 121
Db 334 EYTVADKGLTINIKFAGKKEPEEPKEEVTIKVNLIFADGKTQTAEFKGTFEATAKA 393
QY 122 YRYADALKKONGEYTVADKGYTINIKFAGKE--KTPPEEPKEEVTIKANLIYADGKTQT 179
Db 394 YAYADLLAKENGEXTADLEDGGNTINIKFAGKETPETPEEPKEEVTIKVNLIFADGKIQT 453
QY 180 AEFKGTFEATABAARYADLLAKENGKYTVADKGYTINIKFAGKE--KTPPEEPKEEVT 237
Db 454 AEFKGTFEATAKAYAYANLLAKENGEXTADLEDGGNTINIKFAGKETPETPEEPKEEVT 513
QY 238 IKANLIYADGKTQTAEFKGTFAEATABAARYADLLAKENGKYTADLEDGGYTTINIRFAGK 297
Db 514 IKVNLIFADGKTQTAEFKGTPEEATAEARYADLLAKVNGEYTTADLEDGGYTTINIKFAGK 573
QY 298 KVDEKPEE 305
Db 574 ---EQPGE 578

RESULT 4
US-08-446-137B-4
; Sequence 4, Application US/08446137B
; Patent No. 6162903
; GENERAL INFORMATION:
; APPLICANT: Trowern, Angus R.
; APPLICANT: Ackinson, Anthony
; APPLICANT: Murphy, Jonathan P.
; APPLICANT: Laurence, Oliver S.
; APPLICANT: Duggleby, Clive J.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEINS DERIVED
; TITLE OF INVENTION: FROM L PROTEIN AND THEIR USES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446.137B
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 100084.406
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 291 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-446-137B-4

Query Match 77.7%; Score 1216; DB 3; Length 291;
Best Local Similarity 82.5%; Pred. No. 2.8e-96;
Matches 241; Conservative 20; Mismatches 25; Indels 6; Gaps 3;
QY 10 ETPETDSEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYADTLKONGEYTVAD 69
|||||

Db 2 ETPE--PEEVTIKANLIFADGSTONAEFKGTFAKAVSDAYAYADALKKONGEYTVAD 59
QY 70 KGYTINIKFAGKKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEATABAYADALK 129
Db 60 KGLTINIKFAGKKEPEEPKEEVTIKVNLIFADGKTQTAEFKGTFEATAKAYADLLA 119
QY 130 KONGEYTVADKGYTINIKFAGKE--KTPPEEPKEEVTIKANLIYADGKTQTAEFKGTFE 187
Db 120 KENGEXTADLEDGGNTINIKFAGKETPETPEEPKEEVTIKVNLIFADGKIQTAEFKGTFE 179
QY 188 EATAEARYADLLAKENGKYTVADKGYTINIKFAGKE--KTPPEEPKEEVTIKANLIYA 245
Db 180 EATAKAYAYANLLAKENGEXTADLEDGGNTINIKFAGKETPETPEEPKEEVTIKVNLIFA 239
QY 246 DGKTQTAEFKGTFAEATABAARYADLLAKENGKYTADLEDGGYTTINIRFAGK 297
Db 240 DGKTQTAEFKGTPEEATAEARYADLLAKVNGEYTTADLEDGGYTTINIKFAGK 291

RESULT 5
US-08-828-741B-6
; Sequence 6, Application US/08828741B
; Patent No. 6043069
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Sues, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
; TITLE OF INVENTION: PRODUCING SAME
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828.741B
; FILING DATE: 26-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10591
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 342 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-828-741B-6

Query Match 39.5%; Score 618; DB 3; Length 342;
Best Local Similarity 75.9%; Pred. No. 3.6e-45;
Matches 126; Conservative 5; Mismatches 15; Indels 20; Gaps 1;
QY 16 SEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYADTLKONGEYTVADKGYTLN 75
Db 174 SAEVTIKANLIFANGSTQTAEFKGTFEKATSEAYADTLKONGEYTVADKGYTLN 233
QY 76 IKFAGKKTPEE-----PKEEVTIKANLIYADGKTQTAEFKGTFE 115
|||||

Db 234 IKFAGKEATNRNTDSTDYGIQLNSRWGLTSAEVTIKANLIFANGSTQTAEPKGTPE 293
 QY 116 EATAAYRYADALKKONGEYTVVDVADKGYTLNKKAGKEKTPPEPK 161
 Db 294 KATSEAYAYADTLKKDNGEYTVVDVADKGYTLNKKAGKESAWRHPQ 339

RESULT 6

US-09-160-567-6
 ; Sequence 6, Application US/09160567
 ; Patent No. 6326179
 ; GENERAL INFORMATION:
 ; APPLICANT: Koentgen, Frank
 ; APPLICANT: Suesse, Gabriele M.
 ; APPLICANT: Tarlinton, David M.
 ; APPLICANT: Treutlein, Herbert R.
 ; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: New York
 ; COUNTRY: United States of America
 ; ZIP: 11530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09160,567
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/828,741
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Digiglio, Frank S.
 ; REGISTRATION NUMBER: 31,346
 ; REFERENCE/DOCKET NUMBER: 10591
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (516) 742-4343
 ; TELEFAX: (516) 742-4366
 ; TELEX: 230 901 SANS UR
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 342 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-160-567-6

Query Match 39.5%; Score 618; DB 4; Length 342;
 Best Local Similarity 75.9%; Pred. No. 3.6e-45;
 Matches 126; Conservative 5; Mismatches 15; Indels 20; Gaps 1;

QY 16 SEEEVTIKANLIFANGSTQTAEPKGTPEKATSEAYAYADTLKKDNGEYTVVDVADKGYTLN 75
 Db 174 SAEVTIKANLIFANGSTQTAEPKGTPEKATSEAYAYADTLKKDNGEYTVVDVADKGYTLN 233
 QY 76 IKFAGKEKTPPE-----PKEEVTIKANLIYADGKTQTAEPKGTPE 115
 Db 234 IKFAGKEATNRNTDSTDYGIQLNSRWGLTSAEVTIKANLIFANGSTQTAEPKGTPE 293
 QY 116 EATAAYRYADALKKONGEYTVVDVADKGYTLNKKAGKEKTPPEPK 161
 Db 294 KATSEAYAYADTLKKDNGEYTVVDVADKGYTLNKKAGKESAWRHPQ 339

RESULT 7

US-09-710-299-6

; Sequence 6, Application US/09710299
 ; Patent No. 6521741
 ; GENERAL INFORMATION:
 ; APPLICANT: Koentgen, Frank
 ; APPLICANT: Suesse, Gabriele M.
 ; APPLICANT: Tarlinton, David M.
 ; APPLICANT: Treutlein, Herbert R.
 ; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: New York
 ; COUNTRY: United States of America
 ; ZIP: 11530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09710,299
 ; FILING DATE: 09-NO. 6521741-2000
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/828,741
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Digiglio, Frank S.
 ; REGISTRATION NUMBER: 31,346
 ; REFERENCE/DOCKET NUMBER: 10591
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (516) 742-4343
 ; TELEFAX: (516) 742-4366
 ; TELEX: 230 901 SANS UR
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 342 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 ; US-09-710-299-6

Query Match 39.5%; Score 618; DB 4; Length 342;
 Best Local Similarity 75.9%; Pred. No. 3.6e-45;
 Matches 126; Conservative 5; Mismatches 15; Indels 20; Gaps 1;

QY 16 SEEEVTIKANLIFANGSTQTAEPKGTPEKATSEAYAYADTLKKDNGEYTVVDVADKGYTLN 75
 Db 174 SAEVTIKANLIFANGSTQTAEPKGTPEKATSEAYAYADTLKKDNGEYTVVDVADKGYTLN 233
 QY 76 IKFAGKEKTPPE-----PKEEVTIKANLIYADGKTQTAEPKGTPE 115
 Db 234 IKFAGKEATNRNTDSTDYGIQLNSRWGLTSAEVTIKANLIFANGSTQTAEPKGTPE 293
 QY 116 EATAAYRYADALKKONGEYTVVDVADKGYTLNKKAGKEKTPPEPK 161
 Db 294 KATSEAYAYADTLKKDNGEYTVVDVADKGYTLNKKAGKESAWRHPQ 339

RESULT 8

US-08-828-741B-13
 ; Sequence 13, Application US/08828741B
 ; Patent No. 6043069
 ; GENERAL INFORMATION:
 ; APPLICANT: Koentgen, Frank
 ; APPLICANT: Suesse, Gabriele M.
 ; APPLICANT: Tarlinton, David M.
 ; APPLICANT: Treutlein, Herbert R.
 ; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF


```

; TITLE OF INVENTION: PRODUCING SAME
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,741B
; FILING DATE: 26-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10591
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-828-741B-13

Query Match 39.3%; Score 615; DB 3; Length 178;
Best Local Similarity 76.2%; Pred. No. 2.7e-45;
Matches 125; Conservative 5; Mismatches 14; Indels 20; Gaps 1;

QY 18 BEVTIKANLIFANGSTQTAEFGTPEKATSEAYAYADTLKKONGEYTVDVADKGYTLNIK 77
DB 12 BEVTIKANLIFANGSTQTAEFGTPEKATSEAYAYADTLKKONGEYTVDVADKGYTLNIK 71

QY 78 FAGKEKTPPEE-----PKBEVTIKANLIYADGKTQTAEFGKTFPEA 117
DB 72 FAGKEATNRNTDGTGYILQINRWGGLTSAEVTIKANLIFANGSTQTAEFGKTFPEKA 131

QY 118 TAEAYRYADALKKONGEYTVDVADKGYTLNIKFAKGEKTPPEPK 161
DB 132 TSEAYAYADTLKKONGEYTVDVADKGYTLNIKFAKGESAWRHPQ 175

RESULT 9
US-09-160-567-13
; Sequence 13, Application US/09160567
; Patent No. 6326179
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Sues, Gabriele M.
; APPLICANT: Tarlington, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
; TITLE OF INVENTION: PRODUCING SAME
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/710,299
; FILING DATE: 09-NOV-2000
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,741
; FILING DATE: <unknown>

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/160,567
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,741
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10591
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-160-567-13

Query Match 39.3%; Score 615; DB 4; Length 178;
Best Local Similarity 76.2%; Pred. No. 2.7e-45;
Matches 125; Conservative 5; Mismatches 14; Indels 20; Gaps 1;

QY 18 BEVTIKANLIFANGSTQTAEFGTPEKATSEAYAYADTLKKONGEYTVDVADKGYTLNIK 77
DB 12 BEVTIKANLIFANGSTQTAEFGTPEKATSEAYAYADTLKKONGEYTVDVADKGYTLNIK 71

QY 78 FAGKEKTPPEE-----PKBEVTIKANLIYADGKTQTAEFGKTFPEA 117
DB 72 FAGKEATNRNTDGTGYILQINRWGGLTSAEVTIKANLIFANGSTQTAEFGKTFPEKA 131

QY 118 TAEAYRYADALKKONGEYTVDVADKGYTLNIKFAKGEKTPPEPK 161
DB 132 TSEAYAYADTLKKONGEYTVDVADKGYTLNIKFAKGESAWRHPQ 175

RESULT 10
US-09-710-299-13
; Sequence 13, Application US/09710299
; Patent No. 6521741
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Sues, Gabriele M.
; APPLICANT: Tarlington, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
; TITLE OF INVENTION: PRODUCING SAME
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/710,299
; FILING DATE: 09-NOV-2000
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,741
; FILING DATE: <unknown>

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ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 178 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-710-299-13

Query Match 39.3%; Score 615; DB 4; Length 178;
Best Local Similarity 76.2%; Pred. No. 2.7e-45;
Matches 125; Conservative 5; Mismatches 14; Indels 20; Gaps 1;

QY 18 EVVTIKANLIFANGSTQTAEPKGTPEKATSEAYAYADTLKKNNGEYTVDVADKGYTLNIK 77
Db 12 EVVTIKANLIFANGSTQTAEPKGTPEKATSEAYAYADTLKKNNGEYTVDVADKGYTLNIK 71
QY 78 FAGKEKTPEE-----PKKEVTIKANLIYADGKTQTAEPKGTPEEA 117
Db 72 FAGKEATNRTDGTGYILQINSRWGLTSAEVVTIKANLIFANGSTQTAEPKGTPEKA 131
QY 118 TAEAYRYADALKKNGEYTVDVADKGYTLNIKFKAGKEKTPEEPK 161
Db 132 TSEAYAYADTLKKNNGEYTVDVADKGYTLNIKFKAGKESAWRHPQ 175

RESULT 11
US-08-828-741B-8
; Sequence 8, Application US/08828741B
; Patent No. 6043069
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
; TITLE OF INVENTION: PRODUCING SAME
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,741B
; FILING DATE: 26-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10591
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 198 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-828-741B-8

Query Match 39.3%; Score 615; DB 3; Length 198;
Best Local Similarity 76.2%; Pred. No. 3.1e-45;
Matches 125; Conservative 5; Mismatches 14; Indels 20; Gaps 1;

QY 18 EVVTIKANLIFANGSTQTAEPKGTPEKATSEAYAYADTLKKNNGEYTVDVADKGYTLNIK 77
Db 32 EVVTIKANLIFANGSTQTAEPKGTPEKATSEAYAYADTLKKNNGEYTVDVADKGYTLNIK 91
QY 78 FAGKEKTPEE-----PKKEVTIKANLIYADGKTQTAEPKGTPEEA 117
Db 92 FAGKEATNRTDGTGYILQINSRWGLTSAEVVTIKANLIFANGSTQTAEPKGTPEKA 151
QY 118 TAEAYRYADALKKNGEYTVDVADKGYTLNIKFKAGKEKTPEEPK 161
Db 152 TSEAYAYADTLKKNNGEYTVDVADKGYTLNIKFKAGKESAWRHPQ 195

RESULT 12
US-09-160-567-8
; Sequence 8, Application US/09160567
; Patent No. 6326179
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
; TITLE OF INVENTION: PRODUCING SAME
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/160,567
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,741
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10591
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 198 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-160-567-8

Query Match 39.3%; Score 615; DB 4; Length 198;
Best Local Similarity 76.2%; Pred. No. 3.1e-45;
Matches 125; Conservative 5; Mismatches 14; Indels 20; Gaps 1;

QY 18 EVVTIKANLIPANGSTQTAEPFGTPEKATSEAYAYADTLKONGEYTVDVADKGYTLNKG 77
DB 32 EVVTIKANLIPANGSTQTAEPFGTPEKATSEAYAYADTLKONGEYTVDVADKGYTLNKG 91
QY 78 FAGKEKTPPEE-----PKEEVTIKANLIYADGKTOTABFKGTPEEA 117
DB 92 FAGKEATNRTDGTGYGILQINSRWGGLTSABEVTIKANLIPANGSTQTAEPFGTPEKA 151
QY 118 TABAYRYADALKKONGEYTVDVADKGYTLNKGKTEPPEPK 161
DB 152 TSEAYAYADTLKONGEYTVDVADKGYTLNKGKTEPPEPK 195
RESULT 13
US-09-710-299-8
; Sequence 8, Application US/09710299
; Patent No. 6521741
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; Sues, Gabriele M.
; Tarlington, David M.
; Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
; PRODUCING SAME
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/710,299
; FILING DATE: 09-NO. 6521741-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,741
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10591
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 198 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-710-299-8
Query Match 39.3%; Score 615; DB 4; Length 198;
Best Local Similarity 76.2%; Pred. No. 3.1e-45;
Matches 125; Conservative 5; Mismatches 14; Indels 20; Gaps 1;
QY 18 EVVTIKANLIPANGSTQTAEPFGTPEKATSEAYAYADTLKONGEYTVDVADKGYTLNKG 77
DB 32 EVVTIKANLIPANGSTQTAEPFGTPEKATSEAYAYADTLKONGEYTVDVADKGYTLNKG 91
QY 78 FAGKEKTPPEE-----PKEEVTIKANLIYADGKTOTABFKGTPEEA 117
DB 92 FAGKEATNRTDGTGYGILQINSRWGGLTSABEVTIKANLIPANGSTQTAEPFGTPEKA 151

QY 118 TABAYRYADALKKONGEYTVDVADKGYTLNKGKTEPPEPK 161
DB 152 TSEAYAYADTLKONGEYTVDVADKGYTLNKGKTEPPEPK 195
RESULT 14
US-08-828-741B-4
; Sequence 4, Application US/08828741B
; Patent No. 6043069
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; Sues, Gabriele M.
; Tarlington, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
; PRODUCING SAME
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,741B
; FILING DATE: 26-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10591
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 495 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-828-741B-4
Query Match 39.2%; Score 614; DB 3; Length 495;
Best Local Similarity 78.6%; Pred. No. 1.3e-44;
Matches 125; Conservative 4; Mismatches 10; Indels 20; Gaps 1;
QY 16 SEEVTIKANLIPANGSTQTAEPFGTPEKATSEAYAYADTLKONGEYTVDVADKGYTLN 75
DB 174 SAEVTIKANLIPANGSTQTAEPFGTPEKATSEAYAYADTLKONGEYTVDVADKGYTLN 233
QY 76 IKFAGKEKTPPEE-----PKEEVTIKANLIYADGKTOTABFKGTPE 115
DB 234 IKFAGKEATNRTDGTGYGILQINSRWGGLTSABEVTIKANLIPANGSTQTAEPFGTPE 293
RESULT 15
US-09-160-567-4
; Sequence 4, Application US/09160567
; Patent No. 6326179
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; Sues, Gabriele M.

APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
TITLE OF INVENTION: PRODUCING SAME
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,567
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,741
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 495 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-160-567-4

Query Match 39.2%; Score 614; DB 4; Length 495;
Best Local Similarity 78.6%; Pred. NO. 1.3e-44;
Matches 125; Conservative 4; Mismatches 10; Indels 20; Gaps 1;
QY 16 SEEEVTKANLIFANGSTQTAPEKGTSEAYAYADTLKKNNGEYTVDVADKGYTLN 75
Db 174 SAEVTKANLIFANGSTQTAPEKGTSEAYAYADTLKKNNGEYTVDVADKGYTLN 233
QY 76 IKFAGKEKTPPEE-----PKEEVTKANLIYADGKTQTAPEKGTPE 115
Db 234 IKFAGKEATNRNTDGSYDYLQINSRWGLTSAEVTKANLIFANGSTQTAPEKGTPE 293
QY 116 EATAQAYRYADALKKNGEYTVDVADKGYTLNLIKFPAGKE 154
Db 294 KATSEAYAYADTLKKNNGEYTVDVADKGYTLNLIKFPAGKE 332

Search completed: September 3, 2003, 11:04:45
Job time : 12.5562 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 3, 2003, 11:03:32 ; Search time 31.7794 Seconds
(without alignments)
1317.758 Million cell updates/sec

Title: US-08-325-278B-1

Perfect score: 1565

Sequence: 1 AVENKBPETPTDSEEV.....GGYTINIRFAGKKVDEKPEE 305

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513375 seqs, 137303645 residues

Total number of hits satisfying chosen parameters: 513375

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCT05_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1565	100.0	305	US-08-325-278-1	Sequence 1, Appli
2	1565	100.0	434	US-08-325-278-3	Sequence 3, Appli
3	618	39.5	342	US-10-345-618-6	Sequence 6, Appli
4	615	39.3	178	US-10-345-618-13	Sequence 13, Appli
5	615	39.3	198	US-10-345-618-8	Sequence 8, Appli
6	614	39.2	495	US-10-345-618-4	Sequence 4, Appli
7	613	39.2	182	US-10-345-618-2	Sequence 2, Appli
8	608	38.8	482	US-10-345-618-16	Sequence 16, Appli
9	389	24.9	76	US-09-808-212A-4	Sequence 4, Appli
10	371	23.7	72	US-09-808-212A-6	Sequence 6, Appli
11	370	23.6	72	US-09-808-212A-10	Sequence 10, Appli
12	369	23.6	72	US-09-808-212A-8	Sequence 8, Appli
13	341	21.8	82	US-09-808-212A-2	Sequence 2, Appli
14	334	21.3	75	US-09-808-212A-18	Sequence 18, Appli
15	315.5	20.2	71	US-09-808-212A-14	Sequence 14, Appli

16	306	19.6	74	10	US-09-808-212A-16	Sequence 16, Appli
17	303	19.4	71	10	US-09-808-212A-12	Sequence 12, Appli
18	166	10.6	669	9	US-09-878-756-4	Sequence 4, Appli
19	154	9.8	1741	10	US-09-971-536-68	Sequence 68, Appli
20	151.5	9.7	1183	10	US-09-870-759-45	Sequence 45, Appli
21	151.5	9.7	1183	12	US-09-751-708A-45	Sequence 45, Appli
22	149	9.5	448	12	US-10-342-224-82	Sequence 82, Appli
23	131.5	8.4	414	12	US-10-254-995-16	Sequence 16, Appli
24	131.5	8.4	836	10	US-09-858-525A-10	Sequence 10, Appli
25	131.5	8.4	871	10	US-09-858-525A-2	Sequence 2, Appli
26	130.5	8.3	376	11	US-09-056-019-7	Sequence 7, Appli
27	130.5	8.3	413	11	US-09-056-019-35	Sequence 35, Appli
28	130.5	8.3	414	12	US-10-254-995-10	Sequence 10, Appli
29	130.5	8.3	581	11	US-09-298-523B-58	Sequence 58, Appli
30	130.5	8.3	663	11	US-09-298-523B-56	Sequence 56, Appli
31	130.5	8.3	663	11	US-09-056-019-8	Sequence 8, Appli
32	130.5	8.3	663	12	US-09-969-748C-14	Sequence 14, Appli
33	129	8.2	506	15	US-10-125-692-18	Sequence 18, Appli
34	128.5	8.2	483	11	US-09-298-523B-10	Sequence 10, Appli
35	127	8.1	481	11	US-09-298-523B-6	Sequence 6, Appli
36	124.5	8.0	1436	15	US-10-080-505-13	Sequence 13, Appli
37	123	7.9	444	11	US-09-298-523B-5	Sequence 5, Appli
38	122	7.8	487	15	US-10-156-761-11764	Sequence 11764, A
39	121.5	7.8	522	9	US-09-765-272-120	Sequence 120, App
40	121.5	7.8	1040	9	US-09-765-272-118	Sequence 118, App
41	117	7.5	439	11	US-09-056-019-30	Sequence 30, Appli
42	117	7.5	1621	15	US-10-185-990-10	Sequence 10, Appli
43	117	7.5	1626	15	US-10-185-990-11	Sequence 11, Appli
44	116.5	7.4	892	12	US-10-205-219-102	Sequence 102, App
45	116.5	7.4	2353	10	US-09-797-862-33	Sequence 33, Appli

ALIGNMENTS

RESULT 1
US-08-325-278-1
; Sequence 1, Application US/08325278
; Publication No. US20030027283A1
; GENERAL INFORMATION:
; APPLICANT: Bivrock, Lars
; APPLICANT: Sjvdrck, Ulf
; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,278
; FILING DATE: 26-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 450023.401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 305 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown

MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Escherichia coli LE392/pHDL, DSM 7054
US-08-325-278-1

Query Match 100.0%; Score 1565; DB 8; Length 305;
Best Local Similarity 100.0%; Pred. No. 1.1e-116;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVENKEETPETDSEEVITKANLIFANGSTQTAEPKGTPEKATSEAYAYADTLKKDN 60
DB 1 AVENKEETPETDSEEVITKANLIFANGSTQTAEPKGTPEKATSEAYAYADTLKKDN 60

QY 61 GEYTVADVADKGYTLNIPKAGKEKTPPEPKBEVTIKANLIYADGKTQTAEPKGTPEEATAE 120
DB 61 GEYTVADVADKGYTLNIPKAGKEKTPPEPKBEVTIKANLIYADGKTQTAEPKGTPEEATAE 120

QY 121 AYRYADALKKONGEYTVADVADKGYTLNIPKAGKEKTPPEPKBEVTIKANLIYADGKTQTA 180
DB 121 AYRYADALKKONGEYTVADVADKGYTLNIPKAGKEKTPPEPKBEVTIKANLIYADGKTQTA 180

QY 181 EFKGTPEEATAEAYRYADLLAKENGKYTVADVADKGYTLNIPKAGKEKTPPEPKBEVTIKA 240
DB 181 EFKGTPEEATAEAYRYADLLAKENGKYTVADVADKGYTLNIPKAGKEKTPPEPKBEVTIKA 240

QY 241 NLIYADGKTQTAEPKGTPEEATAEAYRYADLLAKENGKYTVADVADKGYTLNIPKAGKVD 300
DB 241 NLIYADGKTQTAEPKGTPEEATAEAYRYADLLAKENGKYTVADVADKGYTLNIPKAGKVD 300

QY 301 EKPEE 305
DB 301 EKPEE 305

RESULT 2
US-08-325-278-3
Sequence 3, Application US/08325278
Publication No. US20030027283A1
GENERAL INFORMATION:
APPLICANT: Bjvrick, Lars
APPLICANT: Sjvbring, Ulf
TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,278
FILING DATE: 26-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McWaters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 450023.401
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown

MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Escherichia coli LE392/pHDLG, DSM 7055
US-08-325-278-3

Query Match 100.0%; Score 1565; DB 8; Length 434;
Best Local Similarity 100.0%; Pred. No. 1.7e-116;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVENKEETPETDSEEVITKANLIFANGSTQTAEPKGTPEKATSEAYAYADTLKKDN 60
DB 1 AVENKEETPETDSEEVITKANLIFANGSTQTAEPKGTPEKATSEAYAYADTLKKDN 60

QY 61 GEYTVADVADKGYTLNIPKAGKEKTPPEPKBEVTIKANLIYADGKTQTAEPKGTPEEATAE 120
DB 61 GEYTVADVADKGYTLNIPKAGKEKTPPEPKBEVTIKANLIYADGKTQTAEPKGTPEEATAE 120

QY 121 AYRYADALKKONGEYTVADVADKGYTLNIPKAGKEKTPPEPKBEVTIKANLIYADGKTQTA 180
DB 121 AYRYADALKKONGEYTVADVADKGYTLNIPKAGKEKTPPEPKBEVTIKANLIYADGKTQTA 180

QY 181 EFKGTPEEATAEAYRYADLLAKENGKYTVADVADKGYTLNIPKAGKEKTPPEPKBEVTIKA 240
DB 181 EFKGTPEEATAEAYRYADLLAKENGKYTVADVADKGYTLNIPKAGKEKTPPEPKBEVTIKA 240

QY 241 NLIYADGKTQTAEPKGTPEEATAEAYRYADLLAKENGKYTVADVADKGYTLNIPKAGKVD 300
DB 241 NLIYADGKTQTAEPKGTPEEATAEAYRYADLLAKENGKYTVADVADKGYTLNIPKAGKVD 300

QY 301 EKPEE 305
DB 301 EKPEE 305

RESULT 3
US-10-345-618-6
Sequence 6, Application US/10345618
Publication No. US20030148484A1
GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF PRODUCING SAME
FILE REFERENCE: 13474
CURRENT APPLICATION NUMBER: US/10/345,618
CURRENT FILING DATE: 2003-01-16
PRIOR APPLICATION NUMBER: US/09/509,031
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 6
LENGTH: 342
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: TLHL protein
OTHER INFORMATION: sequence
US-10-345-618-6

Query Match 39.5%; Score 618; DB 12; Length 342;
Best Local Similarity 75.9%; Pred. No. 1.7e-41;
Matches 126; Conservative 5; Mismatches 15; Indels 20; Gaps 1;

QY 16 SEEEVTIKANLIFANGSTQTAEPKGTPEKATSEAYAYADTLKKONGEYTVADVADKGYTLN 75
DB 174 SAAEVTIKANLIFANGSTQTAEPKGTPEKATSEAYAYADTLKKONGEYTVADVADKGYTLN 233

QY 76 IKFAGKEKTPPEE-----PKEEVTIKANLIYADGKTQTAEPKGTPE 115
DB 234 IKFAGKEATNRNRTDGTGYILOINRWGGGLTSAEVTIKANLIFANGSTQTAEPKGTPE 293


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; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US/09/509,031
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 2
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:LHL protein
; OTHER INFORMATION: sequence
US-10-345-618-2

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Query Match 39.2%; Score 613; DB 12; Length 182;
Best Local Similarity 78.5%; Pred. NO. 1.9e-41;
Matches 124; Conservative 5; Mismatches 9; Indels 20; Gaps 1;

[illegible]

Qy	75	NIKFAGKEKTPBP-----KEEVIKANLIYADGKTQTAEFKGT	114
Db	85	NIKFAGKEATNRNDGSDTYGILOINRWGLT KEEVIKANLI FANGSTOTAEFKGT	144

Oy

115 EPATAEAYRYADALKKONGEYTTVDVADKYTTLNIKFAG 152
|||:
|||:

Dh

145 EPAATSEAYAYAPTKKNGEYTVDVADGYTTLNKEFG 182
||||
||||:

RESULT 8
US-10-345-618-15

Sequence 16, Application US/10345618
Publication No. US20030148484A1
GENERAL INFORMATION:
APPLICANT: Koestgen Frank

APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF PRODUCING SAME

FILE REFERENCE: 13474
CURRENT APPLICATION NUMBER: US/10/345,618
CURRENT FILING DATE: 2003-01-16
PROB. APPLICATION NUMBER: 10/000,000 001

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; PRIOR FILING DATE: 2000-06-09  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1
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;
; LENGTH: 482
;
; TYPE: PRT
;
; ORGANISM: Artificial Sequence
;

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; OTHER INFORMATION: Description of Artificial Sequence: ccMTIGL protein
; OTHER INFORMATION: sequence
US-10-345-618-16

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Query Match	38.8%	Score 608;	DB 12;	Length 482;
Best Local Similarity	80.0%	Pred. No. 1.7e-40;		
Matches 124;	Conservative	5;	Mismatches 10;	Indels 16; Gaps 1;

[illegible]

Qy	76	KIPAGKENT-----PBPPEEVTIKANLIYAOKTQTAEFKCTFEERATA	119
Db	381	KIPAGKEAGGGGGGGGGGGGSGGGSAAEVTIKANLIFANGSTQTAEPFKGTFEKATS	440

Qy	120	EAYRYADALKKONGEYTV	VDVADKGYTLN	KFPAGKE	154
Eb	441	EAYAYADTLKONGEYTV	VDVADKGYTLN	KFPAGKE	475

RESULT 9
US-09-808
; Sequenc

Patent
GENERAL
APPLIC

;
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;
;

CURRENT
CURRENT
NUMBER

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; SEQ ID
; LENGT
; TYPE:

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US-09-808

Oy
Matches

95

Db

US-09-808
; Sequenc
: Patent

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; GENERAL
; APPLIC
; APPLIC
: APPLIC

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; TITLE
; FILE R
; CURREN
; CURREN

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; NUMBER
; SOFTWA
; SEQ ID
; ENC

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;
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US-09-808

Query M
Best Lo
Matches

QY Db

QY Db

RESULT 11
US-09-808

Patent
; GENERAL
; APPLIC


```
; APPLICANT: Beckingham, Jennifer Ann
; APPLICANT: Roberts, Sian Eleri
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN
; FILE REFERENCE: 100084.414US
; CURRENT APPLICATION NUMBER: US/09/808,212A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Peptostreptococcus sp.
US-09-808-212A-10

Query Match      23.6%; Score 370; DB 10; Length 72;
Best Local Similarity 100.0%; Pred. No. 1.1e-22;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 KETPEEPKEEVTIKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTDABLE 284
DB 1 KETPEEPKEEVTIKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTDABLE 60

QY 285 DGGYTINIRFAG 296
DB 61 DGGYTINIRFAG 72

RESULT 12
US-09-808-212A-8
; Sequence 8, Application US/09808212A
; Patent No. US20020137918A1
; GENERAL INFORMATION:
; APPLICANT: Gore, Michael Graham
; APPLICANT: Beckingham, Jennifer Ann
; APPLICANT: Roberts, Sian Eleri
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN
; FILE REFERENCE: 100084.414US
; CURRENT APPLICATION NUMBER: US/09/808,212A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Peptostreptococcus sp.
US-09-808-212A-8

Query Match      23.6%; Score 369; DB 10; Length 72;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 153 KETPEEPKEEVTIKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTVDDVA 212
DB 1 KETPEEPKEEVTIKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTVDDVA 60

QY 213 DKGYTLNFKAG 224
DB 61 DKGYTLNFKAG 72

RESULT 13
US-09-808-212A-2
; Sequence 2, Application US/09808212A
; Patent No. US20020137918A1
; GENERAL INFORMATION:
; APPLICANT: Gore, Michael Graham
; APPLICANT: Beckingham, Jennifer Ann
; APPLICANT: Roberts, Sian Eleri
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN
; FILE REFERENCE: 100084.414US
; CURRENT APPLICATION NUMBER: US/09/808,212A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Peptostreptococcus sp.
US-09-808-212A-2

Query Match      21.8%; Score 341; DB 10; Length 82;
Best Local Similarity 82.9%; Pred. No. 2.6e-20;
Matches 68; Conservative 6; Mismatches 6; Indels 2; Gaps 1;

QY 218 LNIKFAGKE--KTPEEPKEEVTIKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKE 275
DB 1 MNIKFAGKETPETPEEPKEEVTIKVNLIFADGKTQTAEFKGTFAEATAEAYRYADLLAKV 60

QY 276 NGKYTDABLEDGGYTINIRFAGK 297
DB 61 NGEYTDABLEDGGYHNNIKFAGK 82

RESULT 14
US-09-808-212A-18
; Sequence 18, Application US/09808212A
; Patent No. US20020137918A1
; GENERAL INFORMATION:
; APPLICANT: Gore, Michael Graham
; APPLICANT: Beckingham, Jennifer Ann
; APPLICANT: Roberts, Sian Eleri
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN
; FILE REFERENCE: 100084.414US
; CURRENT APPLICATION NUMBER: US/09/808,212A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Peptostreptococcus sp.
US-09-808-212A-18

Query Match      21.3%; Score 334; DB 10; Length 75;
Best Local Similarity 90.1%; Pred. No. 8.3e-20;
Matches 64; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 227 KTPEEPKEEVTIKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTDLEDG 286
DB 5 ETPEEPKEEVTIKVNLIFADGKTQTAEFKGTFAEATAEAYRYADLLAKVNGEYTDLEDG 64

QY 287 GYTINIRFAGK 297
DB 65 GYTINIRFAGK 75

RESULT 15
US-09-808-212A-14
; Sequence 14, Application US/09808212A
; Patent No. US20020137918A1
; GENERAL INFORMATION:
; APPLICANT: Gore, Michael Graham
; APPLICANT: Beckingham, Jennifer Ann
; APPLICANT: Roberts, Sian Eleri
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN
; FILE REFERENCE: 100084.414US
; CURRENT APPLICATION NUMBER: US/09/808,212A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Peptostreptococcus sp.
US-09-808-212A-14
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Query Match 20.2%; Score 315.5; DB 10; Length 71;
Best Local Similarity 87.5%; Pred. No. 2.3e-18;
Matches 63; Conservative 4; Mismatches 4; Indels 1; Gaps 1;
QY 225 KEKTPPEPKPEVTIIKANLIYADGKTQTAEFKGTFEATAEAYRYADLLAKENGKYTDLE 284
Db 1 KEK-PEEPKPEVTIKVNLIFADGKTQTAEFKGTFEATAKAYAYADLLAKENGKYTDLE 59
QY 285 DGGYTINIRFAG 296
Db 60 DGGNTINIKFAG 71

Search completed: September 3, 2003, 11:15:53
Job time : 32.7794 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:01:51 ; Search time 222.869 Seconds
(without alignments)
1191.101 Million cell updates/sec

Title: US-08-325-278B-1

Perfect score: 1565

Sequence: 1 AVENKBPETPTDSREEV.....GGYINIRPAGKVKDEKPEE 305

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 5580241 seqs, 870357830 residues

Total number of hits satisfying chosen parameters: 5580241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA Main:*

1:	/cgn2_6/ptodata/1/paa/PCTUS	COMB.pep.*
2:	/cgn2_6/ptodata/1/paa/US06	COMB.pep.*
3:	/cgn2_6/ptodata/1/paa/US07	COMB.pep.*
4:	/cgn2_6/ptodata/1/paa/US08	COMB.pep.*
5:	/cgn2_6/ptodata/1/paa/US09	COMB.pep.*
6:	/cgn2_6/ptodata/1/paa/US10	COMB.pep.*
7:	/cgn2_6/ptodata/1/paa/US11	COMB.pep.*
8:	/cgn2_6/ptodata/1/paa/US12	COMB.pep.*
9:	/cgn2_6/ptodata/1/paa/US13	COMB.pep.*
10:	/cgn2_6/ptodata/1/paa/US14	COMB.pep.*
11:	/cgn2_6/ptodata/1/paa/US15	COMB.pep.*
12:	/cgn2_6/ptodata/1/paa/US16	COMB.pep.*
13:	/cgn2_6/ptodata/1/paa/US17	COMB.pep.*
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15:	/cgn2_6/ptodata/1/paa/US19	COMB.pep.*
16:	/cgn2_6/ptodata/1/paa/US20	COMB.pep.*
17:	/cgn2_6/ptodata/1/paa/US21	COMB.pep.*
18:	/cgn2_6/ptodata/1/paa/US22	COMB.pep.*
19:	/cgn2_6/ptodata/1/paa/US23	COMB.pep.*
20:	/cgn2_6/ptodata/1/paa/US24	COMB.pep.*
21:	/cgn2_6/ptodata/1/paa/US25	COMB.pep.*
22:	/cgn2_6/ptodata/1/paa/US26	COMB.pep.*
23:	/cgn2_6/ptodata/1/paa/US27	COMB.pep.*
24:	/cgn2_6/ptodata/1/paa/US28	COMB.pep.*
25:	/cgn2_6/ptodata/1/paa/US29	COMB.pep.*
26:	/cgn2_6/ptodata/1/paa/US30	COMB.pep.*
27:	/cgn2_6/ptodata/1/paa/US31	COMB.pep.*
28:	/cgn2_6/ptodata/1/paa/US32	COMB.pep.*
29:	/cgn2_6/ptodata/1/paa/US33	COMB.pep.*
30:	/cgn2_6/ptodata/1/paa/US34	COMB.pep.*
31:	/cgn2_6/ptodata/1/paa/US35	COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1565	100.0	305	7	US-08-325-278-1 Sequence 1, Appli
2	1565	100.0	305	7	US-08-325-278A-1 Sequence 1, Appli

3	1565	100.0	305	7	US-08-325-278B-1 Sequence 1, Appli
4	1565	100.0	434	7	US-08-325-278-3 Sequence 3, Appli
5	1565	100.0	434	7	US-08-325-278A-3 Sequence 3, Appli
6	1565	100.0	434	7	US-08-325-278B-3 Sequence 3, Appli
7	1561	99.7	719	22	US-09-791-537-10210 Sequence 10210, A
8	1561	99.7	719	22	US-09-791-537-96101 Sequence 96101, A
9	1544.5	98.7	467	25	US-09-980-469-12 Sequence 12, Appl
10	1366	87.3	367	23	US-09-889-182A-4 Sequence 4, Appli
11	1226.5	78.4	992	22	US-09-791-537-88366 Sequence 88366, A
12	1226.5	78.4	1027	7	US-08-331-637-2 Sequence 2, Appli
13	1226.5	78.4	1027	8	US-08-446-137A-2 Sequence 2, Appli
14	1226.5	78.4	1027	15	US-09-187-295-2 Sequence 2, Appli
15	1216	77.7	291	8	US-08-446-137A-4 Sequence 4, Appli
16	618	39.5	342	19	US-09-509-031-6 Sequence 6, Appli
17	618	39.5	342	23	US-09-820-048A-6 Sequence 6, Appli
18	615	39.3	178	19	US-09-509-031-13 Sequence 13, Appl
19	615	39.3	178	23	US-09-820-048A-13 Sequence 13, Appl
20	615	39.3	198	19	US-09-509-031-8 Sequence 8, Appli
21	615	39.3	198	23	US-09-820-048A-8 Sequence 8, Appli
22	614	39.2	495	19	US-09-509-031-4 Sequence 4, Appli
23	614	39.2	495	23	US-09-820-048A-4 Sequence 4, Appli
24	613	39.2	182	19	US-09-509-031-2 Sequence 2, Appli
25	613	39.2	182	23	US-09-820-048A-2 Sequence 2, Appli
26	608	38.8	482	19	US-09-509-031-16 Sequence 16, Appl
27	400	25.6	78	22	US-09-791-537-22553 Sequence 22553, A
28	389	24.9	76	23	US-09-808-212A-4 Sequence 4, Appli
29	371	23.7	72	23	US-09-808-212A-6 Sequence 6, Appli
30	370	23.6	72	23	US-09-808-212A-10 Sequence 10, Appl
31	369	23.6	72	23	US-09-808-212A-2 Sequence 2, Appli
32	341	21.8	82	23	US-09-808-212A-18 Sequence 18, Appl
33	334	21.3	75	23	US-09-808-212A-14 Sequence 14, Appl
34	315.5	20.2	71	23	US-09-808-212A-16 Sequence 16, Appl
35	306	19.6	74	23	US-09-808-212A-12 Sequence 12, Appl
36	303	19.4	71	23	US-09-808-212A-12 Sequence 12, Appl
37	167	10.7	664	10	US-08-669-408-2 Sequence 2, Appli
38	167	10.7	664	23	US-09-878-756-4 Sequence 4, Appli
39	166	10.6	669	23	US-09-878-756-4 Sequence 4, Appli
40	156	10.0	1728	28	US-10-282-122A-56997 Sequence 56997, A
41	156	10.0	1747	15	US-09-134-000-5999 Sequence 5999, Ap
42	156	10.0	1747	15	US-09-134-000C-5999 Sequence 5999, Ap
43	156	10.0	1747	30	US-10-434-665-5999 Sequence 2, Appli
44	154.5	9.9	1156	3	US-07-861-804-2 Sequence 2, Appli
45	154.5	9.9	1156	8	US-08-447-031-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-325-278-1
; Sequence 1, Application US/08325278
; GENERAL INFORMATION:
; APPLICANT: Bjvck, Lars
; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,278
; FILING DATE: 26-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 450023.401
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 305 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Escherichia coli LE392/pHDL, DSM 7054
US-08-325-278-1

Query Match 100.0%; Score 1565; DB 7; Length 305;
Best Local Similarity 100.0%; Pred. No. 4.7e-125;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVENKEETPETDSEEEVTTKANLIFANGSTQTAEPKGTPEKATSEAYAYADTLKKN 60
DB 1 AVENKEETPETDSEEEVTTKANLIFANGSTQTAEPKGTPEKATSEAYAYADTLKKN 60
QY 61 GEYTVADVADKGYTLNPKAGKEKTPPEPKKEVTIKANLIYADGKTQTAEPKGTPEEATAE 120
DB 61 GEYTVADVADKGYTLNPKAGKEKTPPEPKKEVTIKANLIYADGKTQTAEPKGTPEEATAE 120
QY 121 AYRYADALKKONGEYTVADVADKGYTLNPKAGKEKTPPEPKKEVTIKANLIYADGKTQTA 180
DB 121 AYRYADALKKONGEYTVADVADKGYTLNPKAGKEKTPPEPKKEVTIKANLIYADGKTQTA 180
QY 181 EFKGTFPEATAEAYRYADLLAKENGYTVADVADKGYTLNPKAGKEKTPPEPKKEVTIKA 240
DB 181 EFKGTFPEATAEAYRYADLLAKENGYTVADVADKGYTLNPKAGKEKTPPEPKKEVTIKA 240
QY 241 NLIYADGKTQTAEPKGTPEATAEAYRYADLLAKENGYTADLEGGYTNIRFAGKKVD 300
DB 241 NLIYADGKTQTAEPKGTPEATAEAYRYADLLAKENGYTADLEGGYTNIRFAGKKVD 300
QY 301 EKPEE 305
DB 301 EKPEE 305

RESULT 2
US-08-325-278A-1
Sequence 1, Application US/08325278A
GENERAL INFORMATION:
APPLICANT: Bjorck, Lars
TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed IP Law Group
STREET: 701 Fifth Avenue Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,278A
FILING DATE: 26-Oct-1994
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E. R.

REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 100084.402
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 305 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Escherichia coli LE392/pHDL, DSM 7054
US-08-325-278A-1

Query Match 100.0%; Score 1565; DB 7; Length 305;
Best Local Similarity 100.0%; Pred. No. 4.7e-125;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVENKEETPETDSEEEVTTKANLIFANGSTQTAEPKGTPEKATSEAYAYADTLKKN 60
DB 1 AVENKEETPETDSEEEVTTKANLIFANGSTQTAEPKGTPEKATSEAYAYADTLKKN 60
QY 61 GEYTVADVADKGYTLNPKAGKEKTPPEPKKEVTIKANLIYADGKTQTAEPKGTPEEATAE 120
DB 61 GEYTVADVADKGYTLNPKAGKEKTPPEPKKEVTIKANLIYADGKTQTAEPKGTPEEATAE 120
QY 121 AYRYADALKKONGEYTVADVADKGYTLNPKAGKEKTPPEPKKEVTIKANLIYADGKTQTA 180
DB 121 AYRYADALKKONGEYTVADVADKGYTLNPKAGKEKTPPEPKKEVTIKANLIYADGKTQTA 180
QY 181 EFKGTFPEATAEAYRYADLLAKENGYTVADVADKGYTLNPKAGKEKTPPEPKKEVTIKA 240
DB 181 EFKGTFPEATAEAYRYADLLAKENGYTVADVADKGYTLNPKAGKEKTPPEPKKEVTIKA 240
QY 241 NLIYADGKTQTAEPKGTPEATAEAYRYADLLAKENGYTADLEGGYTNIRFAGKKVD 300
DB 241 NLIYADGKTQTAEPKGTPEATAEAYRYADLLAKENGYTADLEGGYTNIRFAGKKVD 300
QY 301 EKPEE 305
DB 301 EKPEE 305

RESULT 3
US-08-325-278B-1
Sequence 1, Application US/08325278B
GENERAL INFORMATION:
APPLICANT: Bjorck, Lars
TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed IP Law Group
STREET: 701 Fifth Avenue Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,278B
FILING DATE: 26-Oct-1994
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E. R.

REGISTRATION NUMBER: 33,332
 REFERENCE/DOCKET NUMBER: 100084.402
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 305 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: Escherichia coli LE392/pHDL, DSM 7054
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-08-325-278B-1
 Query Match 100.0%; Score 1565; DB 7; Length 305;
 Best Local Similarity 100.0%; Pred. No. 4.7e-125;
 Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVENKEETPETDSEBEVTIKANLIFANGSTQTAEPKGTPEKATSBAYAYADTLKKON 60
 DB 1 AVENKEETPETDSEBEVTIKANLIFANGSTQTAEPKGTPEKATSBAYAYADTLKKON 60
 QY 61 GEYTVDVADKGYTLNIFKAGKEKTPPEPKKEVTIKANLIYADGKTQTAEPKGTPEEATAE 120
 DB 61 GEYTVDVADKGYTLNIFKAGKEKTPPEPKKEVTIKANLIYADGKTQTAEPKGTPEEATAE 120
 QY 121 AYRYADALKONGEYTVDVADKGYTLNIFKAGKEKTPPEPKKEVTIKANLIYADGKTQTA 180
 DB 121 AYRYADALKONGEYTVDVADKGYTLNIFKAGKEKTPPEPKKEVTIKANLIYADGKTQTA 180
 QY 181 EFKGTFEATAYRYADLLAKENGYTVDVADKGYTLNIFKAGKEKTPPEPKKEVTIKA 240
 DB 181 EFKGTFEATAYRYADLLAKENGYTVDVADKGYTLNIFKAGKEKTPPEPKKEVTIKA 240
 QY 241 NLIYADGKTQTAEPKGTFAEATAEAYRYADLLAKENGYTADLEDGGYTTINIRFAGKKVD 300
 DB 241 NLIYADGKTQTAEPKGTFAEATAEAYRYADLLAKENGYTADLEDGGYTTINIRFAGKKVD 300
 QY 301 EKPEE 305
 DB 301 EKPEE 305

RESULT 4
 US-08-325-278-3
 Sequence 3, Application US/08325278
 GENERAL INFORMATION:
 APPLICANT: Björck, Lars
 APPLICANT: Sjöbring, Ulf
 TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESS: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/325,278
 FILING DATE: 26-OCT-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: McMasters, David D.

REGISTRATION NUMBER: 33,963
 REFERENCE/DOCKET NUMBER: 450023.401
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 434 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: Escherichia coli LE392/pHDL, DSM 7055
 US-08-325-278-3

Query Match 100.0%; Score 1565; DB 7; Length 434;
 Best Local Similarity 100.0%; Pred. No. 7.8e-125;
 Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVENKEETPETDSEBEVTIKANLIFANGSTQTAEPKGTPEKATSBAYAYADTLKKON 60
 DB 1 AVENKEETPETDSEBEVTIKANLIFANGSTQTAEPKGTPEKATSBAYAYADTLKKON 60
 QY 61 GEYTVDVADKGYTLNIFKAGKEKTPPEPKKEVTIKANLIYADGKTQTAEPKGTPEEATAE 120
 DB 61 GEYTVDVADKGYTLNIFKAGKEKTPPEPKKEVTIKANLIYADGKTQTAEPKGTPEEATAE 120
 QY 121 AYRYADALKONGEYTVDVADKGYTLNIFKAGKEKTPPEPKKEVTIKANLIYADGKTQTA 180
 DB 121 AYRYADALKONGEYTVDVADKGYTLNIFKAGKEKTPPEPKKEVTIKANLIYADGKTQTA 180
 QY 181 EFKGTFEATAYRYADLLAKENGYTVDVADKGYTLNIFKAGKEKTPPEPKKEVTIKA 240
 DB 181 EFKGTFEATAYRYADLLAKENGYTVDVADKGYTLNIFKAGKEKTPPEPKKEVTIKA 240
 QY 241 NLIYADGKTQTAEPKGTFAEATAEAYRYADLLAKENGYTADLEDGGYTTINIRFAGKKVD 300
 DB 241 NLIYADGKTQTAEPKGTFAEATAEAYRYADLLAKENGYTADLEDGGYTTINIRFAGKKVD 300
 QY 301 EKPEE 305
 DB 301 EKPEE 305

RESULT 5
 US-08-325-278A-3
 Sequence 3, Application US/08325278A
 GENERAL INFORMATION:
 APPLICANT: Björck, Lars
 APPLICANT: Sjöbring, Ulf
 TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESS: Seed IP Law Group
 STREET: 701 Fifth Avenue Suite 6300
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/325,278A
 FILING DATE: 26-Oct-1994
 CLASSIFICATION: <unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Potter, Jane E. R.
 REGISTRATION NUMBER: 33,332

REFERENCE/DOCKET NUMBER: 100084.402
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 434 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: Escherichia coli LE392/pHDLG, DSM 7055
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-08-325-278A-3

Query Match 100.0%; Score 1565; DB 7; Length 434;
 Best Local Similarity 100.0%; Pred. No. 7.8e-125;
 Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVENKEETPETDSEEVTIKANLI FANGSTQTAEFKGTPEKATSEAYAYADTLKKDN 60
 DB 1 AVENKEETPETDSEEVTIKANLI FANGSTQTAEFKGTPEKATSEAYAYADTLKKDN 60
 QY 61 GEYTVADVADKGYTLNIFKAGKEKTPPEPKKEVTIKANLIYADGKTQTAEFKGTPEEATAE 120
 DB 61 GEYTVADVADKGYTLNIFKAGKEKTPPEPKKEVTIKANLIYADGKTQTAEFKGTPEEATAE 120
 QY 121 AYRYADALKKONGEYTVADVADKGYTLNIFKAGKEKTPPEPKKEVTIKANLIYADGKTQTA 180
 DB 121 AYRYADALKKONGEYTVADVADKGYTLNIFKAGKEKTPPEPKKEVTIKANLIYADGKTQTA 180
 QY 181 EFKGTPEEATAEAYRYADLLAKENGYTVADVADKGYTLNIFKAGKEKTPPEPKKEVTIKA 240
 DB 181 EFKGTPEEATAEAYRYADLLAKENGYTVADVADKGYTLNIFKAGKEKTPPEPKKEVTIKA 240
 QY 241 NLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGYTADLEDGGYTTINIRFAGKKVD 300
 DB 241 NLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGYTADLEDGGYTTINIRFAGKKVD 300
 QY 301 EKPEE 305
 DB 301 EKPEE 305

RESULT 6

US-08-325-278B-3
 Sequence 3, Application US/08325278B
 GENERAL INFORMATION:
 APPLICANT: Bjorck, Lars
 Sjoerling, Ulf
 TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Seed IP Law Group
 STREET: 701 Fifth Avenue Suite 6300
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/325,278B
 FILING DATE: 26-Oct-1994
 CLASSIFICATION: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Potter, Jane E. R.
 REGISTRATION NUMBER: 33,332

REFERENCE/DOCKET NUMBER: 100084.402
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 434 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: Escherichia coli LE392/pHDLG, DSM 7055
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-08-325-278B-3

Query Match 100.0%; Score 1565; DB 7; Length 434;
 Best Local Similarity 100.0%; Pred. No. 7.8e-125;
 Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVENKEETPETDSEEVTIKANLI FANGSTQTAEFKGTPEKATSEAYAYADTLKKDN 60
 DB 1 AVENKEETPETDSEEVTIKANLI FANGSTQTAEFKGTPEKATSEAYAYADTLKKDN 60
 QY 61 GEYTVADVADKGYTLNIFKAGKEKTPPEPKKEVTIKANLIYADGKTQTAEFKGTPEEATAE 120
 DB 61 GEYTVADVADKGYTLNIFKAGKEKTPPEPKKEVTIKANLIYADGKTQTAEFKGTPEEATAE 120
 QY 121 AYRYADALKKONGEYTVADVADKGYTLNIFKAGKEKTPPEPKKEVTIKANLIYADGKTQTA 180
 DB 121 AYRYADALKKONGEYTVADVADKGYTLNIFKAGKEKTPPEPKKEVTIKANLIYADGKTQTA 180
 QY 181 EFKGTPEEATAEAYRYADLLAKENGYTVADVADKGYTLNIFKAGKEKTPPEPKKEVTIKA 240
 DB 181 EFKGTPEEATAEAYRYADLLAKENGYTVADVADKGYTLNIFKAGKEKTPPEPKKEVTIKA 240
 QY 241 NLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGYTADLEDGGYTTINIRFAGKKVD 300
 DB 241 NLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGYTADLEDGGYTTINIRFAGKKVD 300
 QY 301 EKPEE 305
 DB 301 EKPEE 305

RESULT 7

US-09-791-537-10210
 Sequence 10210, Application US/09791537
 GENERAL INFORMATION:
 APPLICANT: Bionomix, Inc.
 APPLICANT: Debe, Derek
 APPLICANT: Danzer, Joseph
 TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
 TITLE OF INVENTION: METHODS OF USE THEREOF
 FILE REFERENCE: 261/210
 CURRENT APPLICATION NUMBER: US/09/791,537
 CURRENT FILING DATE: 2001-02-22
 NUMBER OF SEQ ID NOS: 153055
 SOFTWARE: Patent in version 3.0
 SEQ ID NO 10210
 LENGTH: 719
 TYPE: PRT
 ORGANISM: Peptostreptococcus magnus
 US-09-791-537-10210
 Query Match 99.7%; Score 1561; DB 22; Length 719;
 Best Local Similarity 100.0%; Pred. No. 3.5e-124;
 Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VENKEETPETDSEEVTIKANLI FANGSTQTAEFKGTPEKATSEAYAYADTLKKONG 61
 DB 95 VENKEETPETDSEEVTIKANLI FANGSTQTAEFKGTPEKATSEAYAYADTLKKONG 154

Qy	62	EYTVDVADKGYTLN	KPAGKEKTPPEPK	EYVTKANLI	YADGKTQTAE	PKGTPEAT	ATA	121
Db	155	EYTVDVADKGYTLN	KPAGKEKTPPEPK	EYVTKANLI	YADGKTQTAE	PKGTPEAT	ATA	214
Qy	122	YRYADALKDNGEYTV	DVADKGYTLN	KPAGKEKTPPEK	EYVTKANLI	YADGKTQTAE		181
Db	215	YRYADALKDNGEYTV	DVADKGYTLN	KPAGKEKTPPEK	EYVTKANLI	YADGKTQTAE		274
Qy	182	FKGTPEATAEAYRY	ADLLAKENGKYTV	DVADKGYTLN	KPAGKEKTPPEK	EYVTKAN		241
Db	275	FKGTPEATAEAYRY	ADLLAKENGKYTV	DVADKGYTLN	KPAGKEKTPPEK	EYVTKAN		334
Qy	242	LIYADGKTQTAE	PKGTTFEATAEAYRY	ADLLAKENGKYTV	ADLEGGYTV	INIRPAGKKVDE		301
Db	335	LIYADGKTQTAE	PKGTTFEATAEAYRY	ADLLAKENGKYTV	ADLEGGYTV	INIRPAGKKVDE		394
Qy	302	KPEE	305					
Db	395	KPEE	398					

```

RESULT 8
US-09-791-537-96101
; Sequence 96101, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 96101
; LENGTH: 719
; TYPE: PRT
; ORGANISM: Peptostreptococcus magnus
US-09-791-537-96101

```

RESULT 9
US-09-980-469-12

```

: Sequence 12, Application US/09980469
: GENERAL INFORMATION:
: APPLICANT: Ziv , Shani
: APPLICANT: Shoseyov, Oded
: TITLE OF INVENTION: PROCESS OF EXPRESSING AND ISOLATING RECOMBINANT PROTEIN PRODUCTS FROM PLANTS, PLANT DERIVED TISSUES AND CELL CULTURES
: TITLE OF INVENTION: PROTEIN PRODUCTS FROM PLANTS, PLANT DERIVED TISSUES AND CELL CULTURES
: FILE REFERENCE: 01/22924
: CURRENT APPLICATION NUMBER: 2000-06-07
: CURRENT FILING DATE: 2000-05-07
: NUMBER OF SEQ ID NOS: 26
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 12
: LENGTH: 467
: TYPE: PRT
: ORGANISM: Artificial sequence
: FEATURE:
: OTHER INFORMATION: pUC19-cell-ProEL-cexNG-HDEL fusion encoded product
US-09-980-469-12

```

```

RESULT 10
US-09-889-182A-4
; Sequence 4, Application US/09889182A
; GENERAL INFORMATION:
; APPLICANT: Breitling, Frank
; TITLE OF INVENTION: SELECTION OF MONOCLONAL ANTIBODIES
; FILE REFERENCE: 4121-126
; CURRENT APPLICATION NUMBER: US/09/889,182A
; CURRENT FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: pct/de00/00079
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-889-182A-4

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Query Match	87.3%;	Score 1366;	DB 23;	Length 367;
Best Local Similarity	88.6%;	Pred. No. 6.2e-108;		
Matches 264;	Conservative 15;	Mismatches 15;	Indels 4;	Gaps 1;


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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1027 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-446-137A-2

Query Match      78.4%; Score 1226.5; DB 8; Length 1027;
Best Local Similarity 79.9%; Pred. No. 2.3e-95;
Matches 246; Conservative 22; Mismatches 31; Indels 9; Gaps 4;

QY 2 VENKEETPTPTDSEEEVTIKANLIFANGSTQTAEPKGTPEKATSEAYAYADTLKKONG 61
DB 276 MERKLSKETPTP--PEEEVTIKANLIFADGSGTQNAEFKGTFAKAVSDAYAYADALKKONG 333
QY 62 EYTVADVADKGYTLNIFKAGKKTPEEPKEEVIKANLIYADGKTQTAEPKGTPEEATAEA 121
DB 334 EYTVADVADKGLTNLIFKAGKKEPEEPKEEVIKANLIFADGKTQTAEPKGTPEEATAEA 393
QY 122 YRYADALKKONGEYTVADVADKGYTLNIFKAGKE--KTPEEPKEEVIKANLIYADGKTQT 179
DB 394 YAYADLLAKENGEXTADLEDGGNTINIKFAGKETPETPEEPKEEVIKANLIFADGKIQT 453
QY 180 AEFKGTPEEATAEAAYRYADLLAKENGKYYTVADVADKGYTLNIFKAGKE--KTPEEPKEEVT 237
DB 454 AEFKGTPEEATAKAYAYANLLAKENGEXTADLEDGGNTINIKFAGKETPETPEEPKEEVT 513
QY 238 IKANLIYADGKTQTAEPKGTPEEATAEAAYRYADLLAKENGKYYTADLEDGGYTNIRFAGK 297
DB 514 IKVNLIFADGKTQTAEPKGTPEEATAEAAYRYADLLAKENGEXTADLEDGGYTNIRFAGK 573
QY 298 KVDEKPEE 305
DB 574 ---EQPGE 578

```

```

RESULT 14
US-09-187-295-2
; Sequence 2, Application US/09187295
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROTEIN L AND PROCESS FOR ITS PREPARATION BY
; RECOMBINANT DNA TECHNOLOGY
; NUMBER OF SEQUENCES: 23
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/187,295
;   FILING DATE: 05-NOV-1998
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/331,637
;   FILING DATE: 13-MARCH-1995
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1027 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-09-187-295-2

```

```

Query Match      78.4%; Score 1226.5; DB 15; Length 1027;
Best Local Similarity 79.9%; Pred. No. 2.3e-95;
Matches 246; Conservative 22; Mismatches 31; Indels 9; Gaps 4;

QY 2 VENKEETPTPTDSEEEVTIKANLIFANGSTQTAEPKGTPEKATSEAYAYADTLKKONG 61
DB 276 MERKLSKETPTP--PEEEVTIKANLIFADGSGTQNAEFKGTFAKAVSDAYAYADALKKONG 333
QY 62 EYTVADVADKGYTLNIFKAGKKTPEEPKEEVIKANLIYADGKTQTAEPKGTPEEATAEA 121

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DB 334 EYTVADVADKGLTNLIFKAGKKEPEEPKEEVIKANLIFADGKTQTAEPKGTPEEATAEA 393
QY 122 YRYADALKKONGEYTVADVADKGYTLNIFKAGKE--KTPEEPKEEVIKANLIYADGKTQT 179
DB 394 YAYADLLAKENGEXTADLEDGGNTINIKFAGKETPETPEEPKEEVIKANLIFADGKIQT 453
QY 180 AEFKGTPEEATAEAAYRYADLLAKENGKYYTVADVADKGYTLNIFKAGKE--KTPEEPKEEVT 237
DB 454 AEFKGTPEEATAKAYAYANLLAKENGEXTADLEDGGNTINIKFAGKETPETPEEPKEEVT 513
QY 238 IKANLIYADGKTQTAEPKGTPEEATAEAAYRYADLLAKENGKYYTADLEDGGYTNIRFAGK 297
DB 514 IKVNLIFADGKTQTAEPKGTPEEATAEAAYRYADLLAKENGEXTADLEDGGYTNIRFAGK 573
QY 298 KVDEKPEE 305
DB 574 ---EQPGE 578

RESULT 15
US-08-446-137A-4
; Sequence 4, Application US/08446137A
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEINS DERIVED
; FROM PROTEIN L AND THEIR USES
; NUMBER OF SEQUENCES: 4
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/446,137A
;   FILING DATE: 22-05-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
;   NAME: MITCHARD, LEONARD C.
;   REGISTRATION NUMBER: 29,009
;   REFERENCE/DOCKET NUMBER: 1418-9
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (703) 816-4000
;   TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 291 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-446-137A-4

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Query Match      77.7%; Score 1216; DB 8; Length 291;
Best Local Similarity 82.5%; Pred. No. 2.9e-95;
Matches 241; Conservative 20; Mismatches 25; Indels 6; Gaps 3;

QY 10 ETPETDSEEEVTIKANLIFANGSTQTAEPKGTPEKATSEAYAYADTLKKONGEYTVADVAD 69
DB 2 ETPETDSEEEVTIKANLIFANGSTQTAEPKGTPEKATSEAYAYADTLKKONGEYTVADVAD 59
QY 70 KGYTLNIFKAGKKTPEEPKEEVIKANLIYADGKTQTAEPKGTPEEATAEAAYRYADALK 129
DB 60 KGLTNLIFKAGKKEPEEPKEEVIKANLIFADGKTQTAEPKGTPEEATAEAAYADLLA 119
QY 130 KONGEYTVADVADKGYTLNIFKAGKE--KTPEEPKEEVIKANLIYADGKTQTAEPKGTPE 187
DB 120 KENGEXTADLEDGGNTINIKFAGKETPETPEEPKEEVIKANLIFADGKIQTAEFKGTPE 179
QY 188 EATAEAAYRYADLLAKENGKYYTVADVADKGYTLNIFKAGKE--KTPEEPKEEVIKANLIYA 245
DB 180 EATAKAYAYANLLAKENGEXTADLEDGGNTINIKFAGKETPETPEEPKEEVIKANLIFA 239
QY 246 DGTQTAEPKGTFAEATAEAAYRYADLLAKENGKYYTADLEDGGYTNIRFAGK 297

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Db 240 DDKTQTAEFKGTPEEATAEAYRYADLLAKVNGEYTDADLEGGYTINIKPAGK 291

Search completed: September 3, 2003, 11:13:53
Job time : 224.869 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:02:46 ; Search time 12.3816 Seconds
(without alignments)
773.734 Million cell updates/sec

Title: US-08-325-278B-1

Perfect score: 1565

Sequence: 1 AVENKETPTPTDSEEV.....GGYTINIRFAGKKVDEKPEE 305

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 148256 seqs, 31410045 residues

Total number of hits satisfying chosen parameters: 148256

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA New.*

- 1: /cgm2_6/ptodata/1/paa/PCT_NEW_COMB.pep.*
- 2: /cgm2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
- 3: /cgm2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
- 4: /cgm2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
- 5: /cgm2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
- 6: /cgm2_6/ptodata/1/paa/US10_NEW_COMB.pep.*
- 7: /cgm2_6/ptodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	141	9.0	1849	6	US-10-637-544-2
2	131.5	8.4	1166	5	US-09-200-650E-7
3	129.5	8.3	1742	6	US-10-615-383-4
4	127.5	8.1	701	6	US-10-333-120A-7
5	127.5	8.1	728	6	US-10-467-534-81
6	126	8.1	630	6	US-10-603-113-20275
7	125	8.0	770	5	US-09-897-516A-4453
8	122	7.6	458	6	US-10-467-421-37
9	119.5	7.6	901	6	US-10-603-113-14747
10	116	7.4	916	6	US-10-408-765A-1222
11	116	7.4	916	7	US-60-490-890-475
12	114.5	7.3	930	5	US-09-200-650E-3
13	114.5	7.3	1394	6	US-10-645-655-2
14	113	7.2	1388	6	US-10-408-765A-1139
15	113	7.2	2060	6	US-10-381-596A-2
16	112	7.2	693	6	US-10-333-120A-10
17	111.5	7.1	718	6	US-10-603-108-2753
18	111.5	7.1	2705	1	PCT-US03-21510-97
19	111.5	7.1	2705	6	US-10-408-765A-2039
20	111.5	7.1	2705	6	US-10-089-320B-44
21	111	7.1	637	6	US-10-617-320-3169
22	111	7.1	864	6	US-10-286-897-2171
23	111	7.1	864	6	US-10-258-898A-2171
24	111	7.1	2138	6	US-10-640-833-5274
25	110	7.0	1315	5	US-09-200-650E-5
26	109.5	7.0	523	6	US-10-333-120A-11

ALIGNMENTS

RESULT 1

US-10-637-544-2

; Sequence 2, Application US/10637544

; GENERAL INFORMATION:

; APPLICANT: Chr. Hansen A/S

; TITLE OF INVENTION: Peptides with anti-hypertensive properties

; FILE REFERENCE: P1032US01

; CURRENT APPLICATION NUMBER: US/10/637,544

; CURRENT FILING DATE: 2003-08-11

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2

; LENGTH: 1849

; TYPE: PRT

; ORGANISM: Lactobacillus helveticus

US-10-637-544-2

Query Match 9.0%; Score 141; DB 6; Length 1849;

Best Local Similarity 27.7%; Pred. No. 0.021;

Matches 76; Conservative 32; Mismatches 108; Indels 58; Gaps 15;

QY 73 TLNKFAGKEKTPPEKPEEVTKANLIYADGKTQTAEFGTFEEATAA--YRVADALKK 130

Db 1415 TLNL---DSENVTVNKKDKFTI-SGTISDDYKFYDLSINGNDVETSWSAVDYHSKEGICK 1470

QY 131 DNGETYVDVADGKGYTLNFK-----FAGKEKTPPEKPEE--VTIKANLIYA 173

Db 1471 -NFKHEVDLKKGKNTFNVKVTDIQGNSSSQALVWVYEPAKTLAEPSVDKLLTKTANLQLL 1529

QY 174 DGKTQTAEFK-----GTFEEATAEAYRVADLLAKENGKYTVDVADGKY-----TL 218

Db 1530 KATTDSEAKVYVSLDNGKTFNDVPADGFK-----VTENGTVQFKAVDK-YGNESKVSXV 1583

QY 219 NIKFAGKEKTPPEKPEEVTKANL---IYADGKTQ---TAEFGKTFEATAEAYRVADL 271

Db 1584 EIKGLNKENQSEDEKELAKENLOAKVDAGEKDLKDYADSKDFNDALKKA---KDV 1640

QY 272 LAKENGKYTADLEGGYTTINIRFAGKKVDEKPEE 305

Db 1641 LADKNK-LADLQDAKALD--KAEQALTEKPAE 1671

RESULT 2

US-09-200-650E-7

; Sequence 7, Application US/09200650E

; GENERAL INFORMATION:

; APPLICANT: Patti, Joseph M.

; APPLICANT: Foster, Timothy J.

; APPLICANT: Hook, Magnus A.O.

```

RESULT 3
US-10-615-383--4
; Sequence 4, Application US/10615383
; GENERAL INFORMATION:
; APPLICANT: FOSTER, Timothy
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES FROM COAGULASE-NEGATIVE STAPHYLOCOCCUS EPIDERMIDIS
; FILE REFERENCE: P06335US03/BAS
; CURRENT APPLICATION NUMBER: US/10/615,383
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: 09/386,962
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/098,443
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/117,119
; PRIOR FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1742
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-615-383--4

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Query Match 7.4%; Score 116; DB 6; Length 916;
Best Local Similarity 25.0%; Pred. No. 0.55; Mismatches 34; Conservative 81; Indels 118; Gaps 19;
Matches 81; Conservative 34; Mismatches 34; Indels 118; Gaps 19;

QY 1 AVENKEETPETDSEBVTIKANLI FANGSTOTAEFGTPEKATSEAYAVADTLKDN 60
DB AAEKEEPEA-----EEEVAAKSPVKAT-APEVKEEG--EKEEEOQEEB--EED 541
QY 61 GYTVVDVADKGYTLNIK FAKGKTPPEPKKEVTIKANLIYADGKTQTAEFGTPEATAE 120
DB GAKS-DAEAG-----GSEKGSSEKEGE-----QEEGETE-AEAG--EAEAK 583
QY 121 ATRYADALKONGEYTVVDVADKGYTLNIK FAKGKTPPEPKKEVTIKANLIYADGKTQT 180
DB -----EKKVEKSEVATKEELV-ADAKVEKP 610
QY 181 E-FKGTFEATAEAYRYADLLAKENGKYTV---DVADKGYT---LNIFAKGKTPPEP 232
DB EKAKSPVKSPVE-----EKGKSPVKSPVEEKGKSPVKSPVEEKGKSPVKSP 660
QY 233 KEEVTIKANLIYADGKTQTAEF-----KGTFAEATAEAYRYADLLAKENGKYTA 281
DB VEE-----KGKSPVKSPVEEAKSPVKSPVEEAKSKA-----EVGKGEQ 701
QY 282 DLEDGGYTINIRFAGKVKDEKPEE 305
DB 702 KEE-----EKEVKEAPKE 715

RESULT 11
US-60-490-890-475
; Sequence 475, Application US/60490890
; GENERAL INFORMATION:
; APPLICANT: Li, Martha
; APPLICANT: Rudnow, Brent A.
; APPLICANT: Webster, Kevin R.
; APPLICANT: Jackson, Donald
; APPLICANT: Wong, Tai W.
; TITLE OF INVENTION: BIOMARKERS OF CYCLIN-DEPENDENT KINASE MODULATION
; FILE REFERENCE: D0310 PSP
; CURRENT APPLICATION NUMBER: US/60/490,890
; CURRENT FILING DATE: 2003-07-29
; NUMBER OF SEQ ID NOS: 2779
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 475
; LENGTH: 916
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-490-890-475

Query Match 7.4%; Score 116; DB 7; Length 916;
Best Local Similarity 25.0%; Pred. No. 0.55; Mismatches 34; Conservative 81; Indels 118; Gaps 19;
Matches 81; Conservative 34; Mismatches 34; Indels 118; Gaps 19;

QY 1 AVENKEETPETDSEBVTIKANLI FANGSTOTAEFGTPEKATSEAYAVADTLKDN 60
DB AAEKEEPEA-----EEEVAAKSPVKAT-APEVKEEG--EKEEEOQEEB--EED 541
QY 61 GYTVVDVADKGYTLNIK FAKGKTPPEPKKEVTIKANLIYADGKTQTAEFGTPEATAE 120
DB GAKS-DAEAG-----GSEKGSSEKEGE-----QEEGETE-AEAG--EAEAK 583
QY 121 ATRYADALKONGEYTVVDVADKGYTLNIK FAKGKTPPEPKKEVTIKANLIYADGKTQT 180
DB -----EKKVEKSEVATKEELV-ADAKVEKP 610
QY 181 E-FKGTFEATAEAYRYADLLAKENGKYTV---DVADKGYT---LNIFAKGKTPPEP 232
DB EKAKSPVKSPVE-----EKGKSPVKSPVEEKGKSPVKSPVEEKGKSPVKSP 660
QY 233 KEEVTIKANLIYADGKTQTAEF-----KGTFAEATAEAYRYADLLAKENGKYTA 281
DB VEE-----KGKSPVKSPVEEAKSPVKSPVEEAKSKA-----EVGKGEQ 701

QY 282 DLEDGGYTINIRFAGKVKDEKPEE 305
DB 702 KEE-----EKEVKEAPKE 715

RESULT 12
US-09-200-650E-3
; Sequence 3, Application US/09200650E
; GENERAL INFORMATION:
; APPLICANT: Patti, Joseph M.
; APPLICANT: Foster, Timothy J.
; APPLICANT: Hook, Magnus A.O.
; APPLICANT: Eidhinn, Deirdre Ni
; APPLICANT: Perkins, Samuel L.
; TITLE OF INVENTION: Extracellular Matrix-Binding Proteins from Staphylococcus aureus
; FILE REFERENCE: P06283US2/BAS
; CURRENT APPLICATION NUMBER: US/09/200,650E
; CURRENT FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/066,815
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: 60/098,427
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 3
; LENGTH: 930
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-200-650E-3

Query Match 7.3%; Score 114.5; DB 5; Length 930;
Best Local Similarity 22.1%; Pred. No. 0.71;
Matches 77; Conservative 44; Mismatches 91; Indels 137; Gaps 22;

QY 11 TPETDSEBVTIKANLI FAN-GSTQTAE-FKGTFEATSEAY-----AYADTLKONG-- 61
DB 407 TPTDSKLADVTDQFDVIYSNDNKATATVLMKG--QTSSNKQVYIIQQVAYPDNSSTDNGKI 464
QY 62 EYTVVDVADKGYTLNIKFA--GKKTPEPKKEVTIKANL-----IYADGKTQTAE-- 109
DB 465 DYTLDTKYKSWNSYNSVNGSSTANGDQK-----KYNLGDYWNEDTKNKGQDANEKG 519
QY 110 FKGTPE-----EATAE--AYRYADALKONGEYTVVDVA-DKGYTLNIKFAKGE 154
DB 520 IKGVVVILKDSNGKELDRITTTDENGKYQFTGL---SNGTYSVEFSTPAGYTTTANVGTD 576
QY 155 KTPPEPKKEVTIKANLIYADGKTQTAEFGTPEATAEAYRYADLLAKENG-----KYTV 209
DB 577 -----DAVSDGLTTTGVTKD-----ADNMTLDSGFYKTPKYSL 610
QY 210 -----DVADKGYTLNIKFAKGEKTPPEPKKEVTIKANLIYADGKTQTAEFK 255
DB 611 GDYVWYDKNKGKRDSTENG-----IKGVVTLQNEKEGVI-----GTTET-- 651
QY 256 GTFEATAEAYRYADLLAKENGKYTAD-LEBGGYTINIRFAGKVKDEKPE 303
DB 652 -----DENGKRYFDNLDGSKY-----KVIFEX 674

RESULT 13
US-10-645-655-2
; Sequence 2, Application US/10645655
; GENERAL INFORMATION:
; APPLICANT: St. Geme III, Joseph W.
; Falkow, Stanley
; TITLE OF INVENTION: Haemophilus Adherence and Penetration Protein
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco

STATE: California
 COUNTRY: United States
 ZIP: 94111-4187
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA: US/10/645,655
 FILING DATE: 20-AUG-2003
 CLASSIFICATION DATA:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/296,791
 FILING DATE: 25-AUG-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Treccartin, Richard F.
 REGISTRATION NUMBER: 31,801
 REFERENCE/DOCKET NUMBER: A-59941/RET/RMS
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1989
 TELEFAX: (415) 398-3249
 TELEX: 910 277299
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1394 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-10-645-655-2

Query Match 7.3%; Score 114.5; DB 6; Length 1394;
 Best Local Similarity 24.7%; Pred. No. 1.1; Mismatches 45; Indels 49; Gaps 17;
 Matches 74; Conservative 45; Mismatches 131; Indels 49; Gaps 17;
 QY 7 ETPETDSEBEVITKANLIIFANGSTQTAEPKGTPEKATSEAYAY-ADTLKONGEYTV 65
 Db 863 ETETTP-TSAER----RFTLTVNGKLSG----QGTFQ-PTSSLFGYKSDKLSND---- 909
 QY 66 DVADKGYTLNIFKAGKEKTPPEKPEVITKANLIYADGKTQTAEPKGTPE--EATAEAYR 123
 Db 910 --AEGDITLSVRNTGK----PETLEQLTLVES----KDNQPLSDKLFLENDHVDAGALR 961
 QY 124 YADALKKONGEYTVVDVADKGYTLNIFKAGKEKTPPEKPEVITKANLIYADGKTQTAEPK 183
 Db 962 Y--KLVDNGEPLHNPIKEQELHNDLVRAEQA------ERTLEAKQVEPTAKTQTGEPK 1013
 QY 184 GTFEEATAEAY------RYADLLAKENGYTVVDVADKGYTLNIFKAGKEKTPPEP--K 233
 Db 1014 VRSRAARAAPDPTLDPQSLNLALEAKQAEATAE-TQSKAKTKKVRSKRAVFSPLLDQ 1072
 QY 234 EVTTKANLIYADGKTQTAEPKGTPEKATSEAYAYR-YADLLAKENGYTVADLEDGYTIN 291
 Db 1073 SLFALEAALEVIDAPQOSE--KDLRAQEAERQKQKDLISRYNSALSSEL---SATVN 1126

RESULT 14
 US-10-408-765A-1139
 ; Sequence 1139, Application US/10408765A
 ; GENERAL INFORMATION:
 ; APPLICANT: Ghosh, Soumitra S.
 ; APPLICANT: Fahy, Eoin D.
 ; APPLICANT: Zhang, Bing
 ; APPLICANT: Gibson, Bradford W.
 ; APPLICANT: Taylor, Steven W.
 ; APPLICANT: Glenn, Gary M.
 ; APPLICANT: Warnock, Dale E.
 ; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
 ; FILE REFERENCE: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
 ; CURRENT APPLICATION NUMBER: US/10/408,765A
 ; CURRENT FILING DATE: 2003-04-04

NUMBER OF SEQ ID NOS: 3077
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 1139
 ; LENGTH: 1388
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-408-765A-1139

Query Match 7.2%; Score 113; DB 6; Length 1388;
 Best Local Similarity 21.6%; Pred. No. 1.4; Mismatches 40; Indels 102; Gaps 14;
 Matches 76; Conservative 40; Mismatches 134; Indels 102; Gaps 14;
 QY 5 KEETPE----TPETDSE----EVTIKANLI------FANGSTQTA- 36
 Db 1022 REKTPVIDATEEIDLEETEREVSQENGLSEVPLGEMETDLKATGRDSPRGKTPEVI 1081
 QY 37 ----EFKGTPEKATSEAYAYADTLK--KONGEYTVVDVADKGYTLNIFKAGKEKTPPEPK 90
 Db 1082 DAIBEIEIDLEETEREISPOENGLSEVPLGEMQTD-----LKATGREISPREKTP 1132
 QY 91 EVTTKANLIYADGKTQTAEPKGTPEEATAEAYRYADALKKONGEYTVVDVADKGYTLNIFK 150
 Db 1133 EVI-----DATEEIDKLEETGRR-----EISPEENGPEEVKPVDEMET-DLKT 1175
 QY 151 AGKEKTPPEKPEVITKANLIYAD-----GKTQTAEPKGTPEE- 188
 Db 1176 TREGSSREKTRVIDAAEVIEDLEETEREISPOENGPEEVKPVGKMET-DLKEIREEI 1234
 QY 189 -----ATAEAYRYADLLAKENGYTVVDVADK-----GYTLNIFKAGKEKTPPEP 232
 Db 1235 SQREKVLAEPSAIREKEIDLKGTGRDIPIMEKVSQKMAVVEEMEADLKTGKFNFRERG 1294
 QY 233 KEEVTI---KANLIYADGKTQTAEPKGTPEEATAEAYRYADLLAKENGYTA 281
 Db 1295 SEECVTEEKVAELKQTKGTDISPNELEETSTSRQTDTHMQSGSNDFSA 1346

RESULT 15
 US-10-381-596A-2
 ; Sequence 2, Application US/10381596A
 ; GENERAL INFORMATION:
 ; APPLICANT: Biocapto AB
 ; TITLE OF INVENTION: von Willebrand factor-binding proteins from
 ; FILE REFERENCE: 110059600
 ; CURRENT APPLICATION NUMBER: US/10/381,596A
 ; PRIOR FILING DATE: 2003-07-02
 ; PRIOR APPLICATION NUMBER: SE 0003573-3
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 2060
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus lugdunensis
 US-10-381-596A-2

Query Match 7.2%; Score 113; DB 6; Length 2060;
 Best Local Similarity 20.2%; Pred. No. 2.2; Mismatches 54; Indels 36; Gaps 12;
 Matches 62; Conservative 54; Mismatches 155; Indels 36; Gaps 12;
 QY 8 TPETPETDSEBEVITKANLIIFANGSTQTAEPKGTPEKATSEAYAYADTLKONGEYTV-VD 66
 Db 1299 TYEQIPNDAPQETPVALEV-----TRYVDSEGNVEQTEEGTHDAPGIIADKWYTGQT 1352
 QY 67 VADKGYTLNIFKAGKEKTPPEKPEVITKANLI-YADGKTQTAEPKGTPEEATAEAYRYA 125
 Db 1353 AAENGITTHVYQRIQSEIPNEAPQETPVALEVTVCVDS-----EGNEVQETEGTHDA 1405
 QY 126 DALKKONGEYTVVDVADKGYTLNIFKAGKEKTPPEKPEVITKANLIYADGKTQTAEPK 184
 Db 1406 FGIIGDKWQYTGQTTTGGDITTHYQRIQSEIPNEAPQETPVALEV-----TRYVDSEG 1459

Qy	185	TFEATAEAYRADLLAKENGKYT--VDVADKYTLNIKPAGKBKTPEEPKEVTTKANL	242
		: :	
Db	1460	NEVOETEETHQPSSIIGDKWYQTGOTTAD-GITTVYVERIQSEIPNEAPKETPIQLEV	1518
Qy	243	I-YADKGTQTAEBFKGPABEAATAEAYRADLLAKENGYKTAD-LEDGGYTTINI--RPAKK	298
		: :	
Db	1519	TRYVDG-----EGNEVQETEGTHAPGIIGKWYQTQTTSGITTHVYERIQSEI	1571
Qy	299	VDEKPEE	305
		: :	
Db	1572	PNEAQPE	1578

Search completed: September 3, 2003, 11:14:30
Job time : 14.3816 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:04:17 ; Search time 48.3288 Seconds
(without alignments)
236.470 Million cell updates/sec

Title: US-08-325-278b-1_COPY_153_224

Perfect score: 369

Sequence: 1 KEKTPPEPKBVTIKANLIY.....GKYTVADVADKGYTLNIKIFAG 72

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_13Jun03.*

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- 2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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- 19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
- 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	369	100.0	72	21	AA198539
2	369	100.0	305	14	AA198539
3	369	100.0	434	14	AA198539
4	358.5	97.2	467	22	AA198539
5	352	95.4	72	21	AA198538
6	352	95.4	367	21	AA198538
7	339	91.9	72	21	AA198540
8	315	85.4	75	21	AA198544
9	315	85.4	291	14	AA198544

10	315	85.4	1027	14	AA198539
11	315	85.4	1027	14	AA198539
12	301.5	81.7	71	21	AA198542
13	299	81.0	76	21	AA198537
14	293	79.4	82	21	AA198536
15	292	79.1	74	21	AA198543
16	286	77.5	82	21	AA198545
17	286	77.5	82	21	AA198548
18	284	77.0	82	21	AA198546
19	284	77.0	182	18	AA198547
20	284	77.0	182	20	AA198547
21	280	75.9	82	21	AA198547
22	276	74.8	178	18	AA198547
23	276	74.8	178	20	AA198547
24	276	74.8	198	18	AA198548
25	276	74.8	198	20	AA198548
26	276	74.8	342	18	AA198548
27	276	74.8	342	20	AA198548
28	276	74.8	482	20	AA198548
29	276	74.8	495	18	AA198548
30	276	74.8	495	20	AA198548
31	270.5	73.3	71	21	AA198541
32	80.5	21.8	395	22	ABG11860
33	79.5	21.5	463	22	ABG11860
34	67.5	18.3	368	22	ABG11860
35	67	18.2	450	22	AA198543
36	67	18.2	450	20	AA198543
37	67	18.2	544	17	AA198543
38	67	18.2	544	19	AA198543
39	67	18.2	608	22	AA198543
40	67	18.2	695	19	AA198543
41	67	18.2	695	21	AA198543
42	67	18.2	695	21	AA198543
43	67	18.2	924	12	AA198543
44	67	18.2	924	14	AA198543
45	67	18.2	924	14	AA198543

ALIGNMENTS

RESULT 1

AA198539

ID AA198539 standard; Protein; 72 AA.

AC AA198539;

XX 20-JUL-2000 (first entry)

DT 20-JUL-2000 (first entry)

DE Peptostreptococcus strain 312 protein L domain B3 protein sequence.

DE Immunoglobulin light chain binding protein; PpL; protein L;

KW Peptostreptococcus; human immunoglobulin kappa chain;

KW immunospecific chromatography.

XX

OS Peptostreptococcus sp.

XX

PN WO200015803-A1.

XX

PD 23-MAR-2000.

XX

PF 14-SEP-1999; 99WO-GB03048.

XX

PR 14-SEP-1998; 98GB-0019998.

XX

PR 26-APR-1999; 99GB-0009578.

XX

PA (ACTI-) ACTINOVA LTD.

XX

PI Gore MG, Beckingham JA, Roberts SE;

XX

DR WPI; 2000-271441/23.

XX

DR N-PSDB; AAA08428.

XX

PT New modified immunoglobulin light chain binding protein, useful in
PT immunoaffinity chromatography, has a dissociation constant of 400 nM or
XX more at pH8 with respect to human immunoglobulin kappa-chain -
PS Disclosure; Page 43; 56pp; English.

XX The present invention describes an immunoglobulin (Ig) light chain
CC binding protein (P1) which has been modified by one or more amino acid
CC substitutions such that the dissociation constant (Kd) of the protein
CC with respect to human Ig kappa-chain is 400 nM or more at pH8. P1 is
CC useful in immunoaffinity chromatography. The present sequence is a
CC Peptostreptococcus protein L Ig light chain binding domain, which is
CC given in the disclosure of the present invention.

XX Sequence 72 AA;

Query Match 100.0%; Score 369; DB 21; Length 72;
Best Local Similarity 100.0%; Pred. No. 9.4e-37;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEKTPPEPKKEVTIKANLIYADGKTQTAEFKGTFEATAEAYRYADLLAKENGKVTVDVA 60
DB 1 KEKTPPEPKKEVTIKANLIYADGKTQTAEFKGTFEATAEAYRYADLLAKENGKVTVDVA 60

QY 61 DKGYTLINIKFAG 72
DB 61 DKGYTLINIKFAG 72

RESULT 2

AAR42993
ID AAR42993 standard; Protein; 305 AA.

AC AAR42993;

XX 25-MAR-2003 (updated)
DT 16-MAY-1994 (first entry)

DE Immunoglobulin light chain binding protein (Protein L).

XX Immunoglobulin; light chain; binding; identification; purification;
KW separation.

XX E. coli LE392/pHDL, DSM 7054.

XX Key Location/Qualifiers
FH Domain 5..305
FT /label= B1 immunoglobulin light chain binding
FT domain.

FT Domain 81..305
FT /label= B2 immunoglobulin light chain binding
FT domain.

FT Domain 153..305
FT /label= B3 immunoglobulin light chain binding
FT domain.

FT Domain 225..305
FT /label= B4 immunoglobulin light chain binding
FT domain.

FT Domain 297..305
FT /label= B5 immunoglobulin light chain binding
FT domain.

XX WO9322342-A1.

XX 11-NOV-1993.

XX 28-APR-1993; 93WO-SE00375.

XX 28-APR-1992; 92SE-0001331.

XX (HIGH-) HIGHTECH RECEPTOR AB.

XX Bjoerck L, Sjoerbring U;

XX WPI; 1993-368722/46.
DR N-PSDB; AAQ50452.
XX New protein L binding light chains of all immunoglobulin classes
PT - for binding purifying and identifying immunoglobulin, also
PT related DNA, vectors and host cells
XX Claim 1; Page 36; 71pp; English.

XX The protein (Protein L) is capable of binding to immunoglobulin G
CC light chains. It is useful for binding, separating (purifying) and
CC identifying immunoglobulin and for removing immunoglobulin molecules
CC from serum. Hybrid proteins of the L protein can bind all human
CC immunoglobulin classes and many immunoglobulins from other species.
CC They are highly soluble and retain their binding activity at high
CC temperatures over a pH range of 3-10. They can be immobilised
CC without loss of activity.
CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 305 AA;

Query Match 100.0%; Score 369; DB 14; Length 305;
Best Local Similarity 100.0%; Pred. No. 6e-36;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEKTPPEPKKEVTIKANLIYADGKTQTAEFKGTFEATAEAYRYADLLAKENGKVTVDVA 60
DB 153 KEKTPPEPKKEVTIKANLIYADGKTQTAEFKGTFEATAEAYRYADLLAKENGKVTVDVA 212

QY 61 DKGYTLINIKFAG 72
DB 213 DKGYTLINIKFAG 224

RESULT 3

AAR42994
ID AAR42994 standard; Protein; 434 AA.

AC AAR42994;

XX 25-MAR-2003 (updated)
DT 16-MAY-1994 (first entry)

DE Sequence encoding immunoglobulin light chain binding protein.

XX Immunoglobulin; light chain; binding; identification; purification;
KW separation; ss.

XX E. coli L392/pHDLG, DSM 7055.

XX Key Location/Qualifiers
FH Domain 5..305
FT /label= B1 immunoglobulin light chain binding
FT domain.

FT Domain 81..305
FT /label= B2 immunoglobulin light chain binding
FT domain.

FT Domain 153..305
FT /label= B3 immunoglobulin light chain binding
FT domain.

FT Domain 225..305
FT /label= B4 immunoglobulin light chain binding
FT domain.

FT Domain 297..305
FT /label= B5 immunoglobulin light chain binding
FT domain.

FT Domain 309..434
FT /label= C1 immunoglobulin heavy chain binding
FT domain.

FT Domain 364..434
FT /label= D intermediate immunoglobulin heavy
FT chain binding domain.

FT Domain 379..434
FT /label= C2 immunoglobulin heavy chain binding
FT domain.
XX WO9322342-A1.
XX 11-NOV-1993.
XX 28-APR-1993; 93WO-SE00375.
XX 28-APR-1992; 92SE-0001331.
XX (HIGH-) HIGHTECH RECEPTOR AB.
XX Bjoerck L, Sjoerbring U;
XX WPI; 1993-368722/46.
XX P-PSDB; AAR42994.
XX New protein L binding light chains of all immunoglobulin classes
PT - for binding purifying and identifying immunoglobulin, also
PT related DNA, vectors and host cells
XX Claim 6; Page 39-40; 71pp; English.
XX Protein L (AAR42993) is capable of binding to immunoglobulin G light
CC chains. It is useful for binding, separating (purifying) and
CC identifying immunoglobulin and for removing immunoglobulin molecules
CC from serum. This is the coding sequence of one hybrid protein of
CC the L protein. The hybrid proteins can bind all human
CC immunoglobulin classes and many immunoglobulins from other species.
CC They are highly soluble and retain their binding activity at high
CC temperatures over a pH range of 3-10. They can be immobilised
CC without loss of activity.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 434 AA;
Query Match 100.0%; Score 369; DB 14; Length 434;
Best Local Similarity 100.0%; Pred. No. 9.4e-36;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KEKTEPEPEKEVTIKANLIYADGKTQTAEFKGTFFETAEAYRYADLLAKENGKKTVDVA 60
Db 153 KEKTEPEPEKEVTIKANLIYADGKTQTAEFKGTFFETAEAYRYADLLAKENGKKTVDVA 212
QY 61 DKGYTLNIKFPAG 72
Db 213 DKGYTLNIKFPAG 224
RESULT 4
ID AAB31372 standard; Protein; 467 AA.
XX AAB31372;
XX 20-APR-2001 (first entry)
XX Amino acid sequence of protein L/CBD cex/ER retaining peptide fusion.
XX Protein production; food processing; protein antibiotic; feed enzyme;
KW protein L: CBD cex protein; cell signal peptide.
XX Synthetic.
XX WO2000077174-A1.
XX 21-DEC-2000.
XX 07-JUN-2000; 2000WO-IL00330.
XX 10-JUN-1999; 99US-0329234.
XX

XX (CBT-) CBD TECHNOLOGIES LTD.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
XX Shani Z, Shoeyov O;
XX WPI; 2001-112219/12.
DR N-PSDB; AAF24730.
XX Expressing and isolating recombinant protein in a plant, useful for
PT producing large quantities of recombinant proteins, by expressing a
PT fusion protein including a cellulose binding peptide fused to a
PT recombinant protein
XX Example; Fig 2a; 87pp; English.
XX The specification describes a method for expressing and isolating
CC a recombinant protein in a plant. The method comprising expressing a
CC fusion protein including the recombinant protein and a cellulose
CC binding peptide fused to it, where the fusion protein is
CC compartmentalised and sequestered within plant cells, plant derived
CC tissue or cultured plant cells. The method is useful for obtaining large
CC quantities of the recombinant proteins and protein products in a simple
CC and cost-effective manner. Recombinant proteins may be used commercially,
CC such as in the food processing industry, e.g. glucoamylases and glucose
CC isomerases are used for converting starch to high fructose corn syrup,
CC pectinases for the hydrolysis of high molecular weight proteins and in
CC manufacturing leather or alcoholic beverages, pectinesterases for
CC pectin hydrolysis in food industry, lipases for cleaving ester linkage
CC in triglycerides, and for effluent treatment. The recombinant proteins
CC may further be used to produce protein antibiotics, which can be used
CC in healing processes, and to produce animal feed enzymes. The present
CC sequence represents a fusion protein of the invention, and comprises a
CC fusion of a cell signal peptide, protein L, CBD cex, and an endoplasmic
CC reticulum retaining peptide.
XX SQ Sequence 467 AA;
Query Match 97.2%; Score 358.5; DB 22; Length 467;
Best Local Similarity 98.6%; Pred. No. 1.9e-34;
Matches 72; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 KEKTEPEPEKEVTIKANLIYADGKTQTAEFKGTFFETAEAYRYADLLAKENGKKTVDV 59
Db 192 KEKTEPEPEKEVTIKANLIYADGKTQTAEFKGTFFETAEAYRYADLLAKENGKKTVDV 251
QY 60 ADGYTLNIKFPAG 72
Db 252 ADGYTLNIKFPAG 264
RESULT 5
AAY82538
ID AAY82538 standard; Protein; 72 AA.
XX AAY82538;
XX 20-JUL-2000 (first entry)
XX Peptostreptococcus strain 312 protein L domain B2 protein sequence.
XX Immunoglobulin light chain binding protein; Ppl; protein L;
KW Peptostreptococcus; human immunoglobulin kappa chain;
KW immunoaffinity chromatography.
XX Peptostreptococcus sp.
OS WO200015803-A1.
XX 23-MAR-2000.
XX 14-SEP-1999; 99WO-GR03048.
XX

PR 14-SEP-1998; 98GB-0019998.
 PR 26-APR-1999; 99GB-0009578.
 XX (ACTI-) ACTINOVA LTD.
 PI Gore MG, Beckingham JA, Roberts SE;
 XX WPI; 2000-271441/23.
 DR N-PSDB; AAA08427.
 XX New modified immunoglobulin light chain binding protein, useful in
 PT immunoaffinity chromatography, has a dissociation constant of 400 nM or
 PT more at pH8 with respect to human immunoglobulin kappa-chain -
 XX Disclosure; Page 42; 56pp; English.
 XX The present invention describes an immunoglobulin (Ig) light chain
 CC binding protein (p1) which has been modified by one or more amino acid
 CC substitutions such that the dissociation constant (Kd) of the protein
 CC with respect to human Ig kappa-chain is 400 nM or more at pH8. p1 is
 CC useful in immunoaffinity chromatography. The present sequence is a
 CC Peptostreptococcus protein L Ig light chain binding domain, which is
 CC given in the disclosure of the present invention.
 XX
 SQ Sequence 72 AA;
 Query Match 95.4%; Score 352; DB 21; Length 72;
 Best Local Similarity 94.4%; Pred. NO. 1e-34; 2; Mismatches 0; Gaps 0;
 Matches 68; Conservative 2; Indels 0; Gaps 0;
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 DB 1 KEKTEPEPKKEVTIKANLIYADGKTQTAEFKGTPEATAEAYRYADALKONGEYTVDDA 60
 QY 61 DKGTYLNIKFAG 72
 DB 61 DKGTYLNIKFAG 72
 RESULT 6
 AAB10432
 ID AAB10432 standard; Protein; 367 AA.
 XX
 AC AAB10432;
 XX
 DT 01-DEC-2000 (first entry)
 XX
 DE Expression vector pSEX1114 protein G.
 XX
 KW Expression vector; antibody binding protein; monoclonal antibody; Neo-R;
 KW B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.
 XX
 OS Synthetic.
 XX
 PN DE19900635-A1.
 XX
 PD 13-JUL-2000.
 XX
 PF 11-JAN-1999; 99DE-1000635.
 XX
 PR 11-JAN-1999; 99DE-1000635.
 XX
 PA (DEKR-) DEUT KRESSFORSCHUNGSZENTRUM.
 XX
 PI Breitling F, Poustka A, Moldenhauer G;
 XX
 DR WPI; 2000-499832/45.
 DR N-PSDB; AAA71428.
 XX
 XX Selecting monoclonal antibodies, by expressing them on the surface of
 PT hybridomas attached to antibody-binding protein, then reaction with
 PT antibody library -
 XX
 PS Disclosure; Page 44-45; 56pp; English.

PS Claim 16; Fig 1; 22pp; German.
 XX This invention describes a novel method for the selection of monoclonal
 CC antibodies (MAB) which comprises (i) fusing B lymphocytes with myeloma
 CC cells to produce antibody-producing hybridomas such that the antibodies
 CC are presented at the surface of the hybridomas by an antibody-binding
 CC protein (I); and (ii) binding the antibody to antigens (Ag). The
 CC invention also describes antibody-binding proteins (I) that comprise a
 CC combination of the signal peptide of a murine immunoglobulin (Ig) kappa
 CC chain or a murine MHC (major histocompatibility complex) Class I k(k)
 CC molecule; an antibody-binding site of proteins A, G, L or LG, and the
 CC transmembrane domain of PDGFR (platelet-derived growth factor receptor)
 CC or CD52. The method is used to select MAB with specificity for particular
 CC antigens. MAB can be selected without separate culture of hybridomas, ally
 CC and selection can be made against many antigens in a library. Optionally
 CC on the basis of strength of affinity for a particular antigen. Complex
 CC mixtures of hybridomas can be used for selection, reducing the time and
 CC cost involved in MAB selection. This sequence represents the protein G
 CC contained in the expression vector pSEX1114 which contains the protein G,
 CC Neo-R and the bla protein described in the method of the invention.
 XX
 SQ Sequence 367 AA;
 Query Match 95.4%; Score 352; DB 21; Length 367;
 Best Local Similarity 94.4%; Pred. NO. 8.3e-34;
 Matches 68; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 KEKTEPEPKKEVTIKANLIYADGKTQTAEFKGTPEATAEAYRYADLLAKENGKVTVDVA 60
 DB 25 KEKTEPEPKKEVTIKANLIYADGKTQTAEFKGTPEATAEAYRYADALKONGEYTVDDA 84
 QY 61 DKGTYLNIKFAG 72
 DB 85 DKGTYLNIKFAG 96
 RESULT 7
 AAY82540
 ID AAY82540 standard; Protein; 72 AA.
 XX
 AC AAY82540;
 XX
 DT 20-JUL-2000 (first entry)
 XX
 DE Peptostreptococcus strain 312 protein L domain B4 protein sequence.
 XX
 KW Immunoglobulin light chain binding protein; PpL; protein L;
 KW Peptostreptococcus; human immunoglobulin kappa chain;
 KW immunoaffinity chromatography.
 XX
 OS Peptostreptococcus sp.
 XX
 PN WO200015803-A1.
 XX
 PD 23-MAR-2000.
 XX
 PF 14-SEP-1999; 99WO-GB03048.
 XX
 PR 14-SEP-1998; 98GB-0019998.
 PR 26-APR-1999; 99GB-0009578.
 XX
 PA (ACTI-) ACTINOVA LTD.
 XX
 PI Gore MG, Beckingham JA, Roberts SE;
 XX
 DR WPI; 2000-271441/23.
 DR N-PSDB; AAA08429.
 XX
 XX New modified immunoglobulin light chain binding protein, useful in
 PT immunoaffinity chromatography, has a dissociation constant of 400 nM or
 PT more at pH8 with respect to human immunoglobulin kappa-chain -
 XX
 PS Disclosure; Page 44-45; 56pp; English.

XX The present invention describes an immunoglobulin (Ig) light chain
CC binding protein (P1) which has been modified by one or more amino acid
CC substitutions such that the dissociation constant (Kd) of the protein
CC with respect to human Ig kappa-chain is 400 nM or more at pH8. P1 is
CC useful in immunoaffinity chromatography. The present sequence is a
CC Peptostreptococcus protein L Ig light chain binding domain, which is
CC given in the disclosure of the present invention.

XX
SQ Sequence 72 AA;

Query Match 91.9%; Score 339; DB 21; Length 72;
Best Local Similarity 90.3%; Pred. No. 3.7e-33;
Matches 65; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 KEKTEPEPKKEVTIKANLIYADGKTQTAEFKGTFEETAEAYRYADLLAKENGKKTVDVA 60
DB 1 KEKTEPEPKKEVTIKANLIYADGKTQTAEFKGTFAETAEAYRYADLLAKENGKKTADLE 60

QY 61 DGYTLNIRFAG 72
DB 61 DGYTLNIRFAG 72

RESULT 8
AAY82544
ID AAY82544 standard; Protein; 75 AA.

XX
AC AAY82544;
XX
DT 20-JUL-2000 (first entry)
XX
DE Peptostreptococcus strain 3316 protein L domain C4 protein sequence.
XX
KW Immunoglobulin light chain binding protein; PpL; protein L;
KW Peptostreptococcus; human immunoglobulin kappa chain;
KW immunoaffinity chromatography.
XX
OS Peptostreptococcus sp.
XX
PN WO200015803-A1.
XX
PD 23-MAR-2000.
XX
PF 14-SEP-1999; 99WO-GB03048.
XX
PR 14-SEP-1998; 98GB-0019998.
PR 26-APR-1999; 99GB-0009578.
XX
PA (ACTI-) ACTINOVA LTD.
XX
PI Gore MG, Beckingham JA, Roberts SE;
XX
XX WPI; 2000-271441/23.
DR N-PSDB; AAA08433.
XX
PT New modified immunoglobulin light chain binding protein, useful in
PT immunoaffinity chromatography, has a dissociation constant of 400 nM or
PT more at pH8 with respect to human immunoglobulin kappa-chain -
XX
PS Disclosure; Page 49-50; 56pp; English.

XX The present invention describes an immunoglobulin (Ig) light chain
CC binding protein (P1) which has been modified by one or more amino acid
CC substitutions such that the dissociation constant (Kd) of the protein
CC with respect to human Ig kappa-chain is 400 nM or more at pH8. P1 is
CC useful in immunoaffinity chromatography. The present sequence is a
CC Peptostreptococcus protein L Ig light chain binding domain, which is
CC given in the disclosure of the present invention.

XX
SQ Sequence 75 AA;

Query Match 85.4%; Score 315; DB 21; Length 75;

Best Local Similarity 85.7%; Pred. No. 3e-30;
Matches 60; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 3 KTEPEPKKEVTIKANLIYADGKTQTAEFKGTFEETAEAYRYADLLAKENGKKTVDVADK 62
DB 5 ETPPEPKKEVTIKANLIYADGKTQTAEFKGTFEETAEAYRYADLLAKVNGEYTTADLEDG 64

QY 63 GYTINIRFAG 72
DB 65 GYTINIRFAG 74

RESULT 9
AAR42204
ID AAR42204 standard; Protein; 291 AA.

XX
AC AAR42204;
XX
DT 25-MAR-2003 (updated)
DT 18-MAY-1994 (first entry)
XX
DE Immunoglobulin binding protein derived from protein L.
XX
KW Peptide; immunoglobulin; binding; analysis; purification; ELISA;
KW enzyme linked immunoabsorbant assay.
XX
OS Synthetic.
XX
PN WO9322439-A1.
XX
PD 11-NOV-1993.
XX
PF 07-MAY-1993; 93WO-GB00950.
XX
PR 07-MAY-1992; 92GB-0009804.
PR 24-DEC-1992; 92GB-0026928.
XX
PA (PUBL-) PUBLIC HEALTH LAB SERVICE BOARD.
XX
PI Atkinson A, Duggleby CJ, Murphy JP, Trowern AR;
XX
DR WPI; 1993-368798/46.
DR N-PSDB; AAQ50947.
XX
PT New immunoglobulin binding proteins derived from Protein L -
PT which bind immunoglobulin kappa light chains but not albumin or
PT cell walls
XX
PS Claim 12; Figure 2; 28pp; English.

XX The synthetic immunoglobulin binding proteins derived from protein
CC L comprise repeated sequences from protein L which bind
CC immunoglobulin kappa light chains. They can be used in protein
CC analysis, purification procedures and other biochemical processes e.
CC g. ELISA. The synthetic molecules are of particular advantage if
CC they are free of regions in protein L which exhibit albumin and cell
CC wall binding.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 291 AA;

Query Match 85.4%; Score 315; DB 14; Length 291;
Best Local Similarity 85.7%; Pred. No. 1.7e-29;
Matches 60; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 3 KTEPEPKKEVTIKANLIYADGKTQTAEFKGTFEETAEAYRYADLLAKENGKKTVDVADK 62
DB 221 ETPPEPKKEVTIKANLIYADGKTQTAEFKGTFEETAEAYRYADLLAKVNGEYTTADLEDG 280

QY 63 GYTINIRFAG 72
DB 281 GYTINIRFAG 290

RESULT 10
AAR42203
ID AAR42203 standard; Protein; 1027 AA.
XX AC AAR42203;
XX AC AAR42203;
XX 25-MAR-2003 (updated)
DT 18-MAY-1994 (first entry)
XX DE Protein L.
XX KW Peptide; immunoglobulin; binding; analysis; purification; ELISA;
KW enzyme linked immunoabsorbant assay.
XX OS Peptococcus magnus.
XX FH Key Location/Qualifiers
FT Peptide 36..59
FT /label= Signal sequence.
FT Protein 60..968
FT /label= Mature protein L.
XX PN WO9322439-A1.
XX 11-NOV-1993.
XX PF 07-MAY-1993; 93WO-GB00950.
XX PR 07-MAY-1992; 92GB-0009804.
XX PR 24-DEC-1992; 92GB-0026928.
XX PA (PUBL-) PUBLIC HEALTH LAB SERVICE BOARD.
XX PI Atkinson A, Duggleby CJ, Murphy JP, Trowern AR;
XX WPI; 1993-368798/46.
XX DR N-PSDB; AAQ05946.
XX PT New immunoglobulin binding proteins derived from Protein L -
FT which bind immunoglobulin kappa light chains but not albumin or
FT cell walls
XX PS Disclosure; Figure 1; 28pp; English.
XX CC The synthetic immunoglobulin binding proteins derived from protein
CC L correspond to the repeated sequences in protein L which bind
CC immunoglobulin kappa light chains. They can be used in protein
CC analysis, purification procedures and other biochemical processes e.
CC g. ELISA. The synthetic molecules are of particular advantage if
CC they are free of regions in protein L which exhibit albumin and cell
CC wall binding.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 1027 AA;
Query Match 85.4%; Score 315; DB 14; Length 1027;
Best Local Similarity 85.7%; Pred. No. 8.6e-29;
Matches 60; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
OY 3 KTEPEPKKEVTIKANLIYADGKTQTAEFKGTFEETAEAYRYADLLAKENGKYYTDVADK 62
DB 503 ETPEPKKEVTIKVNLIFADGKTQTAEFKGTFEETAEAYRYADLLAKVNGEYTDLEDG 562
OY 63 GYTINIKPAG 72
DB 563 GYTINIKPAG 572
RESULT 11
AAR43699
ID AAR43699 standard; Protein; 1027 AA.
XX

AC AAR43699;
XX 25-MAR-2003 (updated)
DT 18-MAY-1994 (first entry)
XX DE Protein L.
XX KW Protein; immunoglobulin; binding; immobilisation; light chains;
KW antibodies; diagnosis; pharmaceutical; ss.
XX OS Peptococcus magnus.
XX FH Key Location/Qualifiers
FT Peptide 36..59
FT /label= Signal sequence.
FT Protein 60..968
FT /label= Mature protein L.
XX PN WO9322438-A1.
XX 11-NOV-1993.
XX PF 07-MAY-1993; 93WO-GB00949.
XX PR 07-MAY-1992; 92GB-0009804.
XX PA (PUBL-) PUBLIC HEALTH LAB SERVICE BOARD.
XX PI Atkinson A, Duggleby CJ, Murphy JP, Trowern AR;
XX WPI; 1993-368797/46.
XX DR P-PSDB; AAR43699.
XX PT Immunoglobulin binding polypeptide, protein L - used for prodn.
FT of pharmaceuticals and for immobilising antibodies e.g. on
FT columns, in diagnostic tests and in assays
XX PS Claim 4; Figure 1; 29pp; English.
XX CC Protein L forms a complex with immunoglobulin kappa light chain.
CC Purified protein can be used as a reagent for immobilising
CC antibodies e.g. on columns, in diagnostic tests and in assays. It
CC may also be used in the production of pharmaceuticals.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 1027 AA;
Query Match 85.4%; Score 315; DB 14; Length 1027;
Best Local Similarity 85.7%; Pred. No. 8.6e-29;
Matches 60; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
OY 3 KTEPEPKKEVTIKANLIYADGKTQTAEFKGTFEETAEAYRYADLLAKENGKYYTDVADK 62
DB 503 ETPEPKKEVTIKVNLIFADGKTQTAEFKGTFEETAEAYRYADLLAKVNGEYTDLEDG 562
OY 63 GYTINIKPAG 72
DB 563 GYTINIKPAG 572
RESULT 12
AAR82542
ID AAR82542 standard; Protein; 71 AA.
XX AC AAR82542;
XX 20-JUL-2000 (first entry)
XX DE Peptostreptococcus strain 3316 protein L domain C2 protein sequence.
XX KW Immunoglobulin light chain binding protein; PpL; protein L;
KW Peptostreptococcus; human immunoglobulin kappa chain;
KW immunoaffinity chromatography.

XX OS Peptostreptococcus sp.
XX PN WO200015803-A1.
XX XX
XX PD 23-MAR-2000.
XX PF 14-SEP-1999; 99WO-GB03048.
XX PR 14-SEP-1998; 98GB-0019998.
XX PR 26-APR-1999; 99GB-0009578.
XX PA (ACTI-) ACTINOVA LTD.
XX PI Gore MG, Beckingham JA, Roberts SE;
XX DR WPI; 2000-271441/23.
XX DR N-PSDB; AAA08542.
XX PT New modified immunoglobulin light chain binding protein, useful in
PT immunoaffinity chromatography, has a dissociation constant of 400 nM or
PT more at pH8 with respect to human immunoglobulin kappa-chain -
XX PS Disclosure; Page 47; 56pp; English.
XX CC The present invention describes an immunoglobulin (Ig) light chain
CC binding protein (pI) which has been modified by one or more amino acid
CC substitutions such that the dissociation constant (Kd) of the protein
CC with respect to human Ig kappa-chain is 400 nM or more at pH8. pI is
CC useful in immunoaffinity chromatography. The present sequence is a
CC Peptostreptococcus protein L, Ig light chain binding domain, which is
CC given in the disclosure of the present invention.
XX SQ Sequence 71 AA;
Query Match 81.7%; Score 301.5; DB 21; Length 71;
Best Local Similarity 83.3%; Pred. No. 1.2e-28;
Matches 60; Conservative 5; Mismatches 6; Indels 1; Gaps 1;
QY 1 KEKTPPEEPKEEVTIKANLIYADGKTQTAEFKGTFFETAEAYRYADLLAKENGKVTVDVA 60
DB 1 KEK-PEEPKEEVTIKANLIYADGKTQTAEFKGTFFETAEAYRYADLLAKENGKVTVDVA 59
QY 61 DGNTINIKFAG 72
DB 60 DGNTINIKFAG 71
RESULT 13
ID AAY82537
AC AAY82537;
XX 20-JUL-2000 (first entry)
DE Peptostreptococcus strain 312 protein L domain B1 protein sequence.
XX Immunoglobulin light chain binding protein; PpL; protein L;
KW Peptostreptococcus; human immunoglobulin kappa chain;
KW immunoaffinity chromatography.
XX OS Peptostreptococcus sp.
XX PN WO200015803-A1.
XX PD 23-MAR-2000.
XX PF 14-SEP-1999; 99WO-GB03048.
XX PR 14-SEP-1998; 98GB-0019998.
XX PR 26-APR-1999; 99GB-0009578.

PA (ACTI-) ACTINOVA LTD.
XX Gore MG, Beckingham JA, Roberts SE;
XX DR WPI; 2000-271441/23.
XX DR N-PSDB; AAA08426.
XX PT New modified immunoglobulin light chain binding protein, useful in
PT immunoaffinity chromatography, has a dissociation constant of 400 nM or
PT more at pH8 with respect to human immunoglobulin kappa-chain -
XX PS Disclosure; Page 40-41; 56pp; English.
XX CC The present invention describes an immunoglobulin (Ig) light chain
CC binding protein (pI) which has been modified by one or more amino acid
CC substitutions such that the dissociation constant (Kd) of the protein
CC with respect to human Ig kappa-chain is 400 nM or more at pH8. pI is
CC useful in immunoaffinity chromatography. The present sequence is a
CC Peptostreptococcus protein L, Ig light chain binding domain, which is
CC given in the disclosure of the present invention.
XX SQ Sequence 76 AA;
Query Match 81.0%; Score 299; DB 21; Length 76;
Best Local Similarity 77.6%; Pred. No. 2.5e-28;
Matches 59; Conservative 8; Mismatches 5; Indels 4; Gaps 1;
QY 1 KEKTPPEEP---KEEVTIKANLIYADGKTQTAEFKGTFFETAEAYRYADLLAKENGKVT 56
DB 1 KEETPETETSEEEVTIKANLIYADGKTQTAEFKGTFFETAEAYRYADLLAKENGKVT 60
QY 57 VDVAADKGYTLNFKFAG 72
DB 61 VDVAADKGYTLNFKFAG 76
RESULT 14
ID AAY82536
AC AAY82536;
XX 20-JUL-2000 (first entry)
DE Ig light chain binding protein PpL construct protein SEQ ID NO:2.
XX Immunoglobulin light chain binding protein; PpL; protein L;
KW Peptostreptococcus; human immunoglobulin kappa chain;
KW immunoaffinity chromatography.
XX OS Peptostreptococcus sp.
XX PN WO200015803-A1.
XX PD 23-MAR-2000.
XX PF 14-SEP-1999; 99WO-GB03048.
XX PR 14-SEP-1998; 98GB-0019998.
XX PR 26-APR-1999; 99GB-0009578.
XX PA (ACTI-) ACTINOVA LTD.
XX PI Gore MG, Beckingham JA, Roberts SE;
XX DR WPI; 2000-271441/23.
XX DR N-PSDB; AAA08425.
XX PT New modified immunoglobulin light chain binding protein, useful in
PT immunoaffinity chromatography, has a dissociation constant of 400 nM or
PT more at pH8 with respect to human immunoglobulin kappa-chain -
XX PS Claim 1; Page 39; 56pp; English.

XX The present invention describes an immunoglobulin (Ig) light chain
CC binding protein (P1) which has been modified by one or more amino acid
CC substitutions such that the dissociation constant (Kd) of the protein
CC with respect to human Ig kappa-chain is 400 nM or more at pH8. P1 is
CC useful in immunoaffinity chromatography. The present sequence
CC represents an Ig light chain binding PpL construct derived from
CC Peptostreptococcus sp. protein L.
XX
SQ Sequence 82 AA;

Query Match 79.4%; Score 293; DB 21; Length 82;
Best Local Similarity 81.4%; Pred. No. 1.5e-27;
Matches 57; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 3 KTPPEPKKEEVTIKANLIYADGKTOTAEFKGTFEETAEAYRYADLLAKENGKYYTDVADK 62
DB 12 ETPPEPKKEEVTIKVNLIFADGKIQTAEFKGTFEETAEAYRYADLLAKVNGEYTTADLDG 71
QY 63 GYTLNLIKFPAG 72
DB 72 GNHMIKFPAG 81

RESULT 15
AAV82543
ID AAV82543 standard; Protein; 74 AA.
XX
AC AAV82543;
XX
DT 20-JUL-2000 (first entry)
XX
DE Peptostreptococcus strain 3316 protein L domain C3 protein sequence.
XX
KW Immunoglobulin light chain binding protein; PpL; protein L;
KW Peptostreptococcus; human immunoglobulin kappa chain;
KW immunoaffinity chromatography.
XX
OS Peptostreptococcus sp.
XX
PN WO200015803-A1.
XX
PD 23-MAR-2000.
XX
PF 14-SEP-1999; 99WO-GB03048.
XX
PR 14-SEP-1998; 98GB-0019998.
XX
PR 26-APR-1999; 99GB-0009578.
XX
PA (ACTI-) ACTINOVIA LTD.
XX
PI Gore MG, Beckingham JA, Roberts SE;
XX
DR WPI; 2000-271441/23.
DR N-PSDB; AAA08543.
XX
PT New modified immunoglobulin light chain binding protein, useful in
PT immunoaffinity chromatography, has a dissociation constant of 400 nM or
PT more at pH8 with respect to human immunoglobulin kappa-chain -
XX
PS Disclosure; Page 48; 56pp; English.
XX
CC The present invention describes an immunoglobulin (Ig) light chain
CC binding protein (P1) which has been modified by one or more amino acid
CC substitutions such that the dissociation constant (Kd) of the protein
CC with respect to human Ig kappa-chain is 400 nM or more at pH8. P1 is
CC useful in immunoaffinity chromatography. The present sequence is a
CC Peptostreptococcus protein L Ig light chain binding domain, which is
CC given in the disclosure of the present invention.
XX
SQ Sequence 74 AA;

Best Local Similarity 80.0%; Pred. No. 1.7e-27;
Matches 56; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 3 KTPPEPKKEEVTIKANLIYADGKTOTAEFKGTFEETAEAYRYADLLAKENGKYYTDVADK 62
DB 5 ETPPEPKKEEVTIKVNLIFADGKIQTAEFKGTFEETAKAYANLLAKENGGEYTTADLDG 64
QY 63 GYTLNLIKFPAG 72
DB 65 GNTINIKFPAG 74

Search completed: September 3, 2003, 11:19:18
Job time : 48.3288 secs

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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:16:02 ; Search time 15.7808 Seconds
(without alignments)
193.043 Million cell updates/sec

Title: US-08-325-278b-1_copy_153_224

Perfect score: 369

Sequence: 1 KEKTPPEKPEVTKANLIY.....GKYTVADVADKGYTLNIFAG 72

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA.*
- 1: /cgm2_6/ptodata/1/iaa/5A_COMB.pap.*
- 2: /cgm2_6/ptodata/1/iaa/5B_COMB.pap.*
- 3: /cgm2_6/ptodata/1/iaa/6A_COMB.pap.*
- 4: /cgm2_6/ptodata/1/iaa/6B_COMB.pap.*
- 5: /cgm2_6/ptodata/1/iaa/PTCUS_COMB.pap.*
- 6: /cgm2_6/ptodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	369	100.0	305	2	US-08-795-475-1
2	369	100.0	434	2	US-08-795-475-3
3	315	85.4	75	3	US-08-446-137B-8
4	315	85.4	291	3	US-08-446-137B-4
5	315	85.4	1027	3	US-08-446-137B-2
6	301.5	81.7	71	3	US-08-446-137B-6
7	292	79.1	74	3	US-08-446-137B-7
8	284	77.0	182	3	US-08-828-741B-2
9	284	77.0	182	4	US-09-160-567-2
10	284	77.0	182	4	US-09-710-299-2
11	276	74.8	178	3	US-08-828-741B-13
12	276	74.8	178	4	US-09-160-567-13
13	276	74.8	178	4	US-09-710-299-13
14	276	74.8	198	3	US-08-828-741B-8
15	276	74.8	198	4	US-09-160-567-8
16	276	74.8	198	4	US-09-710-299-8
17	276	74.8	342	3	US-08-828-741B-6
18	276	74.8	342	4	US-09-160-567-6
19	276	74.8	342	4	US-09-710-299-6
20	276	74.8	495	3	US-08-828-741B-4
21	276	74.8	495	4	US-09-160-567-4
22	276	74.8	495	4	US-09-710-299-4
23	269.5	73.0	71	3	US-08-446-137B-5
24	67	18.2	490	4	US-09-252-149B-26
25	67	18.2	544	1	US-08-387-156-10
26	67	18.2	544	2	US-08-694-865-10
27	67	18.2	544	2	US-08-878-748-10

28	67	18.2	544	3	US-09-124-491-10	Sequence 10, Appl
29	67	18.2	544	4	US-09-383-912-10	Sequence 10, Appl
30	67	18.2	699	2	US-08-694-865-16	Sequence 16, Appl
31	67	18.2	699	3	US-09-124-491-16	Sequence 16, Appl
32	67	18.2	699	4	US-09-383-912-16	Sequence 16, Appl
33	67	18.2	924	3	US-08-619-812-8	Sequence 8, Appl
34	67	18.2	926	1	US-07-908-253-2	Sequence 2, Appl
35	67	18.2	926	1	US-08-455-970A-2	Sequence 2, Appl
36	67	18.2	926	1	US-08-387-156-6	Sequence 6, Appl
37	67	18.2	926	2	US-08-694-865-6	Sequence 6, Appl
38	67	18.2	926	2	US-08-878-748-6	Sequence 6, Appl
39	67	18.2	926	2	US-08-535-837-2	Sequence 2, Appl
40	67	18.2	926	3	US-09-124-491-6	Sequence 6, Appl
41	67	18.2	926	4	US-09-383-912-6	Sequence 6, Appl
42	67	18.2	926	6	5476657-3	Patent No. 5476657
43	67	18.2	936	1	US-08-455-970A-12	Sequence 12, Appl
44	67	18.2	943	1	US-08-455-970A-10	Sequence 10, Appl
45	67	18.2	951	1	US-08-455-970A-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-08-795-475-1
; Sequence 1, Application US/08795475
; Patent No. 5965390
; GENERAL INFORMATION:
; APPLICANT: Bivvick, Lars
; APPLICANT: Sjvbrink, Ulf
; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,475
; FILING DATE: 11-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/POCKET NUMBER: 100084.402D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 305 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli LE392/pHDL, DSM 7054
US-08-795-475-1

Query Match 100.0%; Score 369; DB 2; Length 305;
Best Local Similarity 100.0%; Pred. No. 4.6e-39;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEKTPPEKPEVTKANLIYADGKTQTAEFKGTTEATAEAYRYADLAKENGKTYDVA 60
|||||

Db 153 KETPEEPKEVITKANLIYADGKTQTAEFKGTFFETAEAYRYADLLAKENGKTYDVDA 212

QY 61 DKGYTLNLIKFG 72

Db 213 DKGYTLNLIKFG 224

RESULT 2

US-08-795-475-3

Sequence 3, Application US/08795475

Patent No. 5965390

GENERAL INFORMATION:

APPLICANT: Bjvick, Lars

APPLICANT: Sivbring, Ulf

TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/795,475

FILING DATE: 11-FEB-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: McMasters, David D.

REGISTRATION NUMBER: 33,963

REFERENCE/DOCKET NUMBER: 100084.402D1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 434 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: Escherichia coli LE392/pHDLG, DSM 7055

US-08-795-475-3

Query Match 100.0%; Score 369; DB 2; Length 434;

Best Local Similarity 100.0%; Pred. No. 7.4e-39;

Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KETPEEPKEVITKANLIYADGKTQTAEFKGTFFETAEAYRYADLLAKENGKTYDVDA 60

Db 153 KETPEEPKEVITKANLIYADGKTQTAEFKGTFFETAEAYRYADLLAKENGKTYDVDA 212

QY 61 DKGYTLNLIKFG 72

Db 213 DKGYTLNLIKFG 224

RESULT 3

US-08-446-137B-8

Sequence 8, Application US/08446137B

Patent No. 6162903

GENERAL INFORMATION:

APPLICANT: Trowern, Angus R.

APPLICANT: Atkinson, Anthony

APPLICANT: Murphy, Jonathan P.

APPLICANT: Laurence, Oliver S.

APPLICANT: Duggleby, Clive J.

TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEINS DERIVED

TITLE OF INVENTION: FROM L PROTEIN AND THEIR USES

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/446,137B

FILING DATE: 22-MAY-1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: McMasters, David D.

REGISTRATION NUMBER: 33,963

REFERENCE/DOCKET NUMBER: 100084.406

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 75 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-08-446-137B-8

Query Match 85.4%; Score 315; DB 3; Length 75;

Best Local Similarity 85.7%; Pred. No. 5.4e-33;

Matches 60; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 3 KTPPEPKEVITKANLIYADGKTQTAEFKGTFFETAEAYRYADLLAKENGKTYDVADK 62

Db 5 ETPEEPKEVITKYNLIFADGKTQTAEFKGTFFETAEAYRYADLLAKVNGEYTDLEDG 64

QY 63 GYTLNLIKFG 72

Db 65 GYTLNLIKFG 74

RESULT 4

US-08-446-137B-4

Sequence 4, Application US/08446137B

Patent No. 6162903

GENERAL INFORMATION:

APPLICANT: Trowern, Angus R.

APPLICANT: Atkinson, Anthony

APPLICANT: Murphy, Jonathan P.

APPLICANT: Laurence, Oliver S.

APPLICANT: Duggleby, Clive J.

TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEINS DERIVED

TITLE OF INVENTION: FROM L PROTEIN AND THEIR USES

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/446,137B
;; FILING DATE: 22-MAY-1995
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mcmasters, David D.
;; REGISTRATION NUMBER: 33,963
;; REFERENCE/DOCKET NUMBER: 100084.406
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206) 622-4900
;; TELEFAX: (206) 682-6031
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 291 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-446-137B-4

Query Match 85.4%; Score 315; DB 3; Length 291;
Best Local Similarity 85.7%; Pred. No. 3.3e-32;
Matches 60; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 3 KTPPEPKKEVTKANLIYADGKTQTAEFGKTFEEATAYRYADLLAKENGKYYTDVADK 62
Db 221 ETPPEPKKEVTKVNLIFADGKTQTAEFGKTFEEATAYRYADLLAKENGKYYTDLEDG 280

QY 63 GYTLNPKFAG 72
Db 281 GYTLNPKFAG 290

RESULT 5
US-08-446-137B-2
; Sequence 2, Application US/08446137B
; Patent No. 6152903
; GENERAL INFORMATION:
; APPLICANT: Trowern, Angus R.
; APPLICANT: Atkinson, Anthony
; APPLICANT: Murphy, Jonathan P.
; APPLICANT: Laurence, Oliver S.
; APPLICANT: Duggleby, Clive J.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEINS DERIVED
; FROM L PROTEIN AND THEIR USES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,137B
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 100084.406
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 291 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

;; MOLECULE TYPE: protein
US-08-446-137B-2

Query Match 85.4%; Score 315; DB 3; Length 1027;
Best Local Similarity 85.7%; Pred. No. 1.8e-31;
Matches 60; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 3 KTPPEPKKEVTKANLIYADGKTQTAEFGKTFEEATAYRYADLLAKENGKYYTDVADK 62
Db 503 ETPPEPKKEVTKVNLIFADGKTQTAEFGKTFEEATAYRYADLLAKENGKYYTDLEDG 562

QY 63 GYTLNPKFAG 72
Db 563 GYTLNPKFAG 572

RESULT 6
US-08-446-137B-6
; Sequence 6, Application US/08446137B
; Patent No. 6162903
; GENERAL INFORMATION:
; APPLICANT: Trowern, Angus R.
; APPLICANT: Atkinson, Anthony
; APPLICANT: Murphy, Jonathan P.
; APPLICANT: Laurence, Oliver S.
; APPLICANT: Duggleby, Clive J.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEINS DERIVED
; FROM L PROTEIN AND THEIR USES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,137B
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 100084.406
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 71 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-446-137B-6

Query Match 81.7%; Score 301.5; DB 3; Length 71;
Best Local Similarity 83.3%; Pred. No. 2.6e-31;
Matches 60; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 1 KEKTPPEPKKEVTKANLIYADGKTQTAEFGKTFEEATAYRYADLLAKENGKYYTDVA 60
Db 1 KEK-PEEPKEEVTKVNLIFADGKTQTAEFGKTFEEATAYRYADLLAKENGKYYTDVA 59

QY 61 DKGYTLNPKFAG 72
Db 60 DGGNTINIKFAG 71

RESULT 7
US-08-446-137B-7
; Sequence 7, Application US/08446137B
; Patent No. 6162903
; GENERAL INFORMATION:
; APPLICANT: Trowern, Angus R.
; APPLICANT: Atkinson, Anthony
; APPLICANT: Murphy, Jonathan P.
; APPLICANT: Laurence, Oliver S.
; APPLICANT: Duggleby, Clive J.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEINS DERIVED
; FROM L PROTEIN AND THEIR USES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSER: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,137B
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 100084.406
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 74 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-446-137B-7

Query Match 79.1%; Score 292; DB 3; Length 74;
Best Local Similarity 80.0%; Pred. No. 4.5e-30;
Matches 56; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
QY 3 KTEPEPKKEVTIKANLIYADGKTQTAEFGKTFEEATAEAYRYADLLAKENGKYYTVDVADK 62
Db 5 ETPEPKKEVTIKVNLIFADGKIQTAEFGKTFEEATAKAYANLLAKENGKYYTADLEDG 64
QY 63 GYTLNLIKFGAG 72
Db 65 GNTINIKFAG 74

RESULT 8
US-08-828-741B-2
; Sequence 2, Application US/08928741B
; Patent No. 6043069
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Sues, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
; PRODUCTION
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSER: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City

STATE: New York
COUNTRY: United States of America
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,741B
FILING DATE: 26-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 182 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-828-741B-2
Query Match 77.0%; Score 284; DB 3; Length 182;
Best Local Similarity 76.1%; Pred. No. 1.6e-28;
Matches 54; Conservative 9; Mismatches 8; Indels 0; Gaps 0;
QY 2 EKTPEPKKEVTIKANLIYADGKTQTAEFGKTFEEATAEAYRYADLLAKENGKYYTVDVAD 61
Db 20 QAAKPDNTEVTIKANLIFANGSTQTAEFGKTFEEATSEAYAYADTLKDNNGEYITVDVAD 79
QY 62 KGYTLNLIKFGAG 72
Db 80 KGYTLNLIKFGAG 90
RESULT 9
US-09-160-567-2
; Sequence 2, Application US/09160567
; Patent No. 6326179
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Sues, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
; PRODUCTION
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSER: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,567
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,741
FILING DATE:
ATTORNEY/AGENT INFORMATION:

```

; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-710-299-2

Query Match          77.0%; Score 284; DB 4; Length 182;
Best Local Similarity 76.1%; Pred. No. 1.6e-28;
Matches 54; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY      2 EKTPEPKSEVITKANLIYADGKQTQAEPKGTPEATAEAYRYADLLAKENGKYTVDVAD 61
DB      :|::|||:|||::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
        20 QAAKPONTEEVITKANLIFANGSTQTAEPKGTPEKATSEAYAVADTLKKONGEYTVDVAD 79
QY      62 KGYTLNIKEAG 72
DB      |||:|||:|||
        80 KGYTLNIKEAG 90

RESULT 11
US-08-828-741B-13
; Sequence 13, Application US/08828741B
; Patent No. 6043069
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlington, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
; TITLE OF INVENTION: PRODUCING SAME
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLI, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,741B
; FILING DATE: 26-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10591
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-828-741B-13

Query Match          74.8%; Score 276; DB 3; Length 178;
Best Local Similarity 84.1%; Pred. No. 1.6e-27;
Matches 53; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY      10 EVVTIKANLIYADGKQTQAEPKGTPEATAEAYRYADLLAKENGKYTVDVADKGTYLNLIK 69
DB      |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
        12 EVVTIKANLIFANGSTQTAEPKGTPEKATSEAYAVADTLKKONGEYTVDVADKGTYLNLIK 71
QY      70 FAG 72
DB      |||
        72 FAG 74

```

RESULT 12
 US-09-160-567-13
 ; Sequence 13, Application US/09160567
 ; Patent No. 6326179
 ; GENERAL INFORMATION:
 ; APPLICANT: Koentgen, Frank
 ; APPLICANT: Suess, Gabriele M.
 ; APPLICANT: Tarlinton, David M.
 ; APPLICANT: Treutlein, Herbert R.
 ; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
 ; TITLE OF INVENTION: PRODUCING SAME
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: New York
 ; COUNTRY: United States of America
 ; ZIP: 11530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/160,567
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/828,741
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Digiglio, Frank S.
 ; REGISTRATION NUMBER: 31,346
 ; REFERENCE/DOCKET NUMBER: 10591
 ; TELEPHONE: (516) 742-4343
 ; TELEFAX: (516) 742-4366
 ; TELEX: 230 901 SANS UR
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 178 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-160-567-13

Query Match 74.8%; Score 276; DB 4; Length 178;
 Best Local Similarity 84.1%; Pred. No. 1.6e-27;
 Matches 53; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
 QY 10 EEVTKANLIYADGKTQTAEFGTPEATAEAYRYADLLAKENGKYYTVDVADKGYTLNIK 69
 Db 12 EEVTKANLIYADGKTQTAEFGTPEATAEAYRYADLLAKENGKYYTVDVADKGYTLNIK 71
 QY 70 FAG 72
 Db 72 FAG 74

RESULT 13
 US-09-710-299-13
 ; Sequence 13, Application US/09710299
 ; Patent No. 6521741
 ; GENERAL INFORMATION:
 ; APPLICANT: Koentgen, Frank
 ; APPLICANT: Suess, Gabriele M.
 ; APPLICANT: Tarlinton, David M.
 ; APPLICANT: Treutlein, Herbert R.
 ; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
 ; TITLE OF INVENTION: PRODUCING SAME
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
 STREET: 400 Garden City Plaza
 CITY: Garden City
 STATE: New York
 COUNTRY: United States of America
 ZIP: 11530
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/710,299
 FILING DATE: 09-NO. 6521741-2000
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/828,741
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Digiglio, Frank S.
 REGISTRATION NUMBER: 31,346
 REFERENCE/DOCKET NUMBER: 10591
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (516) 742-4343
 TELEFAX: (516) 742-4366
 TELEX: 230 901 SANS UR
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 178 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 13:
 US-09-710-299-13
 Query Match 74.8%; Score 276; DB 4; Length 178;
 Best Local Similarity 84.1%; Pred. No. 1.6e-27;
 Matches 53; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
 QY 10 EEVTKANLIYADGKTQTAEFGTPEATAEAYRYADLLAKENGKYYTVDVADKGYTLNIK 69
 Db 12 EEVTKANLIYADGKTQTAEFGTPEATAEAYRYADLLAKENGKYYTVDVADKGYTLNIK 71
 QY 70 FAG 72
 Db 72 FAG 74
 RESULT 14
 US-08-828-741B-8
 ; Sequence 8, Application US/08828741B
 ; Patent No. 6043069
 ; GENERAL INFORMATION:
 ; APPLICANT: Koentgen, Frank
 ; APPLICANT: Suess, Gabriele M.
 ; APPLICANT: Tarlinton, David M.
 ; APPLICANT: Treutlein, Herbert R.
 ; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
 ; TITLE OF INVENTION: PRODUCING SAME
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: New York
 ; COUNTRY: United States of America
 ; ZIP: 11530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/828,741B
FILING DATE: 26-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 198 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-828-741B-8

Query Match 74.8%; Score 276; DB 3; Length 198;
Best Local Similarity 84.1%; Pred. No. 1.9e-27;
Matches 53; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 10 EVTIKANLIYADGKTOTAEKGTPEEATAEAYRYADLLAKENGYTVDVADKGYTLNIK 69
DB 32 EVTIKANLIYADGKTOTAEKGTPEEATAEAYRYADLLAKENGYTVDVADKGYTLNIK 91
QY 70 FAG 72
DB 92 FAG 94

RESULT 15
US-09-160-567-8
Sequence 8, Application US/09160567
Patent No. 6326179
GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
APPLICANT: Suesse, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
TITLE OF INVENTION: PRODUCING SAME
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSER: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,567
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,741
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:

LENGTH: 198 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-160-567-8
Query Match 74.8%; Score 276; DB 4; Length 198;
Best Local Similarity 84.1%; Pred. No. 1.9e-27;
Matches 53; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
QY 10 EVTIKANLIYADGKTOTAEKGTPEEATAEAYRYADLLAKENGYTVDVADKGYTLNIK 69
DB 32 EVTIKANLIYADGKTOTAEKGTPEEATAEAYRYADLLAKENGYTVDVADKGYTLNIK 91
QY 70 FAG 72
DB 92 FAG 94

Search completed: September 3, 2003, 11:25:36
Job time : 15.7808 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:23:22 ; Search time 26.6301 Seconds
(without alignments)
371.228 Million cell updates/sec

Title: US-08-325-278b-1_COPY_153_224

Perfect score: 369

Sequence: 1 KEKTEPEKPEVTTKANLIY.....GKYTVADVADKGYTLNIKFAAG 72

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513375 seqs, 137303645 residues

Total number of hits satisfying chosen parameters: 513375

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/ECT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/ECTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	369	100.0	72	10	US-09-808-212A-8
2	369	100.0	305	8	US-08-325-278-1
3	369	100.0	434	8	US-08-325-278-3
4	352	95.4	72	10	US-09-808-212A-6
5	339	91.9	72	10	US-09-808-212A-10
6	315	85.4	75	10	US-09-808-212A-18
7	301.5	81.7	71	10	US-09-808-212A-14
8	299	81.0	76	10	US-09-808-212A-4
9	293	79.4	82	10	US-09-808-212A-2
10	292	79.1	74	10	US-09-808-212A-16
11	284	77.0	182	12	US-10-345-618-2
12	276	74.8	178	12	US-10-345-618-13
13	276	74.8	198	12	US-10-345-618-8
14	276	74.8	342	12	US-10-345-618-6
15	276	74.8	482	12	US-10-345-618-16

16	276	74.8	495	12	US-10-345-618-4	Sequence 4, Appli
17	270.5	73.3	71	10	US-09-808-212A-12	Sequence 12, Appli
18	67	18.2	695	11	US-09-305-924-13	Sequence 13, Appli
19	67	18.2	953	11	US-09-884-696-3	Sequence 3, Appli
20	66	17.9	448	12	US-10-342-224-82	Sequence 82, Appli
21	66	17.9	1098	10	US-09-797-862-32	Sequence 32, Appli
22	65.5	17.8	271	15	US-10-138-505-30	Sequence 30, Appli
23	65.5	17.8	274	15	US-10-138-505-26	Sequence 26, Appli
24	65.5	17.8	836	10	US-09-858-525A-10	Sequence 10, Appli
25	65.5	17.8	871	10	US-09-858-525A-2	Sequence 2, Appli
26	63.5	17.2	279	14	US-10-059-964-60	Sequence 60, Appli
27	63.5	17.2	279	15	US-10-314-639-60	Sequence 60, Appli
28	63.5	17.2	414	9	US-09-039-927A-4	Sequence 4, Appli
29	63.5	17.2	1588	12	US-10-154-419-37	Sequence 37, Appli
30	63.5	17.2	1588	14	US-10-002-769-5	Sequence 5, Appli
31	63	17.1	284	11	US-09-056-019-3	Sequence 3, Appli
32	63	17.1	406	11	US-09-056-019-1	Sequence 1, Appli
33	63	17.1	428	11	US-09-056-019-24	Sequence 24, Appli
34	63	17.1	435	15	US-10-156-761-11066	Sequence 11066, A
35	63	17.1	446	12	US-10-254-395-9	Sequence 9, Appli
36	63	17.1	451	11	US-09-298-523B-67	Sequence 67, Appli
37	63	17.1	460	11	US-09-056-019-38	Sequence 38, Appli
38	63	17.1	511	11	US-09-298-523B-13	Sequence 13, Appli
39	63	17.1	513	11	US-09-298-523B-12	Sequence 12, Appli
40	63	17.1	655	11	US-09-056-019-2	Sequence 2, Appli
41	63	17.1	693	11	US-09-769-787-185	Sequence 185, App
42	61.5	16.7	136	15	US-10-138-505-8	Sequence 8, Appli
43	61.5	16.7	1179	15	US-10-156-761-13670	Sequence 13670, A
44	61	16.5	187	9	US-09-815-242-10591	Sequence 10591, A
45	61	16.5	841	9	US-09-815-242-5779	Sequence 5779, Ap

ALIGNMENTS

RESULT 1
US-09-808-212A-8
; Sequence 8, Application US/09808212A
; Patent No. US20020137918A1
; GENERAL INFORMATION:
; APPLICANT: Gore, Michael Graham
; APPLICANT: Beckingham, Jennifer Ann
; APPLICANT: Roberts, Sian Eleri
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN
; FILE REFERENCE: 100084.414US
; CURRENT APPLICATION NUMBER: US/09/808,212A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Peptostreptococcus sp.
US-09-808-212A-8

Query Match	100.0%	Score 369;	DB 10;	Length 72;
Best Local Similarity	100.0%	Pred. No. 1.6e-35;		
Matches	72;	Conservative	0;	Mismatches 0;
		Indels	0;	Gaps 0;
QY	1	KEKTEPEKPEVTTKANLIYADGKTQTAEFKGTFTTEATAEAYRYADILAKENGKTYDVA	60	
Db	1	KEKTEPEKPEVTTKANLIYADGKTQTAEFKGTFTTEATAEAYRYADILAKENGKTYDVA	60	
QY	61	DKGYTLNIKFAAG	72	
Db	61	DKGYTLNIKFAAG	72	
RESULT 2				
US-08-325-278-1				
; Sequence 1, Application US/08325278				
; Publication No. US20030027283A1				
; GENERAL INFORMATION:				

APPLICANT: Bjvrck, Lars
APPLICANT: Sjvbring, Ulf
TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,278
FILING DATE: 26-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCES/DOCKET NUMBER: 450023.401
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 305 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Escherichia coli LE392/pHDL, DSM 7054
US-08-325-278-1

Query Match 100.0%; Score 369; DB 8; Length 305;
Best Local Similarity 100.0%; Pred. No. 1e-34;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KEKTPPEPKKEVTIKANLIYADGKTQTAEFKGTPEEATAEAYRYADLLAKENGKKTVDVA 60
Db 153 KEKTPPEPKKEVTIKANLIYADGKTQTAEFKGTPEEATAEAYRYADLLAKENGKKTVDVA 212
QY 61 DKGYTLNIKFPAG 72
Db 213 DKGYTLNIKFPAG 224

RESULT 3
US-08-325-278-3
Sequence 3, Application US/08325278
Publication No. US20030027283A1
GENERAL INFORMATION:
APPLICANT: Bjvrck, Lars
APPLICANT: Sjvbring, Ulf
TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,278
FILING DATE: 26-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCES/DOCKET NUMBER: 450023.401
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Escherichia coli LE392/pHDL, DSM 7055
US-08-325-278-3

Query Match 100.0%; Score 369; DB 8; Length 434;
Best Local Similarity 100.0%; Pred. No. 1.6e-34;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KEKTPPEPKKEVTIKANLIYADGKTQTAEFKGTPEEATAEAYRYADLLAKENGKKTVDVA 60
Db 153 KEKTPPEPKKEVTIKANLIYADGKTQTAEFKGTPEEATAEAYRYADLLAKENGKKTVDVA 212
QY 61 DKGYTLNIKFPAG 72
Db 213 DKGYTLNIKFPAG 224

RESULT 4
US-09-808-212A-6
Sequence 6, Application US/09808212A
Patent No. US20020137918A1
GENERAL INFORMATION:
APPLICANT: Gore, Michael Graham
APPLICANT: Beckingham, Jennifer Ann
APPLICANT: Roberts, Sian Eleri
TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN
FILE REFERENCE: 100084.414US
CURRENT APPLICATION NUMBER: US/09/808,212A
CURRENT FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 72
TYPE: PRT
ORGANISM: Peptostreptococcus sp.
US-09-808-212A-6

Query Match 95.4%; Score 352; DB 10; Length 72;
Best Local Similarity 94.4%; Pred. No. 1.5e-33;
Matches 68; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 KEKTPPEPKKEVTIKANLIYADGKTQTAEFKGTPEEATAEAYRYADLLAKENGKKTVDVA 60
Db 1 KEKTPPEPKKEVTIKANLIYADGKTQTAEFKGTPEEATAEAYRYADLLAKENGKKTVDVA 60
QY 61 DKGYTLNIKFPAG 72
Db 61 DKGYTLNIKFPAG 72

RESULT 5
US-09-808-212A-10
Sequence 10, Application US/09808212A
Patent No. US20020137918A1

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; GENERAL INFORMATION:
; APPLICANT: Gore, Michael Graham
; APPLICANT: Beckingham, Jennifer Ann
; APPLICANT: Roberts, Sian Eleri
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN
; FILE REFERENCE: 100084.414US
; CURRENT APPLICATION NUMBER: US/09/808,212A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Peptostreptococcus sp.
; US-09-808-212A-10

Query Match      91.9%; Score 339; DB 10; Length 72;
Best Local Similarity 90.3%; Pred. No. 4.6e-32;
Matches 65; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KEKTPPEPKKEVTIKANLIYADGKTQTAEFGKTFEEATAEAYRYADLLAKENGKYTVDA 60
Db 1 KEKTPPEPKKEVTIKANLIYADGKTQTAEFGKTFEEATAEAYRYADLLAKENGKYTVDA 60

Qy 61 DKGTYTLNIKFPAG 72
Db 61 DGGYTINIRFAG 72

; RESULT 6
; US-09-808-212A-18
; Sequence 18, Application US/09808212A
; Patent No. US20020137918A1
; GENERAL INFORMATION:
; APPLICANT: Gore, Michael Graham
; APPLICANT: Beckingham, Jennifer Ann
; APPLICANT: Roberts, Sian Eleri
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN
; FILE REFERENCE: 100084.414US
; CURRENT APPLICATION NUMBER: US/09/808,212A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Peptostreptococcus sp.
; US-09-808-212A-18

Query Match      85.4%; Score 315; DB 10; Length 75;
Best Local Similarity 85.7%; Pred. No. 2.9e-29;
Matches 60; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 3 KTPPEPKKEVTIKANLIYADGKTQTAEFGKTFEEATAEAYRYADLLAKENGKYTVDA 62
Db 5 ETPPEPKKEVTIKANLIYADGKTQTAEFGKTFEEATAEAYRYADLLAKENGKYTVDA 64

Qy 63 GYTLNIKFPAG 72
Db 65 GYTINIKFPAG 74

; RESULT 7
; US-09-808-212A-14
; Sequence 14, Application US/09808212A
; Patent No. US20020137918A1
; GENERAL INFORMATION:
; APPLICANT: Gore, Michael Graham
; APPLICANT: Beckingham, Jennifer Ann
; APPLICANT: Roberts, Sian Eleri
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN
; FILE REFERENCE: 100084.414US
; CURRENT APPLICATION NUMBER: US/09/808,212A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Peptostreptococcus sp.
; US-09-808-212A-14

Query Match      81.7%; Score 301.5; DB 10; Length 71;
Best Local Similarity 83.3%; Pred. No. 9.8e-28;
Matches 60; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

Qy 1 KEKTPPEPKKEVTIKANLIYADGKTQTAEFGKTFEEATAEAYRYADLLAKENGKYTVDA 60
Db 1 KEKTPPEPKKEVTIKANLIYADGKTQTAEFGKTFEEATAEAYRYADLLAKENGKYTVDA 59

Qy 61 DKGTYTLNIKFPAG 72
Db 60 DGGTINIKFPAG 71

; RESULT 8
; US-09-808-212A-4
; Sequence 4, Application US/09808212A
; Patent No. US20020137918A1
; GENERAL INFORMATION:
; APPLICANT: Gore, Michael Graham
; APPLICANT: Beckingham, Jennifer Ann
; APPLICANT: Roberts, Sian Eleri
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN
; FILE REFERENCE: 100084.414US
; CURRENT APPLICATION NUMBER: US/09/808,212A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Peptostreptococcus sp.
; US-09-808-212A-4

Query Match      81.0%; Score 299; DB 10; Length 76;
Best Local Similarity 77.6%; Pred. No. 2.1e-27;
Matches 59; Conservative 8; Mismatches 5; Indels 4; Gaps 1;

Qy 1 KEKTPPEPKKEVTIKANLIYADGKTQTAEFGKTFEEATAEAYRYADLLAKENGKYTV 56
Db 1 KEETPTPTDSEEEVTIKANLIYADGKTQTAEFGKTFEEATAEAYRYADLLAKENGKYTV 60

Qy 57 VDVAADKGTYTLNIKFPAG 72
Db 61 VDVAADKGTYTLNIKFPAG 76

; RESULT 9
; US-09-808-212A-2
; Sequence 2, Application US/09808212A
; Patent No. US20020137918A1
; GENERAL INFORMATION:
; APPLICANT: Gore, Michael Graham
; APPLICANT: Beckingham, Jennifer Ann
; APPLICANT: Roberts, Sian Eleri
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN
; FILE REFERENCE: 100084.414US
; CURRENT APPLICATION NUMBER: US/09/808,212A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Peptostreptococcus sp.
; US-09-808-212A-2
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RESULT 11
US-10-345-618-2
; Sequence 2, Application US/10345618
; Publication No. US20030148484A1
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF PRODUCING SAME
; FILE REFERENCE: 13474
; CURRENT APPLICATION NUMBER: US/10/345,618
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US/09/509,031
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:LHL protein
; OTHER INFORMATION: sequence
US-10-345-618-2

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RESULT 13
US-10-345-618-8
; Sequence 8, Application US/10345618
; Publication No. US20030148494A1
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF PRODUCING SAME
; FILE REFERENCE: 13474
; CURRENT APPLICATION NUMBER: US/10/345,618
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US/09/509,031
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 198
; TYPE: PRT

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:LHL.seq
; OTHER INFORMATION: protein sequence
US-10-345-618-8

Query Match      74.8%; Score 276; DB 12; Length 198;
Best Local Similarity 84.1%; Pred. No. 3.2e-24;
Matches 53; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 10 EVVTIKANLIYADGKTQTAEFKGTPEATAEAYRYADLLAKENGYTVDDVADKGYTLNIK 69
Db 32 EVVTIKANLIYADGKTQTAEFKGTPEATAEAYRYADLLAKENGYTVDDVADKGYTLNIK 91

QY 70 FAG 72
Db 92 FAG 94

RESULT 14
US-10-345-618-6
; Sequence 6, Application US/10345618
; Publication No. US20030148484A1
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Suesse, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF PRODUCING SAME
; FILE REFERENCE: 13474
; CURRENT APPLICATION NUMBER: US/10/345,618
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US/09/509,031
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:TLHL protein
; OTHER INFORMATION: sequence
US-10-345-618-6

Query Match      74.8%; Score 276; DB 12; Length 342;
Best Local Similarity 84.1%; Pred. No. 6.4e-24;
Matches 53; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 10 EVVTIKANLIYADGKTQTAEFKGTPEATAEAYRYADLLAKENGYTVDDVADKGYTLNIK 69
Db 176 EVVTIKANLIYADGKTQTAEFKGTPEATAEAYRYADLLAKENGYTVDDVADKGYTLNIK 235

QY 70 FAG 72
Db 236 FAG 238

RESULT 15
US-10-345-618-16
; Sequence 16, Application US/10345618
; Publication No. US20030148484A1
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Suesse, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF PRODUCING SAME
; FILE REFERENCE: 13474
; CURRENT APPLICATION NUMBER: US/10/345,618
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US/09/509,031
; PRIOR FILING DATE: 2000-06-09

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 3, 2003, 11:19:27; Search time 213.041 Seconds
(without alignments)
294.149 Million cell updates/sec

Title: US-08-325-278B-1_COPY_153_224

Perfect score: 369

Sequence: 1 KEKTPPEPKERVTKANLIYADGKQTAFKGTFTFEATPAAYRYADLLAKENGKTYDVA 72

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 5580241 seqs, 870357830 residues

Total number of hits satisfying chosen parameters: 5580241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Pending Patents AA Main:

- 1: /cgn2_6/ptodata/1/paa/PCTUS COMB.pcp.*
- 2: /cgn2_6/ptodata/1/paa/US06 COMB.pcp.*
- 3: /cgn2_6/ptodata/1/paa/US07 COMB.pcp.*
- 4: /cgn2_6/ptodata/1/paa/US080 COMB.pcp.*
- 5: /cgn2_6/ptodata/1/paa/US081 COMB.pcp.*
- 6: /cgn2_6/ptodata/1/paa/US082 COMB.pcp.*
- 7: /cgn2_6/ptodata/1/paa/US083 COMB.pcp.*
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- 10: /cgn2_6/ptodata/1/paa/US086 COMB.pcp.*
- 11: /cgn2_6/ptodata/1/paa/US087 COMB.pcp.*
- 12: /cgn2_6/ptodata/1/paa/US088 COMB.pcp.*
- 13: /cgn2_6/ptodata/1/paa/US089 COMB.pcp.*
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- 20: /cgn2_6/ptodata/1/paa/US096 COMB.pcp.*
- 21: /cgn2_6/ptodata/1/paa/US097A COMB.pcp.*
- 22: /cgn2_6/ptodata/1/paa/US097B COMB.pcp.*
- 23: /cgn2_6/ptodata/1/paa/US098 COMB.pcp.*
- 24: /cgn2_6/ptodata/1/paa/US099A COMB.pcp.*
- 25: /cgn2_6/ptodata/1/paa/US099B COMB.pcp.*
- 26: /cgn2_6/ptodata/1/paa/US100 COMB.pcp.*
- 27: /cgn2_6/ptodata/1/paa/US101 COMB.pcp.*
- 28: /cgn2_6/ptodata/1/paa/US102 COMB.pcp.*
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- 30: /cgn2_6/ptodata/1/paa/US104 COMB.pcp.*
- 31: /cgn2_6/ptodata/1/paa/US60 COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	369	100.0	72	23	US-09-808-212A-8
2	369	100.0	305	7	US-08-325-278-1

Sequence 8, Appli
Sequence 1, Appli

3	369	100.0	305	7	US-08-325-278A-1	Sequence 1, Appli
4	369	100.0	305	7	US-08-325-278B-1	Sequence 1, Appli
5	369	100.0	434	7	US-08-325-278-3	Sequence 3, Appli
6	369	100.0	434	7	US-08-325-278A-3	Sequence 3, Appli
7	369	100.0	434	7	US-08-325-278B-3	Sequence 3, Appli
8	369	100.0	719	22	US-09-791-537-10210	Sequence 10210, A
9	369	100.0	719	22	US-09-791-537-96101	Sequence 96101, A
10	359.5	97.2	467	25	US-09-980-469-12	Sequence 12, Appli
11	352	95.4	72	23	US-09-808-212A-6	Sequence 6, Appli
12	352	95.4	367	23	US-09-889-182A-4	Sequence 4, Appli
13	339	91.9	72	23	US-09-808-212A-10	Sequence 10, Appli
14	315	85.4	75	23	US-09-808-212A-18	Sequence 18, Appli
15	315	85.4	291	8	US-08-446-137A-4	Sequence 4, Appli
16	315	85.4	992	22	US-09-791-537-88366	Sequence 88366, A
17	315	85.4	1027	7	US-08-331-637-2	Sequence 2, Appli
18	315	85.4	1027	15	US-08-446-137A-2	Sequence 2, Appli
19	315	85.4	1027	15	US-09-187-295-2	Sequence 2, Appli
20	301.5	81.7	71	23	US-09-808-212A-14	Sequence 14, Appli
21	299	81.0	76	23	US-09-808-212A-4	Sequence 4, Appli
22	299	81.0	78	22	US-09-791-537-22553	Sequence 22553, A
23	293	79.4	82	23	US-09-808-212A-2	Sequence 2, Appli
24	292	79.1	74	23	US-09-808-212A-16	Sequence 16, Appli
25	284	77.0	182	19	US-09-509-031-2	Sequence 2, Appli
26	284	77.0	182	23	US-09-820-048A-2	Sequence 2, Appli
27	276	74.8	178	19	US-09-509-031-13	Sequence 13, Appli
28	276	74.8	178	23	US-09-820-048A-13	Sequence 13, Appli
29	276	74.8	198	19	US-09-509-031-8	Sequence 8, Appli
30	276	74.8	198	23	US-09-820-048A-8	Sequence 8, Appli
31	276	74.8	342	19	US-09-509-031-6	Sequence 6, Appli
32	276	74.8	342	23	US-09-820-048A-6	Sequence 6, Appli
33	276	74.8	482	19	US-09-509-031-16	Sequence 16, Appli
34	276	74.8	495	19	US-09-509-031-4	Sequence 4, Appli
35	276	74.8	495	23	US-09-820-048A-4	Sequence 4, Appli
36	270.5	73.3	71	23	US-09-808-212A-12	Sequence 12, Appli
37	80.5	21.8	395	1	PCT-US01-08631-42219	Sequence 42219, A
38	80.5	21.8	395	19	US-09-538-092-857	Sequence 857, App
39	79.5	21.5	463	1	PCT-US01-08631-53631	Sequence 53631, A
40	72	19.5	891	18	US-09-451-320-2418	Sequence 2418, Ap
41	71.5	19.4	1378	31	US-60-167-217-8500	Sequence 8500, Ap
42	70.5	19.1	586	28	US-10-282-122A-53124	Sequence 53124, A
43	69	18.7	321	31	US-60-360-039-3708	Sequence 3708, Ap
44	69	18.7	1447	30	US-10-437-963-198658	Sequence 198658, A
45	68	18.4	414	21	US-09-708-427-20185	Sequence 20185, A

ALIGNMENTS

RESULT 1
US-09-808-212A-8
; Sequence 8, Application US/09808212A
; GENERAL INFORMATION:
; APPLICANT: Gore, Michael Graham
; APPLICANT: Beckingham, Jennifer Ann
; APPLICANT: Roberts, Sian Eleri
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN
; FILE REFERENCE: 100084.414US
; CURRENT APPLICATION NUMBER: US/09/808,212A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 72
; TYPE: PPT
; ORGANISM: Peptostreptococcus sp.
US-09-808-212A-8

Query Match 100.0%; Score 369; DB 23; Length 72;
Best Local Similarity 100.0%; Pred. No. 2.5e-36;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEKTPPEPKERVTKANLIYADGKQTAFKGTFTFEATPAAYRYADLLAKENGKTYDVA 60
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Db 1 KKTPEEPKEVITKANLIYADGKTQTAEFKGTFEATAEAYRYADLLAKENGKTYDVA 60
QY 61 DKGYTLNIKFPAG 72
Db 61 DKGYTLNIKFPAG 72

RESULT 2
US-08-325-278-1
; Sequence 1, Application US/08325278
; GENERAL INFORMATION:
; APPLICANT: Björck, Lars
; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,278
; FILING DATE: 26-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McWaters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 450023.401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 305 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; MOLECULE TYPE: protein
; TOPOLOGY: unknown
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli LE392/pHDL, DSM 7054
US-08-325-278-1

Query Match 100.0%; Score 369; DB 7; Length 305;
Best Local Similarity 100.0%; Pred. No. 1.9e-35;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKTPEEPKEVITKANLIYADGKTQTAEFKGTFEATAEAYRYADLLAKENGKTYDVA 60
Db 153 KKTPEEPKEVITKANLIYADGKTQTAEFKGTFEATAEAYRYADLLAKENGKTYDVA 212

QY 61 DKGYTLNIKFPAG 72
Db 213 DKGYTLNIKFPAG 224

RESULT 3
US-08-325-278A-1
; Sequence 1, Application US/08325278A
; GENERAL INFORMATION:
; APPLICANT: Björck, Lars
; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed IP Law Group
; STREET: 701 Fifth Avenue Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,278B
; FILING DATE: 26-Oct-1994
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.

Query Match 100.0%; Score 369; DB 7; Length 305;
Best Local Similarity 100.0%; Pred. No. 1.9e-35;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKTPEEPKEVITKANLIYADGKTQTAEFKGTFEATAEAYRYADLLAKENGKTYDVA 60
Db 153 KKTPEEPKEVITKANLIYADGKTQTAEFKGTFEATAEAYRYADLLAKENGKTYDVA 212

QY 61 DKGYTLNIKFPAG 72
Db 213 DKGYTLNIKFPAG 224

RESULT 4
US-08-325-278B-1
; Sequence 1, Application US/08325278B
; GENERAL INFORMATION:
; APPLICANT: Björck, Lars
; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed IP Law Group
; STREET: 701 Fifth Avenue Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,278B
; FILING DATE: 26-Oct-1994
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.

; STREET: 701 Fifth Avenue Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,278A
; FILING DATE: 26-Oct-1994
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 100084.402
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 305 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli LE392/pHDL, DSM 7054
US-08-325-278A-1

Query Match 100.0%; Score 369; DB 7; Length 305;
Best Local Similarity 100.0%; Pred. No. 1.9e-35;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKTPEEPKEVITKANLIYADGKTQTAEFKGTFEATAEAYRYADLLAKENGKTYDVA 60
Db 153 KKTPEEPKEVITKANLIYADGKTQTAEFKGTFEATAEAYRYADLLAKENGKTYDVA 212

QY 61 DKGYTLNIKFPAG 72
Db 213 DKGYTLNIKFPAG 224

RESULT 4
US-08-325-278B-1
; Sequence 1, Application US/08325278B
; GENERAL INFORMATION:
; APPLICANT: Björck, Lars
; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed IP Law Group
; STREET: 701 Fifth Avenue Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,278B
; FILING DATE: 26-Oct-1994
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.

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;
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 100084.402
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 305 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORGANISM: Escherichia coli LE392/pHDL, DSM 7054
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-08-325-278B-1

Query Match 100.0%; Score 369; DB 7; Length 305;
Best Local Similarity 100.0%; Pred. No. 1.9e-35;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KEKTPPEPKKEVTKANLIYADGKTQTAEFKGTPEEATAEAYRYADLLAKENGKTYVDVA 60
Db 153 KEKTPPEPKKEVTKANLIYADGKTQTAEFKGTPEEATAEAYRYADLLAKENGKTYVDVA 212

Qy 61 DKGYTLNIKFGAG 72
Db 213 DKGYTLNIKFGAG 224

RESULT 5
US-08-325-278-3
; Sequence 3, Application US/08325278
; GENERAL INFORMATION:
; APPLICANT: Bjvrck, Lars
; APPLICANT: Bjvrck, Lars
; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESS: SEED AND BERRY LLP
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,278
; FILING DATE: 26-Oct-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 450023.401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 434 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli LE392/pHDLG, DSM 7055
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-325-278-3

Query Match 100.0%; Score 369; DB 7; Length 434;
Best Local Similarity 100.0%; Pred. No. 3.1e-35;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KEKTPPEPKKEVTKANLIYADGKTQTAEFKGTPEEATAEAYRYADLLAKENGKTYVDVA 60
Db 153 KEKTPPEPKKEVTKANLIYADGKTQTAEFKGTPEEATAEAYRYADLLAKENGKTYVDVA 212

Qy 61 DKGYTLNIKFGAG 72
Db 213 DKGYTLNIKFGAG 224

RESULT 7
US-08-325-278B-3
; Sequence 3, Application US/08325278A
; GENERAL INFORMATION:
; APPLICANT: Bjvrck, Lars
; APPLICANT: Bjvrck, Lars
; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESS: Seed IP Law Group
; STREET: 701 Fifth Avenue Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,278A
; FILING DATE: 26-Oct-1994
; CLASSIFICATION: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 100084.402
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 434 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli LE392/pHDLG, DSM 7055
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-325-278A-3

Query Match 100.0%; Score 369; DB 7; Length 434;
Best Local Similarity 100.0%; Pred. No. 3.1e-35;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KEKTPPEPKKEVTKANLIYADGKTQTAEFKGTPEEATAEAYRYADLLAKENGKTYVDVA 60
Db 153 KEKTPPEPKKEVTKANLIYADGKTQTAEFKGTPEEATAEAYRYADLLAKENGKTYVDVA 212

Qy 61 DKGYTLNIKFGAG 72
Db 213 DKGYTLNIKFGAG 224
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Sequence 3, Application US/08325278B
GENERAL INFORMATION:
APPLICANT: Bjorck, Lars
TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed IP Law Group
STREET: 701 Fifth Avenue Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,278B
FILING DATE: 26-Oct-1994
CLASSIFICATION: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 100084.402
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Escherichia coli LE392/pHDLG, DSM 7055
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-325-278B-3
Query Match 100.0%; Score 369; DB 7; Length 434;
Best Local Similarity 100.0%; Pred. No. 3.1e-35;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KEKTPPEPKKEVTIKANLIYADGKTQTAEFKGTFEATAEAYRYADLLAKENGKYYTDVA 60
DB 153 KEKTPPEPKKEVTIKANLIYADGKTQTAEFKGTFEATAEAYRYADLLAKENGKYYTDVA 212
QY 61 DKGYTLNIKFPAG 72
DB 213 DKGYTLNIKFPAG 224
RESULT 8
US-09-791-537-10210
Sequence 10210, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 10210
LENGTH: 719
TYPE: PRT
ORGANISM: Peptostreptococcus magnus

US-09-791-537-10210
Query Match 100.0%; Score 369; DB 22; Length 719;
Best Local Similarity 100.0%; Pred. No. 6.2e-35;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KEKTPPEPKKEVTIKANLIYADGKTQTAEFKGTFEATAEAYRYADLLAKENGKYYTDVA 60
DB 246 KEKTPPEPKKEVTIKANLIYADGKTQTAEFKGTFEATAEAYRYADLLAKENGKYYTDVA 305
QY 61 DKGYTLNIKFPAG 72
DB 306 DKGYTLNIKFPAG 317
RESULT 9
US-09-791-537-96101
Sequence 96101, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 96101
LENGTH: 719
TYPE: PRT
ORGANISM: Peptostreptococcus magnus
US-09-791-537-96101
Query Match 100.0%; Score 369; DB 22; Length 719;
Best Local Similarity 100.0%; Pred. No. 6.2e-35;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KEKTPPEPKKEVTIKANLIYADGKTQTAEFKGTFEATAEAYRYADLLAKENGKYYTDVA 60
DB 246 KEKTPPEPKKEVTIKANLIYADGKTQTAEFKGTFEATAEAYRYADLLAKENGKYYTDVA 305
QY 61 DKGYTLNIKFPAG 72
DB 306 DKGYTLNIKFPAG 317
RESULT 10
US-09-980-469-12
Sequence 12, Application US/09980469
GENERAL INFORMATION:
APPLICANT: Shoseyov, Oded
APPLICANT: Ziv, Shani
TITLE OF INVENTION: PROCESS OF EXPRESSING AND ISOLATING RECOMBINANT PROTEINS AND RECOMBINANT TISSUES OR CULTURED
FILE REFERENCE: 01/22924
CURRENT APPLICATION NUMBER: US/09/980,469
CURRENT FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 467
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: pUC19-cell-ProL-cexNG-HDEL fusion encoded product
US-09-980-469-12
Query Match 97.2%; Score 358.5; DB 25; Length 467;
Best Local Similarity 98.6%; Pred. No. 6.3e-34;
Matches 72; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 KKTPEEPKEEVTIKANLIYADGKTQTAEFKGTPEATAEAYRYADLL-AKENGKYYTDV 59
DB 192 KKTPEEPKEEVTIKANLIYADGKTQTAEFKGTPEATAEAYRYADLLAAKENGKYYTDV 251
QY 60 ADGTYTLNKFAG 72
DB 252 ADGTYTLNKFAG 264

RESULT 11
US-09-808-212A-6
; Sequence 6, Application US/09808212A
; GENERAL INFORMATION:
; APPLICANT: Gore, Michael Graham
; APPLICANT: Beckingham, Jennifer Ann
; APPLICANT: Roberts, Sian Eleri
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN
; FILE REFERENCE: 100084.414US
; CURRENT APPLICATION NUMBER: US/09/808,212A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Peptostreptococcus sp.
US-09-808-212A-6

Query Match 95.4%; Score 352; DB 23; Length 72;
Best Local Similarity 94.4%; Pred. No. 2.8e-34;
Matches 68; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 KKTPEEPKEEVTIKANLIYADGKTQTAEFKGTPEATAEAYRYADLLAAKENGKYYTDVA 60
DB 1 KKTPEEPKEEVTIKANLIYADGKTQTAEFKGTPEATAEAYRYADALKKONGEYTDVA 60
QY 61 DKGYTLNKFAG 72
DB 61 DKGYTLNKFAG 72

RESULT 12
US-09-889-182A-4
; Sequence 4, Application US/09889182A
; GENERAL INFORMATION:
; APPLICANT: Breitling, Frank
; TITLE OF INVENTION: SELECTION OF MONOCLONAL ANTIBODIES
; FILE REFERENCE: 4121-126
; CURRENT APPLICATION NUMBER: US/09/889,182A
; CURRENT FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: pct/de00/00079
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-889-182A-4

Query Match 95.4%; Score 352; DB 23; Length 367;
Best Local Similarity 94.4%; Pred. No. 2.7e-33;
Matches 68; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 KKTPEEPKEEVTIKANLIYADGKTQTAEFKGTPEATAEAYRYADLLAAKENGKYYTDVA 60
DB 25 KKTPEEPKEEVTIKANLIYADGKTQTAEFKGTPEATAEAYRYADALKKONGEYTDVA 84
QY 61 DKGYTLNKFAG 72
DB 85 DKGYTLNKFAG 96

RESULT 13
US-09-808-212A-10
; Sequence 10, Application US/09808212A
; GENERAL INFORMATION:
; APPLICANT: Gore, Michael Graham
; APPLICANT: Beckingham, Jennifer Ann
; APPLICANT: Roberts, Sian Eleri
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN
; FILE REFERENCE: 100084.414US
; CURRENT APPLICATION NUMBER: US/09/808,212A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Peptostreptococcus sp.
US-09-808-212A-10

Query Match 91.9%; Score 339; DB 23; Length 72;
Best Local Similarity 90.3%; Pred. No. 1e-32;
Matches 65; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 KKTPEEPKEEVTIKANLIYADGKTQTAEFKGTPEATAEAYRYADLLAAKENGKYYTDVA 60
DB 1 KKTPEEPKEEVTIKANLIYADGKTQTAEFKGTPEATAEAYRYADLLAAKENGKYYTDLE 60
QY 61 DKGYTLNKFAG 72
DB 61 DGYTYTINIRFAG 72

RESULT 14
US-09-808-212A-18
; Sequence 18, Application US/09808212A
; GENERAL INFORMATION:
; APPLICANT: Gore, Michael Graham
; APPLICANT: Beckingham, Jennifer Ann
; APPLICANT: Roberts, Sian Eleri
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN
; FILE REFERENCE: 100084.414US
; CURRENT APPLICATION NUMBER: US/09/808,212A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Peptostreptococcus sp.
US-09-808-212A-18

Query Match 85.4%; Score 315; DB 23; Length 75;
Best Local Similarity 85.7%; Pred. No. 8.7e-30;
Matches 60; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 3 KKTPEEPKEEVTIKANLIYADGKTQTAEFKGTPEATAEAYRYADLLAAKENGKYYTDVADK 62
DB 5 ETPPEEPKEEVTIKANLIYADGKTQTAEFKGTPEATAEAYRYADLLAAKENGKYYTDLEDG 64
QY 63 GYTLNKFAG 72
DB 65 GYTLNKFAG 74

RESULT 15
US-08-446-137A-4
; Sequence 4, Application US/08446137A
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEINS DERIVED
; FROM PROTEIN L AND THEIR USES

```

; NUMBER OF SEQUENCES: 4
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,137A
; FILING DATE: 22-05-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MITCHARD, LEONARD C.
; REGISTRATION NUMBER: 29,009
; REFERENCE/DOCKET NUMBER: 1418-9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 291 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-446-137A-4

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Query Match      85.4%; Score 315; DB 8; Length 291;
Best Local Similarity 85.7%; Pred. No. 5.8e-29;
Matches 60; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 3 KTEPEPKKEVTIKANLIYADGKTQTAEFKGTFEETAEAYRYADLLAKENGKTYTDVADK 62
Db 221 ETEPEPKKEVTIKVNLIFADGKTQTAEFKGTFEETAEAYRYADLLAKENGKTYTDVADK 280

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QY 63 GYTINIKFAG 72
Db 281 GYTINIKFAG 290

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Search completed: September 3, 2003, 11:40:08
Job time : 214.041 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:20:12 ; Search time 10.1096 Seconds
(without alignments)
223.701 Million cell updates/sec

Title: US-08-325-278b-1_COPY_153_224

Perfect score: 369

Sequence: 1 KEKTPPEKPEVTKANLIY.....GKYTVDVADKGYTLNIKIPAG 72

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 148256 seqs, 31410045 residues

Total number of hits satisfying chosen parameters: 148256

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA.New.*

- 1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep.*
- 2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
- 3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
- 4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
- 5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
- 6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep.*
- 7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	65.5	17.8	271	6	US-10-221-131-95
2	65.5	17.8	271	6	US-10-221-131-96
3	63.5	17.2	914	6	US-10-631-467-789
4	63.5	17.2	1019	1	PCT-US03-21510-62
5	63	17.1	693	6	US-10-333-120A-10
6	62.5	16.9	423	7	US-60-491-156-12
7	62.5	16.9	1849	6	US-10-637-544-2
8	61.5	16.7	136	6	US-10-221-131-91
9	61	16.5	930	5	US-09-200-650E-3
10	61	16.5	1166	5	US-09-200-650E-7
11	60.5	16.4	636	6	US-10-613-520-1638
12	60.5	16.4	637	5	US-09-897-516A-7157
13	60.5	16.4	638	6	US-10-613-520-1341
14	60.5	16.4	638	6	US-10-613-520-1356
15	60.5	16.4	713	6	US-10-467-534-97
16	60.5	16.4	2315	6	US-10-603-114-5434
17	60	16.3	291	6	US-10-640-833-4201
18	60	16.3	328	6	US-10-617-320-3318
19	60	16.3	728	6	US-10-467-534-81
20	59	16.0	242	5	US-09-674-546A-244
21	59	16.0	1646	6	US-10-640-833-4667
22	59	16.0	1653	6	US-10-617-320-4155
23	58	15.7	335	6	US-10-640-833-4355
24	58	15.7	342	6	US-10-617-320-3303
25	58	15.7	722	5	US-09-897-516A-6073
26	58	15.7	820	6	US-10-640-833-4219

27	58	15.7	834	6	US-10-617-320-4760	Sequence 4760, Ap
28	58	15.7	1684	6	US-10-408-765A-811	Sequence 811, App
29	57.5	15.6	245	6	US-10-221-131-100	Sequence 100, App
30	57.5	15.6	271	6	US-10-221-131-98	Sequence 98, Appl
31	57.5	15.6	274	6	US-10-221-131-97	Sequence 97, Appl
32	57.5	15.6	533	6	US-10-221-131-101	Sequence 101, Appl
33	57.5	15.6	753	6	US-10-603-114-5022	Sequence 5022, Ap
34	57.5	15.6	1096	6	US-10-451-901-1	Sequence 1, Appl
35	57.5	15.6	1262	6	US-10-293-244-1125	Sequence 1125, Ap
36	57.5	15.6	1289	6	US-10-293-244-3093	Sequence 3093, Ap
37	57	15.4	224	6	US-10-286-897-5675	Sequence 5675, Ap
38	57	15.4	224	6	US-10-258-898A-5675	Sequence 5675, Ap
39	57	15.4	311	6	US-10-286-897-2103	Sequence 2103, Ap
40	57	15.4	311	6	US-10-258-898A-2103	Sequence 2103, Ap
41	57	15.4	513	6	US-10-603-114-4981	Sequence 4981, Ap
42	57	15.4	977	6	US-10-293-244-1201	Sequence 1201, Ap
43	57	15.4	977	7	US-60-490-890-580	Sequence 580, App
44	57	15.4	1003	6	US-10-293-244-3169	Sequence 3169, Ap
45	57	15.4	2073	7	US-60-490-890-980	Sequence 980, App

ALIGNMENTS

RESULT 1
US-10-221-131-95
; Sequence 95, Application US/10221131
; GENERAL INFORMATION:
; APPLICANT: FUKUSHIMA, NAOSHI
; APPLICANT: TSUCHIYA, MASAYUKI
; APPLICANT: OH-EDA, MASAYOSHI
; APPLICANT: UNO, SHINSUKE
; APPLICANT: KIKUCHI, YASUFUMI
; TITLE OF INVENTION: POLYPEPTIDE INDUCING APOPTOSIS
; FILE REFERENCE: 065678/0106
; CURRENT APPLICATION NUMBER: US/10/221,131
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: PCT/JP01/01912
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 09/523,095
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: JP 2000-115246
; PRIOR FILING DATE: 2000-04-17
; PRIOR APPLICATION NUMBER: JP 2000-321822
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 95
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: pscml. MABL1-scfv
US-10-221-131-95

Query Match 17.8%; Score 65.5; DB 6; Length 271;
Best Local Similarity 30.3%; Pred. No. 1.9;
Matches 20; Conservative 9; Mismatches 24; Indels 13; Gaps 2;
QY 20 YADGKTQTAEPKG-----TFEATATAYRYADLLAKEN-----GKYTVDVADKGYTL 66
Db 76 YNDGTYNEKFKGKATLTSEKSSAAVMELSSLASDSAVTYCARGYYSDMDMGQGTTL 135
QY 67 NIKFAG 72
Db 136 TVSSGG 141

RESULT 2
US-10-221-131-96
; Sequence 96, Application US/10221131
; GENERAL INFORMATION:
; APPLICANT: FUKUSHIMA, NAOSHI

```

; APPLICANT: TSUCHIYA, MASAYUKI
; APPLICANT: OH-EDA, MASAYOSHI
; APPLICANT: UNO, SHINSUKE
; APPLICANT: KIKUCHI, YASUFUMI
; TITLE OF INVENTION: POLYPEPTIDE INDUCING APOPTOSIS
; FILE REFERENCE: 065678/0106
; CURRENT APPLICATION NUMBER: US/10/221,131
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: PCT/JP01/01912
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 09/523,095
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: JP 2000-115246
; PRIOR FILING DATE: 2000-04-17
; PRIOR APPLICATION NUMBER: JP 2000-321822
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 96
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: pCHOM1. MABLI-scFv
US-10-221-131-96

Query Match 17.8%; Score 65.5; DB 6; Length 271;
Best Local Similarity 30.3%; Pred. No. 1.9;
Matches 20; Conservative 9; Mismatches 24; Indels 13; Gaps 2;

QY 20 YADGKTQTAEPKG---TPEATAEAYRYADLLAKEN-----GKTYTVDVADKGYTL 66
Db 73 YNDGTYKNEKFGKATLTSEKSSAAYMELSLASEDSAVYVCARGGYSDWDGQGTTL 132

QY 67 NIKFAG 72
Db 133 TVSSGG 138

RESULT 3
US-10-631-467-789
; Sequence 789, Application US/10631467
; GENERAL INFORMATION:
; APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive p
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 789
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-631-467-789

Query Match 17.2%; Score 63.5; DB 6; Length 914;
Best Local Similarity 40.5%; Pred. No. 15;
Matches 17; Conservative 5; Mismatches 19; Indels 1; Gaps 1;

QY 3 KTPPEPKVEVTKANLIYADGKTQTAEPKGTPEATAEAYRY 44
Db 434 KTPSITSEAVPEAGLV-IDGKTLNAIFQGLEKKEFLELTQY 474

RESULT 4
PCT-US03-21510-62
; Sequence 62, Application PC/TUS0321510

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; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: MP21S AS MODIFIERS OF THE p21 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX03-046C-PC
; CURRENT APPLICATION NUMBER: PCT/US03/21510
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US 60/394,795
; PRIOR FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US 60/401,739
; PRIOR FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US 60/411,010
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 60/437,158
; PRIOR FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 62
; LENGTH: 1019
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-21510-62

Query Match 17.2%; Score 63.5; DB 1; Length 1019;
Best Local Similarity 40.5%; Pred. No. 17;
Matches 17; Conservative 5; Mismatches 19; Indels 1; Gaps 1;

QY 3 KTPPEPKVEVTKANLIYADGKTQTAEPKGTPEATAEAYRY 44
Db 539 KTPSITSEAVPEAGLV-IDGKTLNAIFQGLEKKEFLELTQY 579

RESULT 5
US-10-333-120A-10
; Sequence 10, Application US/10333120A
; GENERAL INFORMATION:
; APPLICANT: Janulczyk, Robert
; APPLICANT: Iannelli, Francesco
; APPLICANT: Sjöholm, Anders
; APPLICANT: Pozzi, Gianni
; APPLICANT: Björck, Lars
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 13519PCTUS
; CURRENT APPLICATION NUMBER: US/10/333,120A
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: PCT/EP01/08409
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: SE 0002728-4
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 693
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-333-120A-10

Query Match 17.1%; Score 63; DB 6; Length 693;
Best Local Similarity 40.4%; Pred. No. 12;
Matches 21; Conservative 5; Mismatches 20; Indels 6; Gaps 2;

QY 7 EPKEVTKANLIYADGK----TTPAEKGTPEATAEAYRYADLLAKENGK 54
Db 238 EPRDQIKQAEVSEKQAEATRLKIKTDREAEAEAKRRAD--AKEQKG 287

RESULT 6
US-60-491-156-12
; Sequence 12, Application US/60491156
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Karicheti, Venkateswarlu
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Eliasof, Scott

```


;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
;; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 14303, 16816, 17827, 32620, 577,
;; TITLE OF INVENTION: 619, 1423, 2158, 8263, 15402, 16209, 16386, 21165, 30911 OR
;; TITLE OF INVENTION: 41897
;; FILE REFERENCE: MPI03-098PIM
;; CURRENT APPLICATION NUMBER: US/60/491,156
;; CURRENT FILING DATE: 2003-07-30
;; NUMBER OF SEQ ID NOS: 30
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 12
;; LENGTH: 423
;; TYPE: PRT
;; ORGANISM: Homo Sapiens
US-60-491-156-12

Query Match 16.9%; Score 62.5; DB 7; Length 423;
Best Local Similarity 31.1%; Pred. No. 7.4;
Matches 19; Conservative 12; Mismatches 23; Indels 7; Gaps 3;
QY 1 KEKTPPEPKSEVTIKANLIYADGKTQTAEFKGTFFETATB---AYRYADLLAKENGKTYV 57
Db 294 KAQLPKLEEIVVILGMEATG--WTCQARSSY--ITSEILWGVRTFVLTLEDGFYEV 349
QY 58 D 58
Db 350 D 350

RESULT 7
US-10-637-544-2
;; Sequence 2, Application US/10637544
;; GENERAL INFORMATION:
;; APPLICANT: Chr. Hansen A/S
;; TITLE OF INVENTION: Peptides with anti-hypertensive properties
;; FILE REFERENCE: P1032US01
;; CURRENT APPLICATION NUMBER: US/10/637,544
;; CURRENT FILING DATE: 2003-08-11
;; NUMBER OF SEQ ID NOS: 20
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 2
;; LENGTH: 1849
;; TYPE: PRT
;; ORGANISM: Lactobacillus helveticus
US-10-637-544-2

Query Match 16.9%; Score 62.5; DB 6; Length 1849;
Best Local Similarity 33.8%; Pred. No. 47;
Matches 25; Conservative 8; Mismatches 30; Indels 11; Gaps 4;
QY 1 KEKTPPEPKSEVTIKANL---IYADGKTQ---TAEFKGTFFETATBAYRYADLLAKENG 53
Db 1590 KENQPSDEKELAKAKENLQAKVDAGEKDKDKYTADSKKDFNDALKKA---KDVLDKNA 1646
QY 54 KYTVVDVADKGYTLN 67
Db 1647 K-LADLQDAAKALD 1659

RESULT 8
US-10-221-131-91
;; Sequence 91, Application US/10221131
;; GENERAL INFORMATION:
;; APPLICANT: FUKUSHIMA, NAOSHI
;; APPLICANT: TSUCHIYA, MASAYUKI
;; APPLICANT: OH-EDA, MASAYOSHI
;; APPLICANT: UNO, SHINSUKE
;; APPLICANT: KIKUCHI, YASUFUMI
;; TITLE OF INVENTION: POLYPEPTIDE INDUCING APOPTOSIS
;; FILE REFERENCE: 065678/0106
;; CURRENT APPLICATION NUMBER: US/10/221,131
;; CURRENT FILING DATE: 2003-02-11
;; PRIOR APPLICATION NUMBER: PCT/JP01/01912
;; PRIOR FILING DATE: 2001-03-12

;; PRIOR APPLICATION NUMBER: 09/523,095
;; PRIOR FILING DATE: 2000-03-10
;; PRIOR APPLICATION NUMBER: JP 2000-115246
;; PRIOR FILING DATE: 2000-04-17
;; PRIOR APPLICATION NUMBER: JP 2000-321822
;; PRIOR FILING DATE: 2000-10-20
;; NUMBER OF SEQ ID NOS: 103
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 91
;; LENGTH: 136
;; TYPE: PRT
;; ORGANISM: Mus sp.
;; FEATURE:
;; OTHER INFORMATION: pGEM-M1H
US-10-221-131-91

Query Match 16.7%; Score 61.5; DB 6; Length 136;
Best Local Similarity 30.6%; Pred. No. 2.4;
Matches 19; Conservative 9; Mismatches 21; Indels 13; Gaps 2;
QY 20 YADGKTQTAEFKG---TFEETATBAYRYADLLAKEN-----GKTYVDVADKGYTL 66
Db 73 YNDGTYKNEKFKGKATLTSEKSSSAAYMELSSLAEDSAVYVCARGYYSYDDMGQGTTL 132
QY 67 NI 68
Db 133 TV 134

RESULT 9
US-09-200-650E-3
;; Sequence 3, Application US/09200650E
;; GENERAL INFORMATION:
;; APPLICANT: Patti, Joseph M.
;; APPLICANT: Foster, Timothy J.
;; APPLICANT: Hook, Magnus A.O.
;; APPLICANT: Eihinn, Deirdre Ni
;; APPLICANT: Perkins, Samuel L.
;; TITLE OF INVENTION: Extracellular Matrix-Binding Proteins from Staphylococcus aureus
;; FILE REFERENCE: P06283US2/BAS
;; CURRENT APPLICATION NUMBER: US/09/200,650E
;; CURRENT FILING DATE: 1998-11-25
;; PRIOR APPLICATION NUMBER: 60/066,815
;; PRIOR FILING DATE: 1997-11-26
;; PRIOR APPLICATION NUMBER: 60/098,427
;; PRIOR FILING DATE: 1998-08-31
;; NUMBER OF SEQ ID NOS: 23
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 3
;; LENGTH: 930
;; TYPE: PRT
;; ORGANISM: Staphylococcus aureus
US-09-200-650E-3

Query Match 16.5%; Score 61; DB 5; Length 930;
Best Local Similarity 31.4%; Pred. No. 30;
Matches 22; Conservative 16; Mismatches 24; Indels 8; Gaps 5;
QY 4 TPEEPK-BEVTIKANLIYA-DGKTQTAE-FKG---TFEETATBAYRYADLLAKENGK--Y 55
Db 407 TPDTSKLKDVTDFQDFVIYSDNDKNTATVLMKGTSSNKQYIIQQVAYPONSSTDNGKIDY 466
QY 56 TVDVADKGYT 65
Db 467 TLDTDKTKYS 476

RESULT 10
US-09-200-650E-7
;; Sequence 7, Application US/09200650E
;; GENERAL INFORMATION:
;; APPLICANT: Patti, Joseph M.
;; APPLICANT: Foster, Timothy J.

261 BEFAVSEKNSRITIKROAPSYRETTOQNTNLAY-----TGKDLGFVEKLDANAY----- 309

Db

Qy 48 LAKENGKYTVDDVADKGYTLNIK 69
Db 310 -VLEKKRYSAADDKONGYAGNVK 330

Search completed: September 3, 2003, 11:40:56
Job time : 11.1096 secs

RESULT 14
US-10-613-520-1356
; Sequence 1356, Application US/10613520
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Laurie, Cathy C
; APPLICANT: Wu, Wei
; APPLICANT: Maolong, Lu
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)E
; CURRENT APPLICATION NUMBER: US/10/613,520
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 10/389,566
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2578
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1356
; LENGTH: 638
; TYPE: PRT
; ORGANISM: Salmonella typhimurium
US-10-613-520-1356

Query Match 16.4%; Score 60.5; DB 6; Length 638;
Best Local Similarity 32.0%; Pred. No. 21;
Matches 24; Conservative 4; Mismatches 32; Indels 15; Gaps 3;
Qy 2 EKTPE-----EPKEVTIKANLIYADGKCTA-----EPKGTFEATAEAYADLL 48
Db 124 KKTAEIDYLGEPTEAVITVPYFNDQORQATKDGRIAGLEVRIINEPTAAALAYG--L 181
Qy 49 AKENGKYTVDDVADKG 63
Db 182 DKEVGNRIAVYDLG 196

RESULT 15
US-10-467-534-97
; Sequence 97, Application US/10467534
; GENERAL INFORMATION:
; APPLICANT: Berthet, Francois-Xavier Jacques
; APPLICANT: Lobet, Yves
; APPLICANT: Poolman, Jan
; APPLICANT: Verilant, Vincent Georges Christian Louis
; TITLE OF INVENTION: Vaccine Composition
; FILE REFERENCE: B45261
; CURRENT APPLICATION NUMBER: US/10/467,534
; CURRENT FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: PCT/EP02/01356
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: GB 0103169.9
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 713
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-534-97
Query Match 16.4%; Score 60.5; DB 6; Length 713;
Best Local Similarity 26.8%; Pred. No. 25;
Matches 22; Conservative 7; Mismatches 28; Indels 25; Gaps 3;
Qy 1 KEKTEEPKKEVTIK-----ANLIYADGKTOTAEFKGTFEATAEAYADL 47

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:04:52 ; Search time 9.12329 Seconds
(without alignments)
371.130 Million cell updates/sec

Title: US-08-325-278B-1_COPY_153_224

Perfect score: 369

Sequence: 1 KEKTEPEKPEVTKANLIY.....GKYTVDVADKGYTLNKFAG 72

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	88.5	24.0	398	1 RPC4 HUMAN	P05423 homo sapien
2	83.5	22.6	398	1 RPC4 MOUSE	Q91wd1 mus musculus
3	67	18.2	953	1 LKAI PASHA	P16535 pasteurrella
4	67	18.2	953	1 LKAB PASHA	P55118 pasteurrella
5	65.5	17.8	471	1 TNAE ECO57	Q8xb34 escherichia
6	65.5	17.8	471	1 TNAE ECO57	P00913 escherichia
7	65.5	17.8	1179	1 DE3A STRCO	Q9z618 streptomyce
8	65	17.6	371	1 SYA AQUPI	Q9xcms aquifex pyr
9	64.5	17.5	367	1 GPR OCEIH	Q8cxc9 oceanobacil
10	64	17.3	621	1 LAMC DROME	Q03427 drosophila
11	64	17.3	634	1 GYRB BORHE	Q9zfk1 borrelia he
12	63.5	17.2	425	1 IRK6 MOUSE	P48542 mus musculus
13	63.5	17.2	425	1 IRK6 MOUSE	P48542 mus musculus
14	63.5	17.2	1461	1 A10B HUMAN	Q94823 homo sapien
15	63	17.1	6632	1 UNB9 CABEL	Q01761 caenorhabdi
16	62.5	16.9	263	1 YC33 ASTLO	P58147 astasia lon
17	62.5	16.9	423	1 IRK6 HUMAN	P48051 homo sapien
18	62.5	16.9	425	1 IRK6 MESAU	P49658 mesocricetu
19	61.5	16.7	300	1 SIAL PIG	P31936 sus scrofa
20	61.5	16.7	451	1 Y996 METJA	Q58403 methanococc
21	61.5	16.7	550	1 THS FYRAB	Q9vzq7 pyrococcus
22	61.5	16.7	892	1 IF2 YERPE	Q82bc2 versinia pe
23	61	16.5	420	1 ASSY YEAST	P22768 saccharomyc
24	60.5	16.4	238	1 RNPH VIBCH	Q9kvd6 vibrio chol
25	60.5	16.4	269	1 T2S1 STRFI	Q52512 streptomyce
26	60.5	16.4	345	1 QUER LACLA	Q9cfa6 lactococcus
27	60.5	16.4	444	1 SLAP LACAC	P35829 lactobacill
28	60.5	16.4	636	1 DNKX YERPE	Q8zlm7 versinia pe
29	60.5	16.4	637	1 DNKX SALT1	Q8z9r1 salmonella
30	60.5	16.4	637	1 DNKX SALT1	Q56073 salmonella
31	60.5	16.4	1023	1 HLY1 ECOLI	P09983 escherichia
32	60	16.3	436	1 RBL EUGST	P48074 euglena ste
33	60	16.3	1131	1 PMA1 DUNBI	P54211 dunaliella

34	59.5	16.1	373	1 CONS ARATH	Q39057 arabidopsis
35	59.5	16.1	390	1 IRKB_CAVPO	Q9jhj9 cavia porce
36	59.5	16.1	796	1 YE29 YEAST	P39956 saccharomyc
37	59.5	16.1	1454	1 C9P2 HUMAN	O60244 h cofactor
38	59.5	16.1	1857	1 FAS2 PENPA	P15368 p fatty aci
39	59	16.0	322	1 MTRH_METKA	Q32869 methanopyru
40	59	16.0	366	1 RUVE_ANASP	Q8yt32 anabaena pp
41	59	16.0	776	1 RTNI_HUMAN	Q16799 homo sapien
42	59	16.0	1829	1 Y296 HUMAN	O15015 homo sapien
43	58.5	15.9	417	1 PUR2 THETN	Q8rc54 thermonaer
44	58.5	15.9	424	1 PUR2 AQUAE	O66949 aquifex aeo
45	58.5	15.9	1001	1 ORK1_DROME	Q94526 drosophila

ALIGNMENTS

RESULT 1
RPC4_HUMAN STANDARD; PRT; 398 AA.
AC P05423; Q9BPV7; Q9BP21; Q9BXB3;
DT 01-NOV-1988 (Rel. 09, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE DNA-directed RNA polymerase III 47 kDa polypeptide (EC 2.7.7.6) (RNA
DE polymerase C subunit 4) (RPC4) (RPC53) (BNS1 protein).
GN GN BNS1 OR BNS1 OR POLR3D.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88065472; PubMed=3683386;
RA Ittmann M., Greco A., Basilico C.;
RT "Isolation of the human gene that complements a temperature-sensitive
RT cell cycle mutation in BHK cells.";
RL Mol. Cell. Biol. 7:3386-3393(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22278866; PubMed=12391170;
RA Hu P., Wu S., Sun Y., Yuan C.-C., Kobayashi R., Myers M.P.,
RA Hernandez N.;
RT "Characterization of human RNA polymerase III identifies orthologues
RT for Saccharomyces cerevisiae RNA polymerase III subunits.";
RL Mol. Cell. Biol. 22:8044-8055(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung, and Lymph;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield A.S., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 1-50 FROM N.A.
RX MEDLINE=21282972; PubMed=11279001;

Chong S.S., Hu P., Hernandez N.;
 "Reconstitution of transcription from the human U6 small nuclear RNA
 promoter with eight recombinant polypeptides and a partially purified
 RNA polymerase III complex.";
 J. Biol. Chem. 276:20727-20734(2001).
 [5]
 RN SEQUENCE OF 1-12 FROM N.A.
 RA Ittmann M.;
 RA "Promoter structure and cell cycle control of the BMS1 cell cycle
 gene, which encodes a subunit of RNA polymerase III.";
 Submitted (Oct-1993) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription
 of DNA into RNA using the four ribonucleoside triphosphates as
 CC substrates. Complements a temperature-sensitive cell cycle
 CC mutation in BHK cells.
 CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
 CC (RNA)(N).
 CC -!- SUBUNIT: RNA polymerase III consists of about 15 different
 CC subunits. Interacts with RPC5.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- CAUTION: Ref.3 (AAH03039 and AAH00516) sequence differs from that
 CC shown due to a frameshift in position 175.
 CC -----
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 CC -----
 DR EMBL; M17754; AAA51838.1; -;
 DR EMBL; AY092086; AAM18216.1; -;
 DR EMBL; BC002603; AAH02603.1; -;
 DR EMBL; BC003039; AAH03039.1; ALT_FRAME.
 DR EMBL; BC004484; AAH04484.1; -;
 DR EMBL; BC000516; AAH00516.1; ALT_FRAME.
 DR EMBL; AF346574; AAK15371.1; -;
 DR EMBL; L15301; AAAT2377.1; -;
 DR PIR; A43700; A43700.
 DR Genew; HGNC:1080; BMS1T.
 DR MIM; 187280; -;
 DR GO; GO:0000074; P:regulation of cell cycle; TAS.
 DR Pfam; PF05132; RNA pol Rpc4; 1.
 KW Transferase; DNA-directed RNA polymerase; Transcription;
 FT Nucleic acid protein.
 FT CONFLICT 9 18 EPSTGGPRP -> RPARGPDL (IN REF. 1).
 FT CONFLICT 9 12 EPST -> RPAR (IN REF. 5).
 FT CONFLICT 26 40 LIGRRPAPLTPGRL -> SSGGGGLSPPAV (IN REF.
 1).
 FT CONFLICT 98 98 G -> R (IN REF. 1).
 FT CONFLICT 233 233 K -> R (IN REF. 2).
 FT CONFLICT 286 286 P -> L (IN REF. 2).
 SQ SEQUENCE 398 AA; 44396 MW; CDBAFF3257B78410 CRC64;
 Query Match 24.0%; Score 88.5; DB 1; Length 398;
 Best Local Similarity 33.3%; Pred. No. 0.052;
 Matches 27; Conservative 9; Mismatches 26; Indels 19; Gaps 3;
 QY 3 KTPBPKPKEVTKAMLIYAD-----GKTQTAEFKGTFTAEATAYRYADLLAK 50
 Db 66 KIKEPKPKEVTKKREKRDQRQEGHGRGRPEVQSHIFEGGPAEMMK-----KK 120
 QY 51 ENGYKTVDVADKG--YTLNIK 69
 Db 121 GNWDKTVDSVDMGPGSHIINIK 141
 RESULT 2
 RPC4_MOUSE
 ID RPC4_MOUSE STANDARD; PRT; 398 AA.
 AC Q91WD1; Q9CZ02;
 DT 15-SEP-2003 (Rel. 42, Created)

DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE DNA-directed RNA polymerase III 47 kDa polypeptide (EC 2.7.7.6) (RNA
 DE polymerase C subunit 4) (RPC4).
 GN ENS1T OR POLR3D.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RP [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RC MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Mateu Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staub J.F., Suzuki R., Tonita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RA "Functional annotation of a full-length mouse cDNA collection";
 RA Nature 409:685-690(2001).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Salivary gland;
 RC MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription
 CC of DNA into RNA using the four ribonucleoside triphosphates as
 CC substrates (By similarity).
 CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
 CC (RNA)(N).
 CC -!- SUBUNIT: RNA polymerase III consists of about 15 different
 CC subunits. Interacts with RPC5 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -----
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 CC -----

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CC -----
DR EMBL; AK013165; BAB28687.1; -.
DR EMBL; BC016102; AAH16102.1; -.
DR MGD; MGI:1914315; 2810426M17R1k.
DR Pfam; PF05132; RNA pol Rpc4; 1.
KW Transferrase; DNA-directed RNA polymerase; Transcription;
KW Nuclear protein.
FT CONFLICT 201 201 L -> F (IN REF. 2).
SQ SEQUENCE 398 AA; 44323 MW; D509DB632C656FFD CRC64;

Query Match
Best Local Similarity 22.6%; Score 83.5; DB 1; Length 398;
Matches 26; Conservative 10; Mismatches 26; Indels 19; Gaps 3;

QY 3 KTPPEPKKEVTIKANLIYAD-----GKTQTAEFKGTPEATAEAYRYADLLAK 50
Db 66 KIKPEPKKEVTMKKEKRDQRQHGGRGRGRVIGSHSIFQGPAAEMK-----KK 120
QY 51 ENKQYTVADKG--YTLNIK 69
Db 121 GNWDKTVDSMDGSPSHIINIK 141

RESULT 3
LKAB_PASHA
ID LKAB_PASHA STANDARD; PRT; 953 AA.
AC P16535;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leukotoxin from serotype A1.
GN LKTA.
OS Pasteurella haemolytica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Mannheimia.
OX NCBI_TaxID=75985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Serotype A1;
RX MEDLINE=87306837; PubMed=3040588;
RA Lo R.Y.C., Strathee C.A., Shewen P.B.;
RT "Nucleotide sequence of the leukotoxin genes of Pasteurella
RL haemolytica A1."
RL Infect. Immun. 55:1987-1996 (1987).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Serotype A1 / PHL101;
RX MEDLINE=89210283; PubMed=2707120;
RA Highlander S.K., Chidambaram M., Engler M.J., Weinstock G.M.;
RT "DNA sequence of the Pasteurella haemolytica leukotoxin gene
RN cluster."
RN DNA 8:15-28 (1989).
RN [3]
RP SEQUENCE OF 884-953 FROM N.A.
RC STRAIN=Serotype A1 / PHL101;
RX MEDLINE=90236888; PubMed=2185213;
RA Highlander S.K., Engler M.J., Weinstock G.M.;
RT "Secretion and expression of the Pasteurella haemolytica Leukotoxin."
RL J. Bacteriol. 172:2343-2350 (1990).
CC -!- FUNCTION: Bacterial hemolysins are exotoxins that attack blood
CC cell membranes and cause cell rupture by mechanisms not clearly
CC defined.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DOMAIN: The Gly-rich region is probably involved in binding
CC calcium, which is required for target cell-binding or cytolytic
CC activity.
CC -!- DOMAIN: The three transmembrane domains are believed to be
CC involved in pore formation by the cytotoxin (By similarity).
CC -!- PTM: Palmitoylated by lktC. The toxin only becomes active when
CC modified (By similarity).
CC -!- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
CC -----

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CC -----
DR EMBL; M20730; AAA25529.1; -.
DR EMBL; M24197; AAA25543.1; -.
DR PIR; B30169; B30169.
DR InterPro; IPR001343; Hemlyen_Ca_bind.
DR InterPro; IPR003995; RtxA.
DR Pfam; PF00353; hemolysinCbind; 5.
DR Pfam; PF02382; RTX; 1.
DR PRINTS; PR00313; CAENDNGRPT.
DR PROSITE; PR01488; RTXTOXINA.
DR PROSITE; PS00330; HEMOLYSIN_CALCIIUM; 4.
KW Hemolysis; Toxin; Cytolysis; Repeat; Calcium; Transmembrane;
KW Lipoprotein; Palmitate.
FT TRANSMEM 229 249
FT TRANSMEM 297 318
FT TRANSMEM 366 390
FT DOMAIN 734 784
FT REPEAT 734 739
FT REPEAT 743 748
FT REPEAT 752 757
FT REPEAT 761 766
FT REPEAT 770 775
FT REPEAT 779 784
FT CONFLICT 409 414 PEHVAN -> LSTLOI (IN REF. 2).
FT CONFLICT 742 742 D -> Y (IN REF. 2).
SQ SEQUENCE 953 AA; 101996 MW; 7F93D113A118C05F CRC64;

Query Match
Best Local Similarity 18.2%; Score 67; DB 1; Length 953;
Matches 21; Conservative 8; Mismatches 25; Indels 10; Gaps 1;

QY 9 KKEVTIKANLIYADKQTQTAEFKGTPEATAE-----AYRYADLLAKENKQYTD 58
Db 832 KEKVTIQNWFEADFAKEVPVNYKATKDEIIGQNGERITSKQVDDLIAGNGKITQD 891
QY 59 VADK 62
Db 892 ELKS 895

RESULT 4
LKAB_PASHA
ID LKAB_PASHA STANDARD; PRT; 953 AA.
AC P55118;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leukotoxin from serotype A11.
GN LKTA.
OS Pasteurella haemolytica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Mannheimia.
OX NCBI_TaxID=75985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Serotype A11;
RX MEDLINE=94041617; PubMed=8225575;
RA Burrows L.L., Olah-Winfield E., Lo R.Y.C.;
RT "Molecular analysis of the leukotoxin determinants from Pasteurella
RL haemolytica serotypes 1 to 16."
RL Infect. Immun. 61:5001-5007 (1993).
CC -!- FUNCTION: Bacterial hemolysins are exotoxins that attack blood
CC cell membranes and cause cell rupture by mechanisms not clearly
CC defined.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DOMAIN: The Gly-rich region is probably involved in binding
CC calcium, which is required for target cell-binding or cytolytic
CC -----

```

CC activity.

CC -!- DOMAIN: The three transmembrane domains are believed to be

CC involved in pore formation by the cytotoxin (BY SIMILARITY).

CC -!- PTM: Palmitoylated by lktC. The toxin only becomes active when

CC modified (by similarity).

CC -!- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.

CC -----

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CC -----

CC EMBL; U01215; AAB36689.1; -

CC InterPro; IPR001343; Hemlysn_Ca_bind.

CC InterPro; IPR003995; RTxA.

CC Pfam; PF00353; hemolysinCbind; 5.

CC Pfam; PF02382; RTX; 1.

CC PRINTS; PR00313; CABNDNGRPT.

CC PROSITE; PS00330; HEMOLYSIN_CALCIIUM; 4.

CC KW Hemolysis; Toxin; Cytolysis; Repeat; Calcium; Transmembrane;

CC Lipoprotein; Palmitate.

CC FT TRANSMEM 230 250 POTENTIAL.

CC FT TRANSMEM 297 317 POTENTIAL.

CC FT TRANSMEM 381 401 POTENTIAL.

CC FT DOMAIN 734 784 6 X REPEATS, GLY-RICH.

CC FT REPEAT 734 739 1.

CC FT REPEAT 743 748 2.

CC FT REPEAT 752 757 3.

CC FT REPEAT 761 766 4.

CC FT REPEAT 770 775 5.

CC FT REPEAT 779 784 6.

CC SQ SEQUENCE 953 AA; 102206 MW; 927FF56CFC884F12 CRC64;

Query Match 18.2%; Score 67; DB 1; Length 953;

Best Local Similarity 32.8%; Pred. No. 23;

Matches 21; Conservative 8; Mismatches 25; Indels 10; Gaps 1;

QY 9 KEVTKANLIYADGKTQTAEPKGTPEATAE-----AYRYADLLAKENGKVTVD 58

Db 832 KKKVTIQDFREADFAKEVRYNKATDKKIEELIGNGRITSKQVDDLLAKNGKITQD 891

QY 59 VADK 62

Db 892 ELSK 895

RESULT 5

TNAA_EC057 STANDARD; PRT; 471 AA.

AC Q8XE34;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Tryptophanase (EC 4.1.99.1) (L-tryptophan indole-lyase) (TNase).

GN TNAA OR 52303 OR ECS4645.

OS Escherichia coli O157:H7.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=83334;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=O157:H7 / EDL933 / ATCC 700927;

RX MEDLINE=21074935; PubMed=11206551;

RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

RA Grobbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamasis K.,

RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

RA Welch R.A., Blattner F.R.;

RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.;"

RL Nature 409:529-533 (2001).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=O157:H7 / RIMD 0509952;

RX MEDLINE=21156231; PubMed=11258796;

RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

RA Iida T., Takami H., Honda T., Sasaki C., Ogasawara N., Yasunaga T.,

RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;

RT "Complete genome sequence of enterohaemorrhagic Escherichia coli

RT O157:H7 and genetic comparison with a laboratory strain K-12.;"

RL DNA Res. 8:11-22 (2001).

CC -!- CATALYTIC ACTIVITY: L-tryptophan + H(2)O = indole + pyruvate +

CC NH(3)

CC -!- COFACTOR: Pyridoxal phosphate (By similarity).

CC -!- PATHWAY: Tryptophan catabolism.

CC -!- SUBUNIT: Homotetramer (By similarity).

CC -!- SIMILARITY: BELONGS TO THE BETA-ELIMINATING LYASE FAMILY.

CC -----

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CC -----

CC EMBL; AB005602; AAG58908.1; ALT_INIT.

CC EMBL; AP002566; BAB38068.1; ALT_INIT.

CC HAMAP; MF 00544; -; 1.

CC InterPro; IPR001597; Beta_elim_lyase.

CC Pfam; PF01212; Beta_elim_lyase; 1.

CC PRODOM; PD005927; Beta_elim_lyase; 1.

CC PROSITE; PS00853; BETA_ELIM_LYASE; 1.

CC KW Tryptophan catabolism; lyase; Pyridoxal phosphate; Complete proteome.

FT BINDING 270 270 PYRIDOXAL PHOSPHATE (BY SIMILARITY).

FT SEQUENCE 471 AA; 52789 MW; 49DD2D41BD9D0034 CRC64;

Query Match 17.8%; Score 65.5; DB 1; Length 471;

Best Local Similarity 51.9%; Pred. No. 16;

Matches 14; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

QY 24 KQTAAEPKGT-TFEEATAEAYRYADLLA 49

Db 239 KQREAYKDWITIEQITRETYKYADMLA 265

RESULT 6

TNAA_EC01 STANDARD; PRT; 471 AA.

AC P00913; P78123;

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Tryptophanase (EC 4.1.99.1) (L-tryptophan indole-lyase) (TNase).

GN TNAA OR IND OR B3708 OR SF3754.

OS Escherichia coli, and

OS Shigella flexneri.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=562, 623;

RN [1]

RP SEQUENCE FROM N.A.

RC SPECIES=E.coli; STRAIN=K12;

RX MEDLINE=82007678; PubMed=6268608;

RA Deeley M.C., Yanofsky C.;

RT "Nucleotide sequence of the structural gene for tryptophanase of

RT Escherichia coli K-12.;"

RL J. Bacteriol. 147:787-796 (1981).

RN [2]

RP SEQUENCE FROM N.A., AND IMPORTANCE OF CYS-298.

RC SPECIES=E.coli; STRAIN=B/1t7-A;

RA Rabinowitch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
 RT Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 CC -!- FUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTICHAIN ENZYME
 CC RESPONSIBLE FOR MOST OF THE REPLICATIVE SYNTHESIS IN BACTERIA.
 CC THIS DNA POLYMERASE ALSO EXHIBITS 3' TO 5' EXONUCLEASE ACTIVITY.
 CC THE ALPHA CHAIN IS THE DNA POLYMERASE (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
 CC + [DNA] (N).
 CC -!- SUBUNIT: DNA polymerase III contains a core (composed of alpha,
 CC epsilon and theta chains) that associates with a tau subunit. This
 CC core dimerizes to form the POLIII' complex. POLIII' associates
 CC with the gamma complex (composed of gamma, delta, delta', psi and
 CC chi chains) and with the beta chain to form the complete DNA
 CC polymerase III complex (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-C FAMILY. DNAE
 CC SUBFAMILY.

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CC -----
 CC EMBL: AF108191; AAD16978.1; -;
 CC EMBL: AL096884; CAB51456.1; -;
 CC PIR: T35093; T35093.
 CC InterPro: IPR004013; PHP_C.
 CC InterPro: IPR003141; PHP_N.
 CC InterPro: IPR004805; PolC_alpha.
 CC InterPro: IPR004365; trNA_anti.
 CC Pfam: PF02811; PHP_C; 1.
 CC Pfam: PF02231; PHP_N; 1.
 CC Pfam: PF01336; trNA_anti; 1.
 CC SMART: SM00481; POLIITAC; 1.
 CC TIGRFAMs: TIGR00594; polC; 1.
 CC Transferase; DNA-directed DNA polymerase; DNA replication;
 CC Complete proteome.
 CC VARIANT 802 E -> K (IN MUTANT TS-38).
 CC SEQUENCE 1179 AA; 130795 MW; 7E4B58675B634CD3 CRC64;

Query Match 17.8%; Score 65.5; DB 1; Length 1179;
 Best Local Similarity 29.9%; Pred. No. 42;
 Matches 20; Conservative 12; Mismatches 28; Indels 7; Gaps 2;

QY 2 EKTPEEPKKEVT-----IKANLIYADGKTQTAEFGTPEATAEAYRVADLLAKENGKYYT 56
 Db 131 QKWPMDKETISQWSEGVASTGCPSEGVQTRLRGLGHFDEALKAAADYDIFGKD--RYF 188

QY 57 VDVAKG 63

Db 189 LELMDHG 195

RESULT 8

SVL_AQUY
 ID SVL_AQUY STANDARD; PRT; 871 AA.
 AC Q9XDM3;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Alanine--trNA synthetase (EC 6.1.1.7) (Alanine--trNA ligase) (Alars).
 GN ALAS.
 OS Aquifex pyrophilus.
 OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
 CC NCBI_TaxID=2714;

RN SEQUENCE FROM N.A.
 RP STRAIN=K015A / DSM 6858;
 RX MEDLINE=99214260; PubMed=10198119;
 RA Klenk H.-P., Meier T.D., Durovic P., Schwass V., Lottepeich F.,
 RA Dennis P.P., Zillig W.;
 RT "RNA polymerase of Aquifex pyrophilus: implications for the evolution
 RT of the bacterial rpoBC operon and extremely thermophilic bacteria.";
 RL J. Mol. Evol. 48:528-541(1999).
 CC -!- CATALYTIC ACTIVITY: ATP + L-alanine + trNA(Ala) = AMP +
 CC diphosphate + L-alanyl-trNA(Ala).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to class-II aminoacyl-trNA synthetase family.
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CC -----
 CC EMBL: AF027500; AAD25871.1; -;
 CC HAMAP: MF_00036; -; 1.
 CC InterPro: IPR003156; DHHA1.
 CC InterPro: IPR002318; trNA-synt 2c.
 CC InterPro: IPR006193; trNA_synt_Ala.
 CC Pfam: PF02272; DHHA1; 1.
 CC Pfam: PF01411; trNA-synt 2c; 1.
 CC PRINTS: PR00980; TRNASYNTHALA.
 CC TIGRFAMs: TIGR00344; alas; 1.
 CC PROSITE: PS00860; AA TRNA LIGASE II ALA; 1.
 CC Aminoacyl-trNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
 CC SEQUENCE 871 AA; 99395 MW; D2D15915FC00CC31 CRC64;

Query Match 17.6%; Score 65; DB 1; Length 871;
 Best Local Similarity 30.2%; Pred. No. 34;
 Matches 19; Conservative 8; Mismatches 20; Indels 16; Gaps 2;

QY 1 KEKTPPEKPEVTIKANLIYADGKTQTAEFGTPEATAEAYRVADLLAKENGKYYTVDV 59
 Db 754 REKVEERHRELT-----YYGVFEDVEPEELRLNLADILRQTGKDVVFI 798

QY 60 ADK 62

Db 799 ASK 801

RESULT 9

GPR_OCEIH
 ID GPR_OCEIH STANDARD; PRT; 367 AA.
 AC Q8XC9;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Germination protease precursor (EC 3.4.99.-) (Spore protease).
 GN GPR OR 0B1975.
 OS Oceanobacillus thelyensis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
 CC NCBI_TaxID=182710;

RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=HTE831 / DSM 14371 / JCM 11309;
 RX MEDLINE=2220767; PubMed=12235376;

RA Takami H., Takaki Y., Uchiyama I.;
 RT "Genome sequence of Oceanobacillus thelyensis isolated from the Iheya
 RT Ridge and its unexpected adaptive capabilities to extreme
 RT environments";
 RL Nucleic Acids Res. 30:3927-3935(2002).
 CC -!- FUNCTION: Initiates the rapid degradation of small, acid-soluble
 CC proteins during spore germination (By similarity).
 CC -!- SUBUNIT: Homotetramer (By similarity).
 CC -!- PTM: Autoproteolytically processed. The inactive tetrameric

EMBL; L07933; AAA28666.1; -.
FlyBase; Fgn0010397; LamC.
GO; GO:0005638; C:lamin filament; NAS.
InterPro; IPR001664; IF.
InterPro; IPR001322; IF_tail.
Pfam; PF00038; filament; 1.
Pfam; PF00932; IF_tail; 1.
DR PROSITE; PS00226; IF; FALSE NEG.
KW Intermediate filament; Coiled coil; Nuclear protein; Phosphorylation;
KW Polymorphism.
FT DOMAIN 1 47 HEAD.
FT DOMAIN 48 403 ROD.
FT DOMAIN 404 621 TAIL.
FT DOMAIN 47 85 COIL 1A.
FT DOMAIN 86 95 LINKER 1.
FT DOMAIN 96 233 COIL 1B.
FT DOMAIN 234 257 LINKER 2.
FT DOMAIN 258 403 COIL 2.
FT DOMAIN 453 458 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT SITE 281 281 HEPTAD CHANGE OF PHASE.
FT SITE 345 345 HEPTAD CHANGE OF PHASE.
FT VARIANT 166 166 S -> A (IN PG-9).
FT VARIANT 528 528 I -> V (IN PG-9).
SQ SEQUENCE 621 AA; 69855 MW; 78FB7375803C2C87 CRC64;

Query Match 17.3%; Score 64; DB 1; Length 621;
Best Local Similarity 27.8%; Pred. No. 31;
Matches 15; Conservative 9; Mismatches 30; Indels 0; Gaps 0;

QY 6 EBPKEVTIKANLIYADGKTQTAEPKGTPEETAARYVADLLAKENGKYTVDV 59
Db 68 ENENSRLTQLNLAQTVNRETSLNKAVYKEKLAARLLDTEAKEKAKLEIDI 121

RESULT 11
GYRB BORHE STANDARD; PRT; 634 AA.
ID ID GYRB BORHE
AC 09ZFK1;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE DNA gyrase subunit B (EC 5.99.1.3).
GN GYRB.
OS Borrelia hermslii.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_Taxid=140;
RN [1]
RC STRAIN=HS1;
RA Samuels D.S., Kimmel B.J., Huang W.M.;
RT "Mutations in Borrelia hermslii gyRB confer resistance to coumermycin
Al.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: DNA GYRASE NEGATIVELY SUPERCOILS CLOSED CIRCULAR DOUBLE-
CC STRANDED DNA IN AN ATP-DEPENDENT MANNER AND ALSO CATALYZES THE
CC INTERCONVERSION OF OTHER TOPOLOGICAL ISOMERS OF DOUBLE-STRANDED
CC DNA RINGS, INCLUDING CATENANES AND KNOTTED RINGS.
CC -!- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC -!- SUBUNIT: MADE UP OF TWO CHAINS. THE A CHAIN IS RESPONSIBLE FOR DNA
CC BREAKAGE AND REJOINING; THE B CHAIN CATALYZES ATP HYDROLYSIS. THE
CC ENZYME FORMS AN A2B2 TETRAMER.
CC -!- SIMILARITY: Belongs to the type II topoisomerase family.
CC
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CC
CC EMBL; AF098862; AAC72846 1.

DR HSSP; P06982; 1AJ6.
 DR InterPro; IPR003594; ATPbind ATPase.
 DR InterPro; IPR002288; DNA_gyraseB_C.
 DR InterPro; IPR000585; DNA_gyraseB.
 DR InterPro; IPR001241; DNA_topoisomII.
 DR InterPro; IPR006171; Topfim dom.
 DR Pfam; PF00204; DNA_gyraseB_1.
 DR Pfam; PF00986; DNA_gyraseB_C_1.
 DR Pfam; PF02518; HATPase_c; 1.
 DR Pfam; PF01751; Toprim; 1.
 DR PRINTS; PR00418; TP12FAMILY.
 DR PROSITE; PD149633; DNA_gyraseB_C; 1.
 DR SMART; SM00387; HATPase_c; 1.
 DR SMART; SM00433; TOP2c; 1.
 DR TIGRFAMs; TIGR01059; Gyrb; 1.
 DR PROSITE; PS00177; TOPOISOMERASE_II; 1.
 DR Topoisomerase; Isomerase; ATP-binding.
 SQ SEQUENCE 634 AA; 70848 MW; 5E58C5F32126833C CRC64;
 Query Match 17.3%; Score 64; DB 1; Length 634;
 Best Local Similarity 32.7%; Pred.No. 31; Mismatches 23; Indels 2; Gaps 1;
 Matches 18; Conservative 12;
 QY 17 NUIYADGKTQTAEFGTGFEEATAEAYRYADLLAKENGKTVVDVADKGYT--LNK 69
 DB 270 NINTREGGTHVAGFGKGLKAMSEAFRDSKISKQVPSLTLDKFKGLTAVISIK 324
 RESULT 12
 IRK6 MOUSE
 ID IRK6 MOUSE STANDARD; PRT; 425 AA.
 AC P48542; O70290; P70216; P70306; P70308; P70309; P70454;
 AC Q9QVH5;
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE 15-GSP-2003 (Rel. 42, Last annotation update)
 DE G protein-activated inward rectifier potassium channel 2 (GIRK2)
 DE (Potassium channel, inwardly rectifying, subfamily J, member 6)
 DE (Inward rectifier K+ channel Kir3.2).
 DE KCNJ6 OR KCNJ7 OR GIRK2 OR W.
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]_TaxID=10090;
 RP SEQUENCE FROM N.A. (ISOFORM GIRK2-1).
 RC TISSUE=Brain;
 RX MEDLINE=95010760; PubMed=7926018;
 RA Lesage F., Duprat F., Fink M., Guillemare E., Coppola T.,
 RA Lazdunski M., Hugnot J.-P.;
 RT "Cloning provides evidence for a family of inward rectifier and G-
 protein coupled K+ channels in the brain."
 RL FEBS Lett. 353:37-42(1994).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM GIRK2A).
 RC TISSUE=Brain;
 RX MEDLINE=96081927; PubMed=7499385;
 RA Lesage F., Guillemare E., Fink M., Duprat F., Heurteaux C.,
 RA Fosset M., Roney G., Barhanin J., Lazdunski M.;
 RT "Molecular properties of neuronal G-protein-activated inwardly
 rectifying K+ channels."
 RL J. Biol. Chem. 270:28660-28667(1995).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM GIRK2B).
 RC TISSUE=Brain;
 RX MEDLINE=96136315; PubMed=8573147;
 RA Isomoto S., Kondo C., Takahashi N., Matsumoto S., Yamada M.,
 RA Takumi T., Horio Y., Kurachi Y.;
 RT "A novel ubiquitously distributed isoform of GIRK2 (GIRK2B) enhances
 GIRK1 expression of the G-protein-gated K+ current in Xenopus
 oocytes."
 RT Biochem. Biophys. Res. Commun. 218:286-291(1996).
 RF [4]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC STRAIN=129/Svj;
 RX MEDLINE=98389623; PubMed=9721208;
 RA Wei J., Hodes M.E., Piva R., Feng Y., Wang Y., Ghetti B., Dlouhy S.R.;
 RT "Characterization of murine Kir2 transcript isoforms: structure and
 differential expression."
 RL Genomics 51:379-390(1998).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM GIRK2D).
 RA Inanobe A., Horio Y., Fujita A., Tanemoto M., Kurachi Y.;
 RT "Molecular cloning and characterization of a novel splicing variant of
 Kir2.2/GIRK2 predominantly expressed in mouse testis."
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP VARIANT WEAVER.
 RX MEDLINE=96024646; PubMed=7550338;
 RA Patil N., Cox D.R., Bhat D., Faham M., Myers R.M., Peterson A.S.;
 RT "A potassium channel mutation in weaver mice implicates membrane
 excitability in granule cell differentiation."
 RL Nat. Genet. 11:126-129(1995).
 CC -!- FUNCTION: THIS POTASSIUM CHANNEL IS CONTROLLED BY G PROTEINS. IT
 CC PLAYS A ROLE IN GRANULE CELL DIFFERENTIATION, POSSIBLY VIA
 CC MEMBRANE HYPERPOLARIZATION. INWARD RECTIFIER K+ CHANNELS ARE
 CC CHARACTERIZED BY A GREATER TENDENCY TO ALLOW POTASSIUM TO FLOW
 CC INTO THE CELL RATHER THAN OUT OF IT. THEIR VOLTAGE DEPENDENCE IS
 CC REGULATED BY THE CONCENTRATION OF EXTRACELLULAR POTASSIUM; AS
 CC EXTERNAL K+ IS RAISED, THE VOLTAGE RANGE OF THE CHANNEL OPENING
 CC SHIFTS TO MORE POSITIVE VOLTAGES. THE INWARD RECTIFICATION IS
 CC MAINLY DUE TO THE BLOCKAGE OF OUTWARD CURRENT BY INTERNAL
 CC MAGNESIUM.
 CC -!- SUBUNIT: MAY ASSOCIATE WITH GIRK1 OR GIRK4 TO FORM A G-PROTEIN-
 CC ACTIVATED HETEROMULTIMER PORE-FORMING UNIT. THE RESULTING INWARD
 CC CURRENT IS MUCH LARGER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC Event-Alternative splicing; Named isoforms=5;
 CC Comment-Additional isoforms seem to exist;
 CC Name=GIRK2A;
 CC IsoId=P48542-1; Sequence=Displayed;
 CC Name=GIRK2-1;
 CC IsoId=P48542-2; Sequence=VSP_002803;
 CC Name=GIRK2B;
 CC IsoId=P48542-3; Sequence=VSP_002804, VSP_002805;
 CC Name=GIRK2C;
 CC IsoId=P48542-4; Sequence=VSP_002806, VSP_002807, VSP_002808;
 CC Name=GIRK2D; Synonyms=KIR3.2D;
 CC IsoId=P48542-5; Sequence=Not described;
 CC -!- TISSUE SPECIFICITY: CEREBELLUM, TESTES, CORTEX, AND SUBSTENTIA
 CC NIGRA.
 CC -!- DISEASE: DEFECTS IN KCNJ6 ARE THE CAUSE OF WEAVER (WV). HOMOZYGOUS
 CC ANIMALS SUFFER FROM SEVERE ATAXIA THAT IS OBVIOUS BY ABOUT THE
 CC SECOND POSTNATAL WEEK. THE CEREBELLUM OF THESE ANIMALS IS
 CC DRASTICALLY REDUCED IN SIZE DUE TO DEPLETION OF THE MAJOR CELL
 CC TYPE OF CEREBELLUM, THE GRANULE CELL NEURON. HETEROZYGOUS ANIMALS
 CC ARE NOT ATAXIC BUT HAVE AN INTERMEDIATE NUMBER OF SURVIVING
 CC GRANULE CELLS. MALE HOMOZYGOES ARE STERILE, BECAUSE OF COMPLETE
 CC FAILURE OF SPERM PRODUCTION. BOTH HETERO- AND HOMOZYGOUS ANIMALS
 CC UNDERGO SPORADIC TONIC-CLONIC SEIZURES.
 CC -!- SIMILARITY: BELONGS TO THE INWARD RECTIFIER-TYPE K+ CHANNEL
 CC FAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC EMBL; U37253; AAA91457.1; -;
 CC EMBL; U11859; AAA53245.1; -;
 CC EMBL; U51122; AAC34141.1; -;
 CC EMBL; U51123; AAC34142.1; -;

DR EMBL; U51124; AAC34143.1; --
 DR EMBL; U51125; AAC34144.1; --
 DR EMBL; U51126; AAC34145.1; --
 DR EMBL; AF040047; AAC34286.1; --
 DR EMBL; AF040047; AAC34286.1; JOINED.
 DR EMBL; AF040050; AAC34287.1; --
 DR EMBL; AF040049; AAC34287.1; JOINED.
 DR EMBL; AF040051; AAC34285.1; --
 DR EMBL; AF040047; AAC34285.1; JOINED.
 DR EMBL; AF040049; AAC34285.1; JOINED.
 DR EMBL; AF040052; AAC34284.1; --
 DR EMBL; AF040047; AAC34284.1; JOINED.
 DR EMBL; AF040049; AAC34284.1; JOINED.
 DR EMBL; D86040; BAA12972.1; --
 DR EMBL; AB029502; BAA88430.1; --
 DR PIR; S48738; S48738.
 DR MGD; MGI:104781; Kcnj6.
 DR GO; GO:0013467; F1G-protein activated inward rectifier potass. . . ; IDA.
 DR InterPro; IPR001838; K-channel_IR.
 DR Pfam; PF01007; IRK; 1.
 DR PRINTS; PR01320; KIRCHANNEL.
 DR ProDom; PD001103; K-channel_IR; 2.
 KW Ionic channel; Ion transport; Voltage-gated channel; Transmembrane;
 KW Alternative splicing; Disease mutation; Potassium transport.
 FT DOMAIN 1 96 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 97 119 M1 (POTENTIAL).
 FT DOMAIN 144 160 H5 (Pore-forming) (POTENTIAL).
 FT TRANSMEM 169 193 M2 (POTENTIAL).
 FT DOMAIN 194 425 INTRACELLULAR MAGNESIUM (BY SIMILARITY).
 FT SITE 184 184 Missing (in isoform GIRK2-1).
 FT VARSPLIC 415 425 /FTID=VSP_002803.
 FT VARSPLIC 319 327 MTCQARSSY -> KMGFALGFL (in isoform GIRK2B).
 FT VARSPLIC 328 425 /FTID=VSP_002804.
 FT VARSPLIC 1 18 Missing (in isoform GIRK2B).
 FT VARSPLIC 319 320 MT -> QF (in isoform GIRK2C).
 FT VARSPLIC 321 425 /FTID=VSP_002807.
 FT VARSPLIC 156 156 /FTID=VSP_002808.
 FT VARSPLIC 313 313 G -> S (IN WEAVER).
 FT VARSPLIC 344 344 I -> M.
 FT VARSPLIC 67 67 M -> L.
 FT CONFLICT 260 260 V -> C (IN REF. 3 AND 4).
 FT CONFLICT 381 381 S -> T (IN REF. 5).
 FT CONFLICT 381 381 V -> L (IN REF. 5).
 SQ SEQUENCE 425 AA; 48651 MW; 285153DCB1B60331 CRC64;
 Query Match 17.2%; Score 63.5; DB 1; Length 425;
 Best Local Similarity 31.1%; Pred. No. 23;
 Matches 19; Conservative 12; Mismatches 23; Indels 7; Gaps 3;
 QY 1 KSKTPEPKKEVTKANLIYAGKTKQTAEKGTFTPEATAT---AVRYADLLAKENGKTV 57
 Db 296 KAQLPKKELEIVILLEGIVEATG--MTCQARSSY--ITSEILWGYRFTPLVLTWEDGFYEV 351
 QY 58 D 58
 Db 352 D 352
 RESULT 13
 IRK6 RAT
 ID IRK6 RAT
 AC P48550; STANDARD; PRT; 425 AA.
 DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE G protein-activated inward rectifier potassium channel 2 (GIRK2)
 DE (Potassium channel, inwardly rectifying, subfamily J, member 6)
 DE (Inward rectifier K+ channel Kir3.2) (KATP-2) (BIR1).
 GN KCNJ6 OR KCNJ7 OR GIRK2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]_TaxID=10116;
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=95324735; PubMed=7601286;
 RA Bond C.T., Aemmelae C., Ashfield R., Blair T.A., Gribble F.,
 RA Khan R.N., Lee K., Proks P., Rowe I.C.M., Sakura H., Ashford M.J.,
 RA Adelman J.P., Ashcroft P.M.;
 RT "Cloning and functional expression of the cDNA encoding an inwardly-
 RT rectifying potassium channel expressed in pancreatic beta-cells and
 RT in the brain.";
 RL FEBS Lett. 367:61-66 (1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95352112; PubMed=7626127;
 RA Stoffel M., Tokuyama Y., Trabb J.B., German M.S., Tsaar M.L.,
 RA Jan L.Y., Polonsky K.S., Bell G.I.;
 RT "Cloning of rat KATP-2 channel and decreased expression in pancreatic
 RT islets of male Zucker diabetic fatty rats.";
 RL Biochem. Biophys. Res. Commun. 212:894-899 (1995).
 CC -!- FUNCTION: THIS POTASSIUM CHANNEL IS CONTROLLED BY G PROTEINS. IT
 CC MAY BE INVOLVED IN THE REGULATION OF INSULIN SECRETION BY GLUCOSE
 CC AND/OR NEUROTRANSMITTERS. INWARD RECTIFIER K+ CHANNELS ARE
 CC CHARACTERIZED BY A GREATER TENDENCY TO ALLOW POTASSIUM TO FLOW
 CC INTO THE CELL RATHER THAN OUT OF IT. THEIR VOLTAGE DEPENDANCE IS
 CC REGULATED BY THE CONCENTRATION OF EXTRACELLULAR POTASSIUM; AS
 CC EXTERNAL K+ IS RAISED, THE VOLTAGE RANGE OF THE CHANNEL OPENING
 CC SHIFTS TO MORE POSITIVE VOLTAGES. THE INWARD RECTIFICATION IS
 CC MAINLY DUE TO THE BLOCKAGE OF OUTWARD CURRENT BY INTERNAL
 CC MAGNESIUM. CAN BE BLOCKED BY EXTERNAL BA2+ OR CS+.
 CC -!- SUBUNIT: ASSOCIATES WITH GIRK1 OR GIRK4 TO FORM A G-PROTEIN-
 CC ACTIVATED HETEROMULTIMER PORE-FORMING UNIT. THE RESULTING INWARD
 CC CURRENT IS MUCH LARGER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: PANCREATIC BETA-CELLS AND BRAIN.
 CC -!- SIMILARITY: BELONGS TO THE INWARD RECTIFIER-TYPE K+ CHANNEL
 CC FAMILY.
 CC -----
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 CC -----
 CC EMBL; X83583; CAA58566.1; --
 DR EMBL; U21087; AAA87002.1; --
 DR PIR; S66266; S52852.
 DR InterPro; IPR001838; K-channel_IR.
 DR InterPro; IPR001622; K-channel_pore.
 DR Pfam; PF01007; IRK; 1.
 DR PRINTS; PR01320; KIRCHANNEL.
 DR ProDom; PD001103; K-channel_IR; 2.
 KW Ionic channel; Ion transport; Voltage-gated channel; Transmembrane;
 KW Potassium transport.
 FT DOMAIN 1 96 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 97 119 M1 (POTENTIAL).
 FT DOMAIN 144 160 H5 (Pore-forming) (POTENTIAL).
 FT TRANSMEM 169 193 M2 (POTENTIAL).
 FT DOMAIN 194 425 CYTOPLASMIC (POTENTIAL).
 FT SITE 184 184 ROLE IN THE CONTROL OF POLYAMINE-MEDIATED
 FT CHANNEL GATING AND IN THE BLOCKING BY
 FT INTRACELLULAR MAGNESIUM (BY SIMILARITY).

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FT CONFLICT 328 328 V -> I (IN REF. 2).
FT CONFLICT 360 360 H -> Y (IN REF. 2).
SQ SEQUENCE 425 AA; 48639 MW; 66CE9599AAAE38D3 CRC64;

Query Match
Best Local Similarity 17.2%; Score 63.5; DB 1; Length 425;
Matches 19; Conservative 12; Mismatches 23; Indels 7; Gaps 3;

QY 1 KEKTPPEKEEVTKANLYADGKTOTAPFKGTFEATAE--AVRYADLLAKENGKVTY 57
Db 296 KAQLPKEELEIVVLEGWVEATG--MTCQARSY--VTSEILWGRFTPTVLEDFYEV 351
QY 58 D 58
Db 352 D 352

RESULT 14
A10B HUMAN
ID A10B HUMAN STANDARD; PRT; 1461 AA.
AC O94823; O9H725;
DC 30-MAY-2000 (Rel. 39, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DE Potential phospholipid-transporting ATPase VB (EC 3.6.3.1).
GN ATP10B OR ATPVB OR KIAA0715.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A. (ISOFORM B).
RC TISSUE=Amygdala;
RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
RA Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saiki K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshina A., Sugiyama A.,
RA Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
RA Isogai T.;
RA "NEDO human cDNA sequencing project.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A. (ISOFORM C).
RC TISSUE=Colon;
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,
RA Tanaka T., Nakamura Y., Isogai T., Sugano S.;
RA "NEDO human cDNA sequencing project.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RA Rowen L., Madan A., Qin S., Abbasi N., Baradarani L., Birditt B.,
RA Bloom S., Dors M., Fleethoff R., Fleetwood P., Harrison G., James R.,
RA Kaur A., Madan A., Owen M.P., Ratcliffe A., Shaffer T., Hood L.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE OF 548-1461 FROM N.A. (ISOFORM A).
RC TISSUE=Brain;
RX MEDLINE=99087487; PubMed=9872452;
RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Miyajima N.,
RA Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XI.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro."
RL DNA Res. 5:277-286(1998).
CC -1- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=A;
CC IsoId=O94823-1; Sequence=Displayed;

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CC Name=B;
CC IsoId=O94823-2; Sequence=VSP_007306, VSP_007307;
CC Note=No experimental confirmation available;
CC Name=C;
CC IsoId=O94823-3; Sequence=VSP_007305, VSP_007306, VSP_007307;
CC Note=No experimental confirmation available;
CC -1- TISSUE SPECIFICITY: Found in brain and in low levels in testis.
CC -1- SIMILARITY: Belongs to the cation transport ATPases family (P-type
CC ATPases). Subfamily IV.
CC
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CC
CC EMBL; AK090832; BAC03528.1; -
CC EMBL; AK025130; BAB15074.1; -
CC EMBL; AC008456; -; NOT ANNOTATED_CDS.
CC EMBL; AB018258; BAA34435.1; -
CC Genew; HGNC:13543; ATP10B.
CC InterPro; IPR001757; ATPase_E1-E2.
CC TIGRFAMs; TIGR01652; ATPase_P-type; 1.
CC TIGRFAMs; TIGR01494; ATPase_P-type; 4.
CC PROSITE; PS00154; ATPASE_E1_E2; 1.
CC Hydrolyase; Transmembrane; Phosphorylation; Magnesium; ATP-binding;
KW Multigene family; Alternative splicing.
FT DOMAIN 1 82
FT TRANSMEM 83 104
FT DOMAIN 105 110
FT TRANSMEM 111 132
FT DOMAIN 133 316
FT TRANSMEM 317 338
FT DOMAIN 339 368
FT TRANSMEM 369 390
FT DOMAIN 391 1111
FT TRANSMEM 1112 1132
FT DOMAIN 1133 1144
FT TRANSMEM 1145 1164
FT DOMAIN 1165 1194
FT TRANSMEM 1195 1216
FT DOMAIN 1217 1223
FT TRANSMEM 1224 1246
FT DOMAIN 1247 1252
FT TRANSMEM 1253 1273
FT DOMAIN 1274 1291
FT TRANSMEM 1292 1316
FT DOMAIN 1317 1461
FT MOD_RES 433 433
FT METAL 1055 1055
FT METAL 1059 1059
FT VARSPLIC 1 156
FT
FT VARSPLIC 461 529
FT
FT VARSPLIC 530 1461
FT
FT CONFLICT 217 217
FT CONFLICT 234 234
FT

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SQ SEQUENCE. 1461 AA; 165390 MW; 2676B90416B6B541 CRC64;
 Query Match 17.2%; Score 63.5; DB 1; Length 1461;
 Best Local Similarity 40.5%; Pred. No. 86;
 Matches 17; Conservative 5; Mismatches 19; Indels 1; Gaps 1;
 QY 3 KTPPEPKKEVTIKANLIYADKGTQTAEPKGTPEETAAYRY 44
 DB 981 KTPSITSEAVPAGLV-IDGKTLNAIFQCKLEKLELTQY 1021
 RESULT 15
 UN89_CABEL STANDARD; PRT; 6632 AA.
 AC O01761; Q17362;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Muscle M-line assembly protein unc-89 (Uncoordinated protein 89).
 GN UNC-89 OR C09D1.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
 RC STRAIN=Bristol N2;
 RX MEDLINE=96180278; PubMed=8603916;
 RA Benian G.M., Tinley T.L., Tang X., Borodovsky M.;
 RT "The Caenorhabditis elegans gene unc-89, required for muscle M-line
 assembly, encodes a giant modular protein composed of Ig and signal
 transduction domains."
 RL J. Cell Biol. 132:835-848(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Du Z., Le T.T., Wilson R.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP REVISIONS.
 RA Waterston R.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Structural component of the muscle M-line. Myofibrillar
 lattice assembly begins with positional cues laid down in the
 basement membrane and muscle cell membrane. UNC-89 responds to
 these signals, localizes, and then participates in assembling an
 M-line.
 CC -!- TISSUE SPECIFICITY: Localizes to the middle of A-bands.
 CC -!- SIMILARITY: Contains 1 DBL-homology (DH) domain.
 CC -!- SIMILARITY: Contains 1 fibronectin type III domain.
 CC -!- SIMILARITY: Contains 49 immunoglobulin-like C2-type domains.
 CC -!- SIMILARITY: Contains 1 PH domain.
 CC -!- SIMILARITY: Contains 5 RCSD domains.
 CC -!- SIMILARITY: Contains 1 SH3 domain.
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 CC -----
 DR EMBL; U33058; AAB00542.1; --
 DR EMBL; AF003131; AAB54132.2; --
 DR PDB; 1FHO; 20-DEC-00.
 DR WormPep; C09D1.1; CE30426.
 DR InterPro; IPR003961; FN III.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR001849; PH.
 DR InterPro; IPR007850; RCSD.
 DR InterPro; IPR000219; RhoGEF.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF00041; fn3; 1.
 DR Pfam; PF00047; ig; 47.
 DR Pfam; PF00169; PH; 1.
 DR Pfam; PF05177; RCSD; 5.
 DR Pfam; PF00621; RhoGEF; 1.
 DR Pfam; PF00018; SH3; 1.
 DR SMART; SM00408; IGC2; 23.
 DR SMART; SM00325; RhoGEF; 1.
 DR SMART; SM00326; SH3; 1.
 DR PROSITE; PS50010; DH_2; 1.
 DR PROSITE; PS50835; IG_LIKE; 49.
 DR PROSITE; PS50003; PH_DOMAIN; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW Muscle protein; Immunoglobulin domain; Repeat; SH3 domain;
 3D-structure.
 FT DOMAIN 63 127 SH3.
 FT DOMAIN 152 330 DH.
 FT DOMAIN 342 498 PH.
 FT DOMAIN 547 633 IG-LIKE C2-TYPE 1.
 FT DOMAIN 648 736 IG-LIKE C2-TYPE 2.
 FT DOMAIN 748 838 IG-LIKE C2-TYPE 3.
 FT DOMAIN 946 1033 IG-LIKE C2-TYPE 4.
 FT DOMAIN 1044 1132 IG-LIKE C2-TYPE 5.
 FT DOMAIN 1140 1227 IG-LIKE C2-TYPE 6.
 FT DOMAIN 1272 1315 THR-RICH.
 FT DOMAIN 1375 1475 RCSD 1.
 FT DOMAIN 1479 1585 RCSD 2.
 FT DOMAIN 1597 1799 RCSD 3.
 FT DOMAIN 1700 1799 RCSD 4.
 FT DOMAIN 1800 1860 RCSD 5.
 FT DOMAIN 1982 2067 IG-LIKE C2-TYPE 7.
 FT DOMAIN 2071 2163 IG-LIKE C2-TYPE 8.
 FT DOMAIN 2171 2261 IG-LIKE C2-TYPE 9.
 FT DOMAIN 2289 2359 IG-LIKE C2-TYPE 10.
 FT DOMAIN 2367 2455 IG-LIKE C2-TYPE 11.
 FT DOMAIN 2463 2564 IG-LIKE C2-TYPE 12.
 FT DOMAIN 2563 2651 IG-LIKE C2-TYPE 13.
 FT DOMAIN 2657 2746 IG-LIKE C2-TYPE 14.
 FT DOMAIN 2754 2858 IG-LIKE C2-TYPE 15.
 FT DOMAIN 2887 2980 IG-LIKE C2-TYPE 16.
 FT DOMAIN 2994 3081 IG-LIKE C2-TYPE 17.
 FT DOMAIN 3087 3183 IG-LIKE C2-TYPE 18.
 FT DOMAIN 3189 3280 IG-LIKE C2-TYPE 19.
 FT DOMAIN 3286 3376 IG-LIKE C2-TYPE 20.
 FT DOMAIN 3384 3469 IG-LIKE C2-TYPE 21.
 FT DOMAIN 3482 3572 IG-LIKE C2-TYPE 22.
 FT DOMAIN 3580 3667 IG-LIKE C2-TYPE 23.
 FT DOMAIN 3686 3777 IG-LIKE C2-TYPE 24.
 FT DOMAIN 3817 3908 IG-LIKE C2-TYPE 25.
 FT DOMAIN 3920 4009 IG-LIKE C2-TYPE 26.
 FT DOMAIN 4018 4106 IG-LIKE C2-TYPE 27.
 FT DOMAIN 4109 4201 IG-LIKE C2-TYPE 28.
 FT DOMAIN 4212 4297 IG-LIKE C2-TYPE 29.
 FT DOMAIN 4302 4387 IG-LIKE C2-TYPE 30.
 FT DOMAIN 4400 4485 IG-LIKE C2-TYPE 31.
 FT DOMAIN 4489 4580 IG-LIKE C2-TYPE 32.
 FT DOMAIN 4588 4678 IG-LIKE C2-TYPE 33.
 FT DOMAIN 4681 4771 IG-LIKE C2-TYPE 34.
 FT DOMAIN 4873 4961 IG-LIKE C2-TYPE 35.
 FT DOMAIN 4965 5057 IG-LIKE C2-TYPE 36.
 FT DOMAIN 5067 5160 IG-LIKE C2-TYPE 37.
 FT DOMAIN 5171 5260 IG-LIKE C2-TYPE 38.
 FT DOMAIN 5277 5366 IG-LIKE C2-TYPE 39.
 FT DOMAIN 5383 5472 IG-LIKE C2-TYPE 40.
 FT DOMAIN 5487 5578 IG-LIKE C2-TYPE 41.
 FT DOMAIN 5595 5685 IG-LIKE C2-TYPE 42.
 FT DOMAIN 5701 5790 IG-LIKE C2-TYPE 43.
 FT DOMAIN 5815 5904 IG-LIKE C2-TYPE 44.
 FT DOMAIN 5925 6014 IG-LIKE C2-TYPE 45.
 FT DOMAIN 6038 6130 IG-LIKE C2-TYPE 46.
 FT DOMAIN 6150 6239 IG-LIKE C2-TYPE 47.

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FT DOMAIN 6275 6368 FIBRONECTIN TYPE-III.
FT DOMAIN 6413 6502 IG-LIKE C2-TYPE 48.
FT DOMAIN 6507 6596 IG-LIKE C2-TYPE 49.
FT DISULFID 568 621 POTENTIAL.
FT DISULFID 2908 2975 POTENTIAL.
FT DISULFID 3015 3065 POTENTIAL.
FT DISULFID 3707 3759 POTENTIAL.
FT DISULFID 3826 3890 POTENTIAL.
FT DISULFID 5092 5157 POTENTIAL.
FT DISULFID 5298 5350 POTENTIAL.
FT DISULFID 5508 5560 POTENTIAL.
FT DISULFID 5616 5669 POTENTIAL.
FT DISULFID 5722 5764 POTENTIAL.
FT DISULFID 5836 5901 POTENTIAL.
FT DISULFID 5946 5998 POTENTIAL.
FT DISULFID 6036 6171 POTENTIAL.
FT DISULFID 6421 6486 POTENTIAL.
FT CONFLICT 2137 2137 A -> P (IN REF. 1).
FT CONFLICT 2245 2247 AKA -> PKP (IN REF. 1).
FT CONFLICT 2258 2258 A -> P (IN REF. 1).
FT CONFLICT 2284 2284 E -> G (IN REF. 1).
FT CONFLICT 2297 2297 M -> I (IN REF. 1).
FT CONFLICT 3531 3531 A -> G (IN REF. 1).
FT CONFLICT 3884 3888 DAGEY -> RRRRI (IN REF. 1).
FT CONFLICT 3929 3929 A -> V (IN REF. 1).
FT CONFLICT 5134 5134 A -> P (IN REF. 1).
FT CONFLICT 5145 5145 T -> S (IN REF. 1).
FT CONFLICT 5185 5185 G -> A (IN REF. 1).
FT CONFLICT 5199 5199 K -> N (IN REF. 1).
FT CONFLICT 5202 5202 L -> F (IN REF. 1).
FT CONFLICT 5213 5213 F -> L (IN REF. 1).
FT CONFLICT 6178 6178 A -> G (IN REF. 1).
FT CONFLICT 6268 6268 K -> E (IN REF. 1).
SQ SEQUENCE 6632 AA; 731665 MW; 262D3EDD62960E89 CRC64;
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Query Match 17.1%; Score 63; DB 1; Length 6632;
Best Local Similarity 30.6%; Pred. No. 4.9e+02;
Matches 26; Conservative 12; Mismatches 33; Indels 14; Gaps 4;

Qy 2 EKTPEEPKEVTIKANLIY----ADGK-TQTAEFKGTFEATAEAYRYADLLAKENGK-- 54
Db 2112 EKIVESRTITTIKTEDVYTLKISNAKIEQTGVTKVTAQNSAGQDSKQADLKVEPNVKAP 2171

Qy 55 -----YTVDVADKGYTL--NIKPAQ 72
Db 2172 KFKSQLTDKVADEGEPLRWNLDDG 2196
```

Search completed: September 3, 2003, 11:20:06
Job time : 11.1233 secs

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:14:37 ; Search time 17.0137 Seconds
(without alignments)
406.975 Million cell updates/sec

Title: US-08-325-278b-1_COPY_153_224

Perfect score: 369

Sequence: 1 KEKTPPEPKKEVTIKANLIY.....GKYTVDVADKGYTLNIKFPAG 72

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_76.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	369	100.0	455	A45063	immunoglobulin-bin
2	369	100.0	719	A42808	Ig light chain-bin
3	315	85.4	992	S54396	protein L precursor
4	162	43.9	74	A34483	Ig light chain-bin
5	82.5	22.4	1576	AE0249	probable hemolysin
6	80.5	21.8	395	A43700	BNS1 protein - hum
7	74	20.1	871	D86355	protein T16E15.12
8	73.5	19.9	256	S54803	merozoite surface
9	72	19.5	1025	E86355	hypothetical prote
10	69	18.7	324	T37931	hypothetical coile
11	68	18.4	448	B48782	late embryogenesis
12	67	18.2	953	H30169	leukotoxin A - Pas
13	66.5	18.0	657	AD1525	probable cell surf
14	66	17.9	448	JC6171	late embryogenesis
15	66	17.9	470	AF2828	PAD dependent oxid
16	66	17.9	477	D97606	glycolate oxidase
17	65.5	17.8	436	T16638	hypothetical prote
18	65.5	17.8	476	1 WZEC	tryptophanase (EC
19	65.5	17.8	476	E91209	tryptophanase (imp
20	65.5	17.8	476	H86055	tryptophanase (imp
21	65.5	17.8	1179	T35093	DNA-directed DNA p
22	65.5	17.8	4558	C82199	RTX toxin RtxA Vcl
23	65	17.6	636	D70184	methyl-accepting c
24	65	17.6	838	D71492	hypothetical prote
25	64.5	17.5	621	D72719	hypothetical prote
26	64	17.3	243	S49020	nuclear lamin C pr
27	64	17.3	722	T21521	hypothetical prote
28	63.5	17.2	414	D48738	potassium channel
29	63.5	17.2	425	S52852	inward rectifier p

ALIGNMENTS

RESULT 1

A45063

immunoglobulin-binding protein LG - Peptostreptococcus magnus

C:Species: Peptostreptococcus magnus

C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 15-Oct-1999

C:Accession: A45063

R:Kihlberg, B.M.; Sjoerding, U.; Kastern, W.; Bjorck, L.

J. Biol. Chem. 267, 25583-25588, 1992

A:Title: Protein LG: a hybrid molecule with unique immunoglobulin binding properties.

A:Reference number: A45063; MUID:93094283; PMID:1460053

A:Accession: A45063

A:Status: preliminary

A:Molecule type: mRNA; protein

A:Residues: 1-455 <KH>

A:Cross-references: GB:S50809; NID:G261705; PIDN:AAA03280.1; PID:G261706

A:Note: sequence extracted from NCBI backbone (NCBIN:120302, NCBIPI:120303)

Query Match 100.0%; Score 369; DB 2; Length 455;

Best Local Similarity 100.0%; Pred. No. 6.8e-31;

Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEKTPPEPKKEVTIKANLIYADGKTQTAFKGTTEATAEAYRYADLAKENGKVTVDVA 60

Db |||||

174 KEKTPPEPKKEVTIKANLIYADGKTQTAFKGTTEATAEAYRYADLAKENGKVTVDVA 233

QY 61 DKGVTLNKFPAG 72

Db |||||

234 DKGVTLNKFPAG 245

RESULT 2

A42808

Ig light chain-binding protein precursor - Peptostreptococcus magnus

N:Alternate names: protein L

C:Species: Peptostreptococcus magnus

C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999

C:Accession: A42808; A41493

R:Kastern, W.; Sjoerding, U.; Bjorck, L.

J. Biol. Chem. 267, 12820-12825, 1992

A:Title: Structure of peptostreptococcal protein L and identification of a repeated immu

A:Reference number: A42808; MUID:92316971; PMID:1618782

A:Accession: A42808

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-719 <KAS>

A:Cross-references: GB:M86697

R:Kastern, W.; Holst, E.; Nielsen, E.; Sjoerding, U.; Bjorck, L.

Infect. Immun. 58, 1217-1222, 1990

A:Title: Protein L, a bacterial immunoglobulin-binding protein and possible virulence de

A:Reference number: A41493; MUID:90215984; PMID:2108927

A:Accession: A41493

A:Status: preliminary

30 63.5 17.2 479 2 T47561 late embryogenesis
31 63 17.1 88 2 C83657 hypothetical prote
32 63 17.1 319 2 E89872 hypothetical prote
33 63 17.1 693 2 H95255 choline binding pr
34 63 17.1 6642 2 T29757 protein UNC-89 - C
35 62.5 16.9 423 2 I38979 inward rectifier p
36 62.5 16.9 425 2 I48202 potassium channel-
37 62 16.8 118 2 S38717 Ig heavy chain V r
38 62 16.8 195 2 A70247 conserved hypother
39 62 16.8 356 2 T37136 hypothetical prote
40 62 16.8 529 2 S62194 hypothetical prote
41 62 16.8 1612 2 A81347 probable peptidogl
42 61.5 16.7 266 2 A12289 hypothetical prote
43 61.5 16.7 280 2 S35103 bone sialoprotein
44 61.5 16.7 451 1 D64424 tLd homolog MJ099
45 61.5 16.7 487 2 T10215 hypothetical prote

A:Molecule type: DNA

A:Residues: 202-275 <KA2>

C:Keywords: immunoglobulin

Query Match 100.0%; Score 369; DB 2; Length 719;
Best Local Similarity 100.0%; Pred. No. 1.1e-30;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEKTPPEKPEVTIKANLIYADGKTQTAEFGKTFPEATAEAYRYADLLAKENGKTYVDVA 60
Db 246 KEKTPPEKPEVTIKANLIYADGKTQTAEFGKTFPEATAEAYRYADLLAKENGKTYVDVA 305

QY 61 DKGYTLNIKFPAG 72

Db 306 DKGYTLNIKFPAG 317

RESULT 3

S54396

protein L precursor - Peptostreptococcus magnus (strain 3316)

C:Species: Peptostreptococcus magnus

A:Variety: strain 3316

C>Date: 27-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 15-Oct-1999

C:Accession: S54396

R:Murphy, J.P.; Duggleby, C.J.; Atkinson, M.A.; Trowern, A.R.; Atkinson, T.; Goward, C.R.

Mol. Microbiol. 12, 911-920, 1994

A:Title: The functional units of a peptostreptococcal protein L.

A:Reference number: S54396; MUID:95020613; PMID:7934898

A:Accession: S54396

A>Status: preliminary; nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-992 <MUR>

A:Cross-references: EMBL:L04466; NID:gl50673; PIDN:AAA67503.1; PID:gl50674

Query Match

Best Local Similarity 85.4%; Score 315; DB 2; Length 992;

Matches 60; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 3 KTEPEKPEVTIKANLIYADGKTQTAEFGKTFPEATAEAYRYADLLAKENGKTYVDVADK 62
Db 468 ETEPEKPEVTIKANLIYADGKTQTAEFGKTFPEATAEAYRYADLLAKENGKTYVDVADK 527

QY 63 GYTINIKFPAG 72

Db 528 GYTINIKFPAG 537

RESULT 4

A34483

Ig light chain-binding protein L - Peptostreptococcus magnus (fragments)

C:Species: Peptostreptococcus magnus

C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 16-Aug-1996

C:Accession: A34483

R:Akerstroem, B.; Bjoerck, L.

J. Biol. Chem. 264, 19740-19746, 1989

A:Title: Protein L: an immunoglobulin light chain-binding bacterial protein. Characteriz

A:Reference number: A34483; MUID:90062074; PMID:2479638

A:Accession: A34483

A:Molecule type: protein

A:Residues: 1-74 <AKB>

C:Keywords: immunoglobulin

Query Match

Best Local Similarity 43.9%; Score 162; DB 2; Length 74;

Matches 35; Conservative 3; Mismatches 2; Indels 16; Gaps 1;

QY 2 EKTPEKPEVTIKANLIYADGKTQTAEFGKTFPEATAEAYRYADLLAKENGKTYVDVA 41

Db 9 ETTPEKPEVTIKANLIYADGKTQTAEFGKTFPEATAEAYRYADLLAKENGKTYVDVA 64

RESULT 5

AS0249

protein T16B15.12 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: D86355

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.

probable hemolysin YPO2045 [imported] - Yersinia pestis (strain CO92)

C:Species: Yersinia pestis

C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001

C:Accession: AS0249

R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;

il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,

Nature 413, 523-527, 2001

A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A:Reference number: AS0001; MUID:21470413; PMID:11586360

A:Accession: AS0249

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1576 <KUR>

A:Cross-references: GB:AL590842; PIDN:CAC50857.1; PID:gl5980056; GSPDB:GN00175

C:Genetics:

A:Gene: YPO2045

Query Match

Best Local Similarity 22.4%; Score 82.5; DB 2; Length 1576;

Matches 30; Conservative 9; Mismatches 27; Indels 43; Gaps 4;

QY 1 KEKTPPEKPEVTIKANLIYADGKTQTAEFGKTFPEATAEAYRYADLLAKENGKTYVDVADK 36

Db 1001 KANTTEQEKGEVSLRG-----GMTATQEIKGHLGVKAETSGDSYAEMLVGNINAKSG 1054

QY 37 ----ATAEAYRYADLLAKENGKTYVD-----VADKGYTLNIKFPAG 72

Db 1055 VSIKTTGDYYYATNIEGGNGDITIDAGNNLYFDQVDSQRSSNIKFSG 1103

RESULT 6

A43700

EN51 protein - human

C:Species: Homo sapiens (man)

C>Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 21-Jul-2000

C:Accession: A43700

R:Ittmann, M.; Greco, A.; Basilico, C.

Mol. Cell. Biol. 7, 3386-3393, 1987

A:Title: Isolation of the human gene that complements a temperature-sensitive cell cycle

A:Reference number: A43700; MUID:88065472; PMID:3683386

A:Accession: A43700

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-395 <ITT>

A:Cross-references: GB:ML7754; NID:gl79512; PIDN:AAA51838.1; PID:gl79513

C:Genetics:

A:Gene: GDB:BN51T

A:Cross-references: GDB:119728; OMIM:187280

A:Map position: 8pter-8q24

Query Match

Best Local Similarity 21.8%; Score 80.5; DB 2; Length 395;

Matches 26; Conservative 9; Mismatches 27; Indels 19; Gaps 3;

QY 3 KTEPEKPEVTIKANLIYAD-----GKTQTAEFGKTFPEATAEAYRYADLLAK 50

Db 63 KKEPEKPEVTIKKEKREDRDRQREGHGRRRPEVLIQSHSIFEQPAEMWK-----KK 117

QY 51 ENGKTYVDVADKG--YTINIK 69

Db 118 GNWDKTVDSWDMGSPSHINIK 138

RESULT 7

D86355

protein T16B15.12 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: D86355

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Frazer, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: D86355
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-871 <STO>
A:Cross-references: GB:AE005172; NID:g9392688; PIDN:AP87265.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

Query Match 20.1%; Score 74; DB 2; Length 871;
Best Local Similarity 26.7%; Pred. No. 9.6;
Matches 20; Conservative 16; Mismatches 27; Indels 12; Gaps 2;
QY 3 KTEPEPKERVIT-----KANLIYADGKTOTAEFKGTFEATAEAYRYADLLAKE 51
DB 429 KTSEDKKQSLKLSLESMESEKCEKIQADQARQVEELE-TLQKESHQADLLAKE 487
QY 52 NGKYTVDDVADKGYTL 66
DB 488 VNQLQTVIEKGHVI 502

RESULT 8
S54803
C:Species: Theileria parva
C:Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Sep-1997
C:Accession: S54803
R:Shiels, B.R.; d'Oliviera, C.; McKellar, S.; Ben-Miled, L.; Kawazu, S.; Hide, G.
submitted to the EMBL Data Library, March 1995
A:Description: Selection of diversity at putative glycosylation sites in the immunodominant
A:Reference number: S54803
A:Accession: S54803
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-256 <SHI>
A:Cross-references: EMBL:Z48740; NID:g807986; PID:g807987
C:Keywords: glycoprotein

Query Match 19.9%; Score 73.5; DB 2; Length 256;
Best Local Similarity 31.7%; Pred. No. 2.8;
Matches 19; Conservative 11; Mismatches 29; Indels 1; Gaps 1;
QY 1 KEKTPPEPKERVITKANLIYADGKTOTAEFKGTFEATAEAYRYADLLAKENGKGYTVDA 60
DB 25 EEEKKKKKEDLVDTLSSWENVTSTPAGGTLLKAN-EGYRFTLKVGDGTLINVDTS 83

RESULT 9
E86355
hypothetical protein T16E15.11 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C:Accession: E86355
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Dewar, K.; Dwar, K.;
ansen, N.F.; Hughes, B.; Huizart, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Frazer, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: E86355
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1025 <STO>
A:Cross-references: GB:AE005172; NID:g9392687; PIDN:AP87264.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

Query Match 19.5%; Score 72; DB 2; Length 1025;
Best Local Similarity 26.7%; Pred. No. 19;
Matches 20; Conservative 17; Mismatches 26; Indels 12; Gaps 2;
QY 3 KTEPEPKERVITKANLIYADGKTOTAEFKGTFEATAEAYRYADLLAKE 51
DB 571 RTSEDKKQSLKLSLESMESEKCEKIQADQARQVEELE-TLQKESHQADLLAKE 629
QY 52 NGKYTVDDVADKGYTL 66
DB 630 VNQLQTVIEKGHVI 644

RESULT 10
T37931
hypothetical coiled-coil protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T37931
R:McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Bothe, G.; Pohl, T.
submitted to the EMBL Data Library, August 1999
A:Reference number: Z21755
A:Accession: T37931
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-324 <MCD>
A:Cross-references: EMBL:AL109820; PIDN:CA852567.1; GSPDB:GN00066; SPDB:SPAC1952.03
A:Experimental source: strain 972h-; cosmid cl952
C:Genetics:
A:Gene: SPDB:SPAC1952.03
A:Map position: 1
A:Introns: 144/3

Query Match 18.7%; Score 69; DB 2; Length 324;
Best Local Similarity 28.6%; Pred. No. 11;
Matches 18; Conservative 15; Mismatches 26; Indels 4; Gaps 1;
QY 1 KEKTPPEPKERVITKANLIYADGKTOTAEFKGTFEATAEAYRYADLLAKENGKGYTVDA 60
DB 126 KENTPQQPKSENROKREL-----ERRKAEKMKQSEKQAELESEKQADLLAKNEKKKFSKILE 181
QY 61 DKG 63
DB 182 EAG 184

RESULT 11
H84782
late embryogenesis abundant protein (AtECP63) [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 17-May-2002
C:Accession: H84782
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Frazer, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: H84782
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-448 <STO>
A:Cross-references: GB:AE002093; NID:g4415909; PIDN:AAD20140.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2G36640

probable cell surface protein (LPXTG motif) - *Listeria innocua* (strain Clp1)

C;Species: *Listeria innocua*

C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001

C;Accession: AD1525

C;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, R.; Dominguez-Bernal, G.; Duclaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A;Authors: Kreft, J.; Kuhn, M.; Kunat, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of *Listeria* species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AD1525

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-657 <GLA>

A;Cross-references: GB:AL592022; PIDN:CAC95972.1; PID:g16413192; GSPDB:GN00178

A;Experimental source: strain Clp1262

C;Genetics:

A;Gene: lin0740

Query Match 18.0%; Score 66.5; DB 2; Length 657;

Best Local Similarity 32.5%; Pred. No. 43;

Matches 26; Conservative 6; Mismatches 29; Indels 19; Gaps 5;

QY 1 KEKTPPEPKEEYTIKANLIYADGK----TQTAEFKG-----TFEATAEAYRYADLLAK 50

381 KQVPKAPK---VTVK---YVDDKGKELAPSETFTGFIDDDYTSKTIETYTLVETPAN 433

Db

QY 51 ENKGYTVD--VADKGYYTLNI 68

434 ANGKLTADQQTVNYIYTKNI 453

Db

RESULT 14

JC6171

N;Alternate names: abundant protein - Arabidopsis thaliana late embryogenesis

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 03-Jun-2002

C;Accession: JC6171

K;Yang, H.; Saitou, T.; Kameda, Y.; Harada, H.; Kamada, H.

Gene 184, 83-88, 1997

A;Title: Arabidopsis thaliana ECP63 encoding a LEA protein is located in chromosome 4.

A;Reference number: JC6171; MUID:97169149; PMID:9016956

A;Accession: JC6171

A;Molecule type: mRNA

A;Residues: 1-448 <YAN>

A;Cross-references: DBJ:D64140; NID:g1526423; PIDN:BAAI1017.1; PID:g1526424

C;Comment: This protein is a phosphotyrosine protein which belongs to late embryogenesis

C;Genetics:

A;Gene: AtECP63

A;Map position: 4, south part

C;Superfamily: pea seed biotin-containing protein

C;Keywords: seed

Query Match 17.9%; Score 66; DB 2; Length 448;

Best Local Similarity 26.4%; Pred. No. 32;

Matches 23; Conservative 16; Mismatches 32; Indels 16; Gaps 3;

QY 1 KEKTPPEPKEEYTIKANLIYADGKTQTAEFKGTPEATAE-----AYRYADLL 48

176 KQKTAEKAKETSNTYADKA-KEAKDKTAEKGYKDYTVDKAVEADYTAEKIAEKQKT 234

Db

QY 49 AKENGK---YTVDDVADKGYYTLNIKIFAG 72

235 AEKTYGYKDYTVKEKATEGKDKVTVSKLG 261

Db

RESULT 15

AF2828

FAD dependent oxidoreductase Atu2053 [imported] - *Agrobacterium tumefaciens* (strain C58,

C;Species: *Agrobacterium tumefaciens*

RESULT 13
AD1525

Search completed: September 3, 2003, 11:24:31
Job time : 19.0137 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model.

Run on: September 3, 2003, 11:14:02 ; Search time 44.137 Seconds
(without alignments)
420.957 Million cell updates/sec

Title: US-08-325-278b-1_COPY_153_224

Perfect score: 369

Sequence: 1 KEKTPPEPKKEVTKANLIY.....GKYTVADVADGKGYTLNIKFPAG 72

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:**

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archepa:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	369	100.0	455	2 Q53291	Q53291 streptococc
2	369	100.0	719	2 Q51912	Q51912 peptostrept
3	315	85.4	992	2 Q51918	Q51918 peptostrept
4	88.5	24.0	216	4 Q3BPV7	Q3BPV7 homo sapien
5	88.5	24.0	398	4 Q9BP21	Q9BP21 homo sapien
6	83.5	22.6	398	11 Q9CZ02	Q9CZ02 mus musculu
7	83.5	22.6	398	11 Q91WD1	Q91WD1 mus musculu
8	82.5	22.4	1576	16 Q8ZEV8	Q8ZEV8 yersinia pe
9	74	20.1	871	10 Q9LME2	Q9LME2 arabisdopsi
10	73.5	19.9	256	5 Q27039	Q27039 theileria p
11	73.5	19.9	256	5 Q27029	Q27029 theileria p
12	73.5	19.9	280	5 Q27030	Q27030 theileria p
13	72	19.5	1025	10 Q9LME3	Q9LME3 arabisdopsi
14	71	19.2	265	10 Q23822	Q23822 dunalialla
15	69	18.7	324	3 Q9UUK3	Q9UUK3 schizosacch
16	68	18.4	448	10 Q9SKP0	Q9SKP0 arabisdopsi

17	67.5	18.3	383	5 Q9VTV4	Q9vtv4 drosophila
18	67	18.2	946	2 Q9EV24	Q9ev24 mannheimia
19	67	18.2	953	2 Q9ETX2	Q9etx2 mannheimia
20	67	18.2	953	2 Q9EV29	Q9ev29 pasteurella
21	67	18.2	953	2 Q9EV25	Q9ev25 mannheimia
22	67	18.2	953	2 Q9ETG5	Q9etg5 pasteurella
23	67	18.2	953	2 Q9EV23	Q9ev23 mannheimia
24	67	18.2	953	2 Q9EV34	Q9ev34 pasteurella
25	67	18.2	1204	2 Q8GM76	Q8gm76 haemophilus
26	66.5	18.0	657	16 Q92DS2	Q92ds2 listeria in
27	66	17.9	448	10 Q96246	Q96246 arabisdopsi
28	66	17.9	477	16 Q8UDR8	Q8udr8 agrobacteri
29	66	17.9	1096	2 Q8GM79	Q8gm79 haemophilus
30	66	17.9	1098	2 Q48152	Q48152 haemophilus
31	66	17.9	1498	5 Q8IDP2	Q8idp2 plasmodium
32	65.5	17.8	436	5 Q21481	Q21481 caenorhabdi
33	65.5	17.8	451	2 Q924J9	Q924j9 lactobacill
34	65.5	17.8	476	16 Q8FBV2	Q8fbv2 escherichia
35	65.5	17.8	1167	17 Q8TUJ9	Q8tuj9 methanosarc
36	65.5	17.8	1210	2 Q8GM75	Q8gm75 haemophilus
37	65.5	17.8	1210	2 Q8GM74	Q8gm74 haemophilus
38	65.5	17.8	4545	2 Q9X4W2	Q9x4w2 vibrio chol
39	65.5	17.8	4558	16 Q9KS12	Q9ks12 vibrio chol
40	65	17.6	284	5 Q76174	Q76174 theileria s
41	65	17.6	284	5 Q9TYA5	Q9tya5 theileria s
42	65	17.6	636	16 Q51624	Q51624 borrelia bu
43	65	17.6	838	16 Q84625	Q84625 chlamydia t
44	64.5	17.5	243	17 Q9YFE6	Q9yfe6 aeropyrum p
45	64.5	17.5	333	3 Q9UVE8	Q9uve8 yarrowia li

ALIGNMENTS

RESULT 1

ID	Q53291	PRELIMINARY;	PRT;	455 AA.
AC	Q53291;			
DT	01-NOV-1996 (TrEMBLrel. 01, Created)			
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)			
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)			
DE	Protein LG (Fragment).			
OS	Streptococcus sp.			
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;			
OC	Streptococcus.			
OX	NCBI_TaxID=1306;			
RP	[1]			
RN	SEQUENCE FROM N.A.			
RX	MEDLINE=93094283; PubMed=1460053;			
RA	Kihlberg B.M., Sjobring U., Kastern W., Bjorck L.;			
RT	"Protein LG: a hybrid molecule with unique immunoglobulin binding			
RT	properties."			
RL	J. Biol. Chem. 267:25583-25588(1992).			
DR	EMBL; S50809; AAA03280.1; -			
DR	HSSP; P06654; IFGX.			
DR	InterPro; IPR003147; BL.			
DR	InterPro; IPR000724; Igg_bind_B.			
DR	Pfam; PF02246; BL; 4.			
DR	Pfam; PF01378; Igg_binding_B; 2.			
FT	NON_TER 455 455			
SQ	SEQUENCE 455 AA; 49926 MW; 381FC235BBC8307B CRC64;			

Query Match 100.0%; Score 369; DB 2; Length 455;

Best Local Similarity 100.0%; Pred. No. 2.4e-29;

Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KEKTPPEPKKEVTKANLIYADGKTYQTAEFGTTEATAEAYRAADLLAKENGYTVDA 60

|||||

Db 174 KEKTPPEPKKEVTKANLIYADGKTYQTAEFGTTEATAEAYRAADLLAKENGYTVDA 233

|||||

Qy 61 DKGYTLNIKFPAG 72

|||||

Db 234 DKGYTLNIKFPAG 245

2


```

Query Match          22.6%; Score 83.5; DB 11; Length 398;
Best Local Similarity 32.1%; Pred. No.2.2;
Matches 26; Conservative 10; Mismatches 26; Indels 19; Gaps 3

QY 3 KTPEEPKEEVTIKANLIYAD-----GKTQTAEFGTGTTEATAEAYRYADLLAK 50
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 66 KIKEEPKEEVTMTKEKRERDRDREGHGRGRPEVIQSHSIFEQGPAAEMMK-----KK 120
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 51 ENKGYTVDVADKG--YTLNIK 69
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 121 GNWDKTVDSMDMGPSHIINIK 141
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 7
Q91WD1 PRELIMINARY; PRT; 398 AA.
ID Q91WD1 AC Q91WD1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE RIKEN CDNA 2810426M17 gene.
GN 2810426M17RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary gland;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016102; AAH16102.1;
DR MGD; MGI:1914315; 2810426M17RIK.
SQ SEQUENCE 398 AA; 44323 MW; D509DE632C656FFD CRC64;

Query Match          22.6%; Score 83.5; DB 11; Length 398;
Best Local Similarity 32.1%; Pred. No.2.2;
Matches 26; Conservative 10; Mismatches 26; Indels 19; Gaps 3

QY 3 KTPEEPKEEVTIKANLIYAD-----GKTQTAEFGTGTTEATAEAYRYADLLAK 50
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 66 KIKEEPKEEVTMTKEKRERDRDREGHGRGRPEVIQSHSIFEQGPAAEMMK-----KK 120
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 51 ENKGYTVDVADKG--YTLNIK 69
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 121 GNWDKTVDSMDMGPSHIINIK 141
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 8
Q8ZEV8 PRELIMINARY; PRT; 1576 AA.
ID Q8ZEV8 AC Q8ZEV8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative hemolysin.
GN YPO2045 OR Y2267.
OS Versinia pestis
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
[1]
RP SEQUENCE FROM N.A.
RC SPRAIN-CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdono-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrall B.G.;
RA "Genome sequence of Yersinia pestis, the causative agent of plague.";
```

RESULT 10
Q27039
QY 1 KEKTPPEPKKEEVTIKANLIYADGKTTQAEFGKTFEATAEAYRYADLLAKENKGYTVDA 60
Matches 19; Conservative 11; Mismatches 29; Indels 1; Gaps 17

GN SPAC1952.03.
OS Schizosaccharomyces pombe (Fission yeast).

```

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972h-;
RA McDougall R.C., Rajandream M.A., Barrell B.G., Bothe G., Pohl T.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL109820; CAB52567.1; -.
DR GeneDB_SPombe; SPAC1952.03; -.
DR InterPro; IPR003323; OTU.
DR Pfam; PF02338; OTU; 1.
DR PROSITE; PS50802; OTU; 1.
SQ SEQUENCE 324 AA; 37516 MW; 48BBB435960D4B9C CRC64;

Query Match      18.7%; Score 69; DB 3; Length 324;
Best Local Similarity 28.6%; Pred. No. 52;
Matches 18; Conservative 15; Mismatches 26; Indels 4; Gaps 1;

QY 1 KKTPEPEKPEVTIKANLIYADGKTQTAEFKGTFEETAEAYRYADLLAKENGKVTVDVA 60
Db 126 KENTPOPKKSRNRQKERL---ERRKAEMKKMQAELESEKMDLKNEEKKFKSKILE 181
QY 61 DKG 63
Db 182 EAG 184

Search completed: September 3, 2003, 11:23:13
Job time : 45.137 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 3, 2003, 11:14:37 ; Search time 17.0137 Seconds
(without alignments)
406.975 Million cell updates/sec

Title: US-08-325-278B-1_COPY_225_296

Perfect score: 370

Sequence: 1 KEKTPPEPKKEVTIKANLIY.....GKYTADLEDGGYTINIRFAG 72

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_76.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	370	100.0	455	2 A45063	immunoglobulin-bin
2	370	100.0	719	2 A42808	Ig light chain-bin
3	329	88.9	992	2 S54396	protein L precursor
4	157	42.4	74	2 A34483	Ig light chain-bin
5	80.5	21.8	1576	2 AE0249	probable hemolysin
6	74	20.0	324	2 T37931	hypothetical colle
7	71.5	19.3	657	2 AD1525	probable cell surf
8	71	19.2	871	2 D86355	protein T16E15.12
9	70.5	19.1	256	2 S54803	merozoite surface
10	69.5	18.8	2062	2 G96602	probable receptor
11	69	18.6	397	2 AC1498	specificity determ
12	69	18.6	401	2 AE1498	specificity determ
13	69	18.5	1025	2 E86355	hypothetical prote
14	68.5	18.5	858	2 E96602	hypothetical prote
15	67	18.1	283	2 S69639	hypothetical prote
16	66.5	18.0	1029	2 F96602	hypothetical prote
17	66	17.8	495	2 D89808	hypothetical prote
18	65.5	17.7	4558	2 C82199	RTX toxin RtxA VCL
19	64.5	17.4	1179	2 T35093	DNA-directed DNA p
20	64	17.3	863	2 S06017	neuraxin - rat
21	64	17.3	2364	2 A56577	microtubule-associ
22	64	17.3	2464	1 QRM5P1	microtubule-associ
23	63.5	17.2	395	2 A43700	BN51 protein - hum
24	63.5	17.2	550	2 F75186	thrombosome, chain
25	63	17.0	356	2 T37136	hypothetical prote
26	63	17.0	490	2 F38462	S-mephenytoin 4'-h
27	63	17.0	1104	1 A36866	microbial collagen
28	62.5	16.9	215	2 AC1156	transcription regu
29	62	16.8	266	2 A12289	hypothetical prote

ALIGNMENTS

RESULT 1

A45063

immunoglobulin-binding protein LG - Peptostreptococcus magnus

C;Species: Peptostreptococcus magnus

C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 15-Oct-1999

C;Accession: A45063

J;Kihlberg, B.M.; Sjoerding, U.; Kastern, W.; Bjorck, L.

J; Biol. Chem. 267, 25583-25588, 1992

A;Title: Protein LG: a hybrid molecule with unique immunoglobulin binding properties.

A;Reference number: A45063; MUID:93094283; PMID:1460033

A;Accession: A45063

A;Status: preliminary

A;Molecule type: mRNA; protein

A;Residues: 1-455 <KIH>

A;Cross-references: GB:S50809; NID:G261705; PID:AAA03280.1; PID:G261706

A;Note: sequence extracted from NCBI backbone (NCBIN:120302, NCBIPI:120303)

Query Match 100.0%; Score 370; DB 2; Length 455;

Best Local Similarity 100.0%; Pred. No. 4.3e-32;

Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEKTPPEPKKEVTIKANLIYADGKTQTAEFKGTFAEATAYRYADLLAKENGYTADLE 60

DB 246 KEKTPPEPKKEVTIKANLIYADGKTQTAEFKGTFAEATAYRYADLLAKENGYTADLE 305

QY 61 DGGYTINIRFAG 72

DB 306 DGGYTINIRFAG 317

RESULT 2

A42808

Ig light chain-binding protein precursor - Peptostreptococcus magnus

N;Alternate names: protein L

C;Species: Peptostreptococcus magnus

C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999

C;Accession: A42808; A41493

R;Kastern, W.; Sjoerding, U.; Bjorck, L.

J. Biol. Chem. 267, 12820-12825, 1992

A;Title: Structure of peptostreptococcal protein L and identification of a repeated i

A;Reference number: A42808; MUID:92316971; PMID:1618782

A;Accession: A42808

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-719 <KAS>

A;Cross-references: GB:M86697

R;Kastern, W.; Holst, E.; Nielsen, E.; Sjoerding, U.; Bjorck, L.

Infect. Immun. 58, 1217-1222, 1990

A;Title: Protein L, a bacterial immunoglobulin-binding protein and possible virulence

A;Reference number: A41493; MUID:90215984; PMID:2108927

A;Accession: A41493

A;Status: preliminary

A:Molecule type: DNA
A:Residues: 202-275 <KA2>
C:Keywords: immunoglobulin

Query Match 100.0%; Score 370; DB 2; Length 719;
Best Local Similarity 100.0%; Pred. No. 7.2e-32;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEKTPPEKKEVTIKANLIYADGKTQTAEPKGTFAEATAEAYRYADLLAKENGYTTADLE 60
|||||
DB 318 KEKTPPEKKEVTIKANLIYADGKTQTAEPKGTFAEATAEAYRYADLLAKENGYTTADLE 377
|||||

QY 61 DGGYTIINRFAG 72
|||||

DB 378 DGGYTIINRFAG 389

RESULT 3
S54396
protein L precursor - Peptostreptococcus magnus (strain 3316)
C:Species: Peptostreptococcus magnus
A:Variety: strain 3316
C:Date: 27-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 15-Oct-1999
C:Accession: S54396
R:Murphy, J.P.; Duggleby, C.J.; Atkinson, M.A.; Trowern, A.R.; Atkinson, T.; Goward, C.R.
Mol. Microbiol. 12, 911-920, 1994
A:Title: The functional units of a peptostreptococcal protein L.
A:Reference number: S54396; MUID:95020613; PMID:7934898
A:Accession: S54396
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-992 <MUR>
A:Cross-references: EMBL:L04466; NID:gl50673; PIDN:AAA67503.1; PID:gl50674

Query Match 88.9%; Score 329; DB 2; Length 992;
Best Local Similarity 90.0%; Pred. No. 2.7e-27;
Matches 63; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 KTPPEKKEVTIKANLIYADGKTQTAEPKGTFAEATAEAYRYADLLAKENGYTTADLE 62
|||||
DB 468 ETPEEPKKEVTIKVNLIFADGKTQTAEPKGTFAEATAEAYRYADLLAKVNGEYTTADLE 527
|||||

QY 63 GYTIINRFAG 72
|||||

DB 528 GYTIINRFAG 537

RESULT 4
A34483
Ig light chain-binding protein L - Peptostreptococcus magnus (fragments)
C:Species: Peptostreptococcus magnus
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 16-Aug-1996
C:Accession: A34483
R:Akerstroem, B.; Bjoerck, L.
J. Biol. Chem. 264, 19740-19746, 1989
A:Title: Protein L: an immunoglobulin light chain-binding bacterial protein. Characteriz
A:Reference number: A34483; MUID:90062074; PMID:2479638
A:Accession: A34483
A:Molecule type: protein
A:Residues: 1-74 <AKE>
C:Keywords: immunoglobulin

Query Match 62.4%; Score 157; DB 2; Length 74;
Best Local Similarity 62.7%; Pred. No. 4.8e-10;
Matches 37; Conservative 2; Mismatches 10; Indels 10; Gaps 2;

QY 2 EKTPPEKKEVTIKANLIYADGKTQTAEPKGTFAEATAE-----AYRYADLLAKE 51
|||||
DB 9 ETTPPEKKEVTIKANLIYADGKTQTAEPKGTFAEATAE-----AYRYADLLAKE 66
|||||

RESULT 5
AE0249

Query Match	19.1%;	Score 70.5;	DB 2;	Length 256;
Best Local Similarity	31.0%;	Pred. No. 4;		
Matches	18.	Conservative	10.	Mismatches
			20.	Indels
				1.
				1.

```

RESULT 10
G96602
probable receptor protein kinase F14G9.24 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: G96602

```

	Matches	21;	Conservative	13;	Mismatches	29;	Indels	1/;	Gaps	1
QY	7	EPKEEVTIKANLIYADGKTTQTAEPKGTFAAT	-----	-----	-----	-----	-----	-----	-----	AAEAYRADLLA 49
db	1473	EREDDI GDASEVVSAGORWAAASVGHFAGSNNIVTSTQSOFVNVTIDSPLEFOSARISA	1532	EREDDI GDASEVVSAGORWAAASVGHFAGSNNIVTSTQSOFVNVTIDSPLEFOSARISA	1532	EREDDI GDASEVVSAGORWAAASVGHFAGSNNIVTSTQSOFVNVTIDSPLEFOSARISA	1532	EREDDI GDASEVVSAGORWAAASVGHFAGSNNIVTSTQSOFVNVTIDSPLEFOSARISA	1532	EREDDI GDASEVVSAGORWAAASVGHFAGSNNIVTSTQSOFVNVTIDSPLEFOSARISA

```

RESULT 11
AC1498
specificity determinant HsdS homolog lin0523 [imported] - Listeria innocua
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AC1498

```

D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Krefft, J., Kuhn, M., Kunst, F., Kurapkat, G.; Madueno, E.; Maitournam, A.;
Ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehler,
A.:Title: Comparative genomics of *Listeria* species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AC1498
D.; Domínguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgey, O.; Entian, K.D.; Fsihi,

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-397 <GLA>
A:Cross-references: GB:AL592022; PIDN:CAC95755.1; PID:g16412963; GSPDB:GN00178
A:Experimental source: strain Clip11262
C:Genetics:
A:Gene: lin0523

Query Match 18.6%; Score 69; DB 2; Length 397;
Best Local Similarity 31.7%; Pred. No. 9.6;
Matches 26; Conservative 8; Mismatches 28; Indels 20; Gaps 4;

QY 2 EKTPEPKKEVTKANLIYADGKTQ--TAE-----FKGTFAEATAEAYRYADLLAKENGK 54

Db 38 EQVEDGKTYIINSKFISTNGKVRQYTNQVEPFIDGFIAMVLSDL-----PNKG 88

QY 55 YTADL-----EDGTYTINIRFAG 72

Db 89 ALAKFLVKEDGKTYTLNQRAG 110

RESULT 12

AE1498

specificity determinant Hsds homolog lin0525 [imported] - Listeria innocua (strain Clip11262)

C:Species: Listeria innocua

C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001

C:Accession: AE1498

R:Glaser, P.; Frangelet, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker

; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl, H.

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma

ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,

A:Title: Comparative genomics of Listeria species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AE1498

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-401 <GLA>

A:Cross-references: GB:AL592022; PIDN:CAC95757.1; PID:g16412965; GSPDB:GN00178

A:Experimental source: strain Clip11262

C:Genetics:

A:Gene: lin0525

Query Match 18.6%; Score 69; DB 2; Length 401;

Best Local Similarity 31.7%; Pred. No. 9.7;

Matches 26; Conservative 8; Mismatches 28; Indels 20; Gaps 4;

QY 2 EKTPEPKKEVTKANLIYADGKTQ--TAE-----FKGTFAEATAEAYRYADLLAKENGK 54

Db 36 EQVEDGKTYIINSKFISTNGKVRQYTNQVEPFIDGFIAMVLSDL-----PNKG 86

QY 55 YTADL-----EDGTYTINIRFAG 72

Db 87 ALAKFLVKEDGKTYTLNQRAG 108

RESULT 13

E86355

hypothetical protein T16E15.11 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001

C:Accession: E86355

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

ansen, N.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luo, J.S.; Maiti, R.; Marzila,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.B.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: E86355

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1025 <STO>

A:Cross-references: GB:AE005172; NID:g9392687; PIDN:AAF87264.1; GSPDB:GN00141

C:Genetics:

A:Map position: 1

Query Match 18.6%; Score 69; DB 2; Length 1025;

Best Local Similarity 28.0%; Pred. No. 28;

Matches 21; Conservative 15; Mismatches 27; Indels 12; Gaps 2;

QY 3 KTEPEKKEVTKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKE 51

Db 571 RTSEDKKKLSIKLSLETSKDYKQLQADARQVGELE-TLQKESHQADLLAKE 629

QY 52 NGKYTADLEGGYTI 66

Db 630 VNQLQTIIEKGHLI 644

RESULT 14

E96602

hypothetical protein T6H22.9 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: E96602

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon,

ansen, N.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luo, J.S.; Maiti, R.; Marzila,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.B.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: E96602

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-858 <STO>

A:Cross-references: GB:AE005173; NID:g6056372; PIDN:AAF02836.1; GSPDB:GN00141

C:Genetics:

A:Gene: T6H22.9

A:Map position: 1

Query Match 18.5%; Score 68.5; DB 2; Length 858;

Best Local Similarity 35.7%; Pred. No. 26;

Matches 20; Conservative 9; Mismatches 22; Indels 5; Gaps 2;

QY 16 ANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKGTADLEGGYTNIREFA 71

Db 305 SNNIYI--ATSLAQFINTM--DSELFQSAFLSASSIRYVGLGLENGYTVTLQFA 355

RESULT 15

S69639

hypothetical protein YDR472w - yeast (Saccharomyces cerevisiae)

C:Species: Saccharomyces cerevisiae

C:Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 19-Apr-2002

C:Accession: S69639

R:Dietrich, F.S.

A:Description: The sequence of S. cerevisiae cosmid 9410, 8035, 8166, and 9787.

A:Reference number: S69554

A:Accession: S69639

A:Molecule type: DNA

A:Residues: 1-283 <DIE>

A:Cross-references: EMBL:U33050; NID:g927726; PID:g927742; GSPDB:GN00004; MIPS:YDR472

C:Genetics:

A:Gene: SGD:TRS31; MIPS:YDR472w

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:14:02 ; Search time 44.137 Seconds
(without alignments)
420.957 Million cell updates/sec

Title: US-08-325-278b-1_COPY_225_296
Perfect score: 370
Sequence: 1 KEKTPPEPKKEVTIKANLIY.....GKYTADLEGGYTINIRFAG 72

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	370	100.0	455	2 Q53291	Q53291 streptococ
2	370	100.0	719	2 Q51912	Q51912 peptostrept
3	329	88.9	992	2 Q51918	Q51918 peptostrept
4	80.5	21.8	1576	16 Q82EW8	Q82EW8 yersinia pe
5	74	20.0	324	3 Q9UUK3	Q9UUK3 schizosacch
6	74	20.0	846	2 Q8RPV1	Q8RPV1 streptococ
7	71.5	19.3	216	4 Q9BPV7	Q9BPV7 homo sapien
8	71.5	19.3	398	4 Q9BPZ1	Q9BPZ1 homo sapien
9	71.5	19.3	657	16 Q82DS2	Q82DS2 listeria in
10	71	19.2	871	10 Q9LME2	Q9LME2 arabisdopsi
11	70.5	19.1	256	5 Q27039	Q27039 theileria p
12	70.5	19.1	256	5 Q27029	Q27029 theileria p
13	70.5	19.1	280	5 Q27030	Q27030 theileria p
14	70.5	19.1	398	11 Q9CZ02	Q9CZ02 mus musculu
15	70.5	19.1	398	11 Q91WD1	Q91WD1 mus musculu
16	70	18.9	549	17 Q8TZL6	Q8TZL6 pyrococcus

17	69.5	18.8	1086	10 Q9SGU0	Q9sgu0 arabisdopsi
18	69.5	18.8	1849	2 Q9S4K2	Q9s4k2 lactobacill
19	69.5	18.8	2062	10 Q9C7J2	Q9c7j2 arabisdopsi
20	69	18.6	397	16 Q92ED7	Q92ed7 listeria in
21	69	18.6	401	16 Q92ED5	Q92ed5 listeria in
22	69	18.6	1025	10 Q9LME3	Q9lme3 arabisdopsi
23	68.5	18.5	858	10 Q9SGT8	Q9sgt8 arabisdopsi
24	67.5	18.2	383	5 Q9VTV4	Q9vtv4 drosophila
25	67	18.1	278	10 Q94KL8	Q94kl8 podophyllum
26	67	18.1	283	3 Q03337	Q03337 saccharomyc
27	66.5	18.0	1029	10 Q9SGT9	Q9sgt9 arabisdopsi
28	66	17.8	495	16 Q9W9G8	Q9w9g8 staphylococ
29	65.5	17.7	225	2 Q9WX49	Q9wx49 onion yello
30	65.5	17.7	4545	2 Q9X4W2	Q9x4w2 vibrio chol
31	65.5	17.7	4558	16 Q9KSI2	Q9ksi2 vibrio chol
32	65	17.6	304	6 Q9BE26	Q9be26 macaca fasc
33	65	17.6	319	4 Q00477	Q00477 homo sapien
34	65	17.6	334	4 Q9NR44	Q00477 homo sapien
35	65	17.6	334	4 Q9BU81	Q9bu81 homo sapien
36	65	17.6	357	4 Q15338	Q15338 homo sapien
37	65	17.6	359	4 P78410	P78410 homo sapien
38	65	17.6	495	4 Q9HCY1	Q9hcy1 homo sapien
39	65	17.6	513	4 Q00481	Q00481 homo sapien
40	65	17.6	584	4 Q00478	Q00478 homo sapien
41	64.5	17.4	279	2 Q9ADV8	Q9adv8 ehrlichia c
42	64	17.3	500	16 Q8NY41	Q8ny41 staphylococ
43	64	17.3	585	16 Q8EJS9	Q8ejs9 shewanella
44	64	17.3	1433	2 Q45616	Q45616 bacillus su
45	63.5	17.2	183	16 Q8EBW9	Q8ebw9 shewanella

ALIGNMENTS

RESULT 1

Q53291 ID Q53291 PRELIMINARY; PRT; 455 AA.
AC Q53291;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Protein LG (Fragment).
OS Streptococcus sp.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1306;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93094283; PubMed=1460053;
RA Kihlberg B.M., Sjobring U., Kastern W., Bjorck L.;
RT "Protein LG: a hybrid molecule with unique immunoglobulin binding properties.";
RL J. Biol. Chem. 267:25583-25588(1992).
DR EMBL; S50809; AAA03280.1; -;
DR HSSP; P06654; IPGX.
DR InterPro; IPR003147; B1.
DR InterPro; IPR000724; IgG_bind_B.
DR Pfam; PF02246; B1; 4.
DR Pfam; PF01378; IgG-binding_B; 2.
FT NON_TER 455
SQ SEQUENCE 455 AA; 49926 MW; 381FC235B8C307B CRC64;

Query Match 100.0%; Score 370; DB 2; Length 455;
Best Local Similarity 100.0%; Pred. No. 6.5e-30;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KEKTPPEPKKEVTIKANLIYADGKGTQTAEFKGTFAEATAEAYRYADLLAKENKYYTADLE 60
Db 246 KEKTPPEPKKEVTIKANLIYADGKGTQTAEFKGTFAEATAEAYRYADLLAKENKYYTADLE 305
QY 61 DGGYTINIRFAG 72
Db 306 DGGYTINIRFAG 317

```
RESULT 2
Q51912
ID Q51912 PRELIMINARY; PRT; 719 AA.
AC Q51912;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Protein L precursor.
OS Peptostreptococcus magnus.
OC Bacteria; Firmicutes; Clostridia; Clostridiales;
OC Peptostreptococcaceae; Finegoldia.
OX NCBI_TaxID=1260;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=312;
RX MEDLINE=90215984; PubMed=2108927;
RA Kastern W., Holst E., Nielsen E., Sjobring U., Bjorck L.;
RT "Protein L, a bacterial immunoglobulin-binding protein and possible
RT virulence determinant.";
RL Infect. Immun. 58:1217-1222(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=312;
RX MEDLINE=92316971; PubMed=1618782;
RA Bjorck L., Sjobring U., Kastern W.;
RT "Structure of peptostreptococcal protein L and identification of
RT repeated immunoglobulin light chain-binding domain.";
RL J. Biol. Chem. 267:12820-12825(1992).
CC -!- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN BY
CC AN AMIDE BOND (BY SIMILARITY).
DR EMBL; M86697; AAA25612.1; -.
DR InterPro; IPR003147; B1.
DR ProDom; PD153432; Csurface_antigen; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Peptidoglycan-anchor; Signal.
KW SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 719 PROTEIN L.
FT CHAIN 19 719
SQ SEQUENCE 719 AA; 78983 MW; 963A8D76D5E34DD2 CRC64;

Query Match 100.0%; Score 370; DB 2; Length 719;
Best Local Similarity 100.0%; Pred. No. 1.1e-29;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEKTEPEKPEVTKANLIYADGKTQTAEFGTFAETAAYRYADLLAKENGYKTADLE 60
Db 318 KEKTEPEKPEVTKANLIYADGKTQTAEFGTFAETAAYRYADLLAKENGYKTADLE 377

QY 61 DGGYTINIRFAG 72
Db 378 DGGYTINIRFAG 389

RESULT 3
Q51918
ID Q51918 PRELIMINARY; PRT; 992 AA.
AC Q51918;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Protein L precursor.
OS Peptostreptococcus magnus.
OC Bacteria; Firmicutes; Clostridia; Clostridiales;
OC Peptostreptococcaceae; Finegoldia.
OX NCBI_TaxID=1260;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=312;
RX MEDLINE=90215984; PubMed=2108927;
RA Kastern W., Holst E., Nielsen E., Sjobring U., Bjorck L.;
RT "Protein L, a bacterial immunoglobulin-binding protein and possible
RT virulence determinant.";
RL Infect. Immun. 58:1217-1222(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=312;
RX MEDLINE=92316971; PubMed=1618782;
RA Bjorck L., Sjobring U., Kastern W.;
RT "Structure of peptostreptococcal protein L and identification of
RT repeated immunoglobulin light chain-binding domain.";
RL J. Biol. Chem. 267:12820-12825(1992).
CC -!- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN BY
CC AN AMIDE BOND (BY SIMILARITY).
DR EMBL; M86697; AAA25612.1; -.
DR InterPro; IPR003147; B1.
DR ProDom; PD153432; Csurface_antigen; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Peptidoglycan-anchor; Signal.
KW SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 719 PROTEIN L.
FT CHAIN 19 719
SQ SEQUENCE 719 AA; 78983 MW; 963A8D76D5E34DD2 CRC64;

Query Match 100.0%; Score 370; DB 2; Length 719;
Best Local Similarity 100.0%; Pred. No. 1.1e-29;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEKTEPEKPEVTKANLIYADGKTQTAEFGTFAETAAYRYADLLAKENGYKTADLE 60
Db 318 KEKTEPEKPEVTKANLIYADGKTQTAEFGTFAETAAYRYADLLAKENGYKTADLE 377

QY 61 DGGYTINIRFAG 72
Db 378 DGGYTINIRFAG 389
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RP SEQUENCE FROM N.A.
RC STRAIN=3316;
RX MEDLINE=95078460; PubMed=7987012;
RA Murphy J.P., Trowern A.R., Dugleby C.J.;
RT "Nucleotide sequence of the gene for peptostreptococcal protein L.";
RL DNA Seq. 4:259-265(1994).
CC -!- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN BY
CC AN AMIDE BOND (BY SIMILARITY).
DR EMBL; L04466; AAA67503.1; -.
DR HSSP; Q51911; IGAB.
DR InterPro; IPR003147; B1.
DR InterPro; IPR002988; GA.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR006192; LPXTG.
DR Pfam; PF02246; B1; 4.
DR Pfam; PF01468; GA; 4.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Peptidoglycan-anchor; Signal.
KW SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 992 PROTEIN L.
FT CHAIN 25 992
SQ SEQUENCE 992 AA; 108700 MW; 9CFF5771578A5DCE CRC64;

Query Match 88.9%; Score 329; DB 2; Length 992;
Best Local Similarity 90.0%; Pred. No. 2.7e-25;
Matches 63; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 KTEPEKPEVTKANLIYADGKTQTAEFGTFAETAAYRYADLLAKENGYKTADLE 62
Db 468 ETEPEKPEVTKANLIYADGKTQTAEFGTFAETAAYRYADLLAKENGYKTADLE 527

QY 63 GYTINIRFAG 72
Db 528 GYTINIRFAG 537

RESULT 4
Q8ZEVS8
ID Q8ZEVS8 PRELIMINARY; PRT; 1576 AA.
AC Q8ZEVS8;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Putative hemolysin.
GN YPO2045 OR Y2267.
OS Versinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM.";
```


OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	[1]
RN	NCBI_TaxID=9606;
RP	SEQUENCE FROM N.A.
RC	TISSUE=Lung, and Lymph;
RA	Strausberg R.;
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR	EMBL; BC004484; AAH04484.1; -
DR	ENML; BC002603; AAH02603.1; -
SO	SEQUENCE 398 AA; 44396 MW; CD8AFF3257B78410 CRC64;
Query Match	19.3%; Score 71.5; DB 4; Length 398;
Best Local Similarity	29.6%; Pred. No. 31;
Matches 24; Conservative	9; Mismatches 29; Indels 19; Gaps 3;
QY	3 KTPPEKPEEVTIKANLIYAD-----GKTQTAEFKGTFAETATAEAAYRYADLLAK 50 : : : : : : : : : :
Db	66 KIREEPKEEVTVKKERERDRDREGHGGRGCRPEVIQSHSIFEQGPAEMMK-----KK 120 : : : : : : : : : :
QY	51 ENCKYATADLEDGG--YTINIR 69 : : : : : : : : : :
Db	121 GNWDKTVDSVDMGPSHIINIK 141 : : : : : : : : : :
RESULT 9	
Q92DS2	PRELIMINARY; PRT; 657 AA.
ID Q92DS2	
AC Q92DS2;	
DT 01-DEC-2001	(TREMBLrel. 19, Created)
DT 01-DEC-2001	(TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003	(TREMBLrel. 23, Last annotation update)
DE	Probable cell surface protein (LPXTG motif).
GN LIN0740.	
OS	Listeria innocua.
OC	Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
NCBI_TaxID=1642;	
[1]	
SEQUENCE FROM N.A.	
STRAIN=CLIP 11262 / Serovar 6a;	
PubMed=11679669;	
Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,	
Bequerro F., Berche P., Bloeker H., Brandt P., Chakraborty T.,	
Charbit A., Chetoui F., Couve E., de Daruvar A., Dehoux P.,	
Doman E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,	
Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,	
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,	
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,	
Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,	
Nordsiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,	
Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,	
Vazquez-Boland J.-A., Voss H., Wehlund J., Cossart P.;	
Comparative genomics of Listeria species.;	
Science 294:849-852(2001).	
EMBL; AL596166; CAC95972.1; -	
LSTlist; LIN00740;	
InterPro; IPR001899; Gram_pos_anchor.	
InterPro; IPR001611; LRR.	
InterPro; IPR003591; LRR_typ.	
Pfam; PF00746; Gram_pos_anchor; 1.	
Pfam; PF00560; LRR; 4.	
TIGRfams; TIGR01167; LPXTG_anchor; 1.	
PROSITE; PS50506; LRR_TYPICAL; 1.	
Complete proteome.	
SEQUENCE 657 AA; 72501 MW; 32C819296AE018B6 CRC64;	
Query Match	19.3%; Score 71.5; DB 16; Length 657;
Best Local Similarity	33.8%; Pred. No. 56;
Matches 27; Conservative	6; Mismatches 28; Indels 19; Gaps 5;
QY	1 KETPPEKPEEVTIKANLIYADGK-----TQTAEFKG-----TFAEATAEAAYRYADLLAK 50 : : : : : : : : : :
Db	381 KDVPAPKP---VFVTK-----YVDKGKELAFSEFTFGFIDDYDTSTETKIETYIVETPAN 433 : : : : : : : : : :

```

RC STRAIN=MUGUGA;
RA Shields B.R., Fox M., McKellar S., Kinnaird J., Swan D.G.;
RT "An upstream element of the Tams1 gene is a site of DNA - protein
RT interactions during differentiation to the merozoite in Theileria
RT annulata.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: L47209; AAA75252.1; -.
DR EMBL: AJ276655; CAB93689.1; -.
DR InterPro: IPR003407; Merozoite_Agen.
DR DR Pfam: PF02488; EMA; 1.
KW SIGNAL.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 280 32 KDA SURFACE ANTIGEN.
SQ SEQUENCE 280 AA; 32047 MW; 6BFF7BB6D44D589F CRC64;

Query Match 19.1%; Score 70.5; DB 5; Length 280;
Best Local Similarity 31.0%; Pred. No. 26;
Matches 18; Conservative 10; Mismatches 29; Indels 1; Gaps 1;

QY 1 KETPEEPKEEVTIKANLIYADGKTQTAEPKGTFAETAABAYRYADLLAKENGYKTAD 58
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
25 EEEKKEKKEDLVDTLSSWENVTSTPEAGGTLKAN-EGYRFKTLKVGDKTLNVND 81

RESULT 14
RC9C202 PRELIMINARY; PRT; 398 AA.
ID Q9C202 AC Q9C202;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE 2810426M17Rik protein.
DE 2810426M17RIK.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RP "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK013165; BAB28687.1; -.
DR MGD; MGI:1914315; 2810426M17Rik.
SQ SEQUENCE 398 AA; 44356 MW; B70179A124C1231B CRC64;

Query Match 19.1%; Score 70.5; DB 11; Length 398;
Best Local Similarity 29.6%; Pred. No. 39;
Matches 24; Conservative 9; Mismatches 29; Indels 19; Gaps 3;

QY 3 KTEPEEPKEEVTIKANLIYAD-----GKTTQTAEPKGTFAETAABAYRYADLLAK 50
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
66 KKEEPKEEVTMKKEKRRDRDRQREHGGRGRGPRVFIQSHSIFEQGPAEMWK-----KK 120

```

1000

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:14:02; Search time 46.589 Seconds
(without alignments)
420.957 Million cell updates/sec

Title: US-08-325-278B-1_COPY_5_80

Perfect score: 389

Sequence: 1 KEETPETPTDSEEEVTKA.....GEYTVADKGYTLNIFKAG 76

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	389	100.0	455	2 Q53291	Q53291 streptococc
2	389	100.0	719	2 Q51912	Q51912 peptostrept
3	298.5	76.7	992	2 Q51918	Q51918 peptostrept
4	85	21.9	1576	16 Q82EV8	Q82EV8 yersinia pe
5	74	19.0	529	1 Q48937	Q48937 methanosarc
6	73.5	18.9	451	2 Q924J9	Q924J9 lactobacill
7	72	18.5	477	10 Q932G9	Q932G9 arabidopsis
8	72	18.5	487	10 Q9STK2	Q9STK2 arabidopsis
9	71.5	18.4	947	2 Q86487	Q86487 staphylococ
10	71	18.3	528	16 Q9KX8	Q9KX8 bacillus ha
11	71	18.3	929	3 P78718	P78718 nectria hae
12	70.5	18.1	955	16 Q8NXX7	Q8NXX7 staphylococ
13	70	18.0	645	5 Q3862	Q3862 ascaris suu
14	69.5	17.9	292	16 Q92FA8	Q92FA8 listeria in
15	69.5	17.9	300	11 Q9JHY1	Q9JHY1 rattus norv
16	69	17.7	190	17 Q8TQF1	Q8TQF1 methanosarc

17	69	17.7	341	3 Q12191	Q12191 saccharomyc
18	69	17.7	1430	5 Q9VMA7	Q9VMA7 drosophila
19	68.5	17.6	401	16 Q8FHX3	Q8FHX3 escherichia
20	68	17.5	574	2 Q9AJD4	Q9AJD4 streptococc
21	67.5	17.4	218	2 Q9RF14	Q9RF14 streptococc
22	67.5	17.4	1022	2 Q93T54	Q93T54 streptococc
23	67.5	17.4	1056	16 Q9PAQ0	Q9PAQ0 xyliella fas
24	67.5	17.4	1876	16 Q8DQNS	Q8DQNS streptococc
25	67	17.2	529	17 Q8TV18	Q8TV18 methanopyru
26	67	17.2	574	16 Q8P2T7	Q8P2T7 streptococc
27	67	17.2	588	2 Q9S0T6	Q9S0T6 escherichia
28	67	17.2	779	10 Q9SZB6	Q9SZB6 arabidopsis
29	67	17.2	890	2 Q01891	Q01891 enterococcu
30	67	17.2	891	2 Q04111	Q04111 enterococcu
31	67	17.2	1433	2 Q45616	Q45616 bacillus su
32	67	17.2	1881	16 Q8RGK2	Q8RGK2 fusobacteri
33	66.5	17.1	255	16 Q99XB4	Q99XB4 staphylococ
34	66.5	17.1	465	2 Q9X775	Q9X775 mycoplasma
35	66.5	17.1	842	16 Q9JTL4	Q9JTL4 neisseria m
36	66.5	17.1	843	2 Q47802	Q47802 enterococcu
37	66	17.0	183	16 Q9KDD6	Q9KDD6 bacillus ha
38	66	17.0	489	17 Q8THX7	Q8THX7 methanosarc
39	66	17.0	498	16 Q8X6R2	Q8X6R2 escherichia
40	66	17.0	653	16 Q67097	Q67097 aquifex aeo
41	66	17.0	1169	16 Q8K5Q0	Q8K5Q0 streptococc
42	66	17.0	1615	2 Q9KKA4	Q9KKA4 rickettsia
43	65.5	16.8	313	5 Q76641	Q76641 caenorhabdi
44	65.5	16.8	456	11 Q9CS77	Q9CS77 mus musculu
45	65.5	16.8	868	17 Q8PZM5	Q8PZM5 methanosarc

ALIGNMENTS

RESULT 1

Q53291 ID Q53291 PRELIMINARY; PRT; 455 AA.
AC Q53291;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Protein LG (Fragment).
OS Streptococcus sp.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1306;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93094283; PubMed=1460053;
RA Kihlberg B.M., Sjobring U., Kastern W., Bjorck L.;
RT "Protein LG: a hybrid molecule with unique immunoglobulin binding properties";
RL J. Biol. Chem. 267:25583-25588(1992).
DR EMBL; S50809; AAA03280.1; -;
DR HSSP; P06654; IPGX.
DR InterPro; IPR003147; B1.
DR InterPro; IPR000724; IgG_bind_B.
DR Pfam; PF02246; B1; 4.
DR Pfam; PF01378; IgG_binding_B; 2.
FT NON_TER 455 455
SQ SEQUENCE 455 AA; 49926 MW; 381FC235B8C8307B CRC64;

Query Match 100.0%; Score 389; DB 2; Length 455;

Best Local Similarity 100.0%; Pred. No. 2.1e-30;

Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEETPETPTDSEEEVTKANLIFANGSTQAEFGTFEKATSEAYAYADTLKKNGEYT 60
|||||

Db 26 KEETPETPTDSEEEVTKANLIFANGSTQAEFGTFEKATSEAYAYADTLKKNGEYT 85
|||||

QY 61 DVADKGYTLNIFKAG 76
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Db 86 DVADKGYTLNIFKAG 101
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RESULT 2
ID Q51912 PRELIMINARY; PRT; 719 AA.
AC Q51912;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Protein L precursor.
OS Peptostreptococcus magnus.
OC Bacteria; Firmicutes; Clostridia; Clostridiales;
OC Peptostreptococcaceae; Finegoldia.
OX NCBI_TaxID=1260;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=312;
RX MEDLINE=90215984; PubMed=2108927;
RA Kasten W., Holst E., Nielsen E., Sjoerding U., Bjorck L.;
RT "Protein L, a bacterial immunoglobulin-binding protein and possible
FT virulence determinant.";
RL Infect. Immun. 58:1217-1222(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=312;
RX MEDLINE=92316971; PubMed=1618782;
RA Bioerck L., Sjoerding U., Kasten W.;
RT "Structure of peptostreptococcal protein L and identification of
FT repeated immunoglobulin light chain-binding domain.";
RL J. Biol. Chem. 267:12820-12825(1992).
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN BY
AN AMIDE BOND (BY SIMILARITY).
EMBL: M86697; AAA25612.1; -
DR InterPro: IPR003147; B1.
DR InterPro: IPR004829; Csurface_antigen.
DR InterPro: IPR001899; Gram_pos_anchor.
DR InterPro: IPR006192; LPXTG.
DR Pfam: PF02246; B1; 5.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR ProDom: PD153432; Csurface_antigen; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR PROSITE: PS0847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 719 PROTEIN L.
SQ SEQUENCE 719 AA; 78983 MW; 963A8D76D5E34DD2 CRC64;

Query Match 100.0%; Score 389; DB 2; Length 719;
Best Local Similarity 100.0%; Pred. No. 3.5e-30;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEETPETDSEEVTKANLIFANGSTQTAFFKGTSEAYAYADTLKNDGEY 60
DB 98 KEETPETDSEEVTKANLIFANGSTQTAFFKGTSEAYAYADTLKNDGEY 157
QY 61 VDVAADKGYTLNKFAG 76
DB 158 VDVAADKGYTLNKFAG 173

RESULT 3
Q51918
ID Q51918 PRELIMINARY; PRT; 992 AA.
AC Q51918;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Protein L precursor.
OS Peptostreptococcus magnus.
OC Bacteria; Firmicutes; Clostridia; Clostridiales;
OC Peptostreptococcaceae; Finegoldia.
OX NCBI_TaxID=1260;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=312;
RX MEDLINE=90215984; PubMed=2108927;
RA Kasten W., Holst E., Nielsen E., Sjoerding U., Bjorck L.;
RT "Protein L, a bacterial immunoglobulin-binding protein and possible
FT virulence determinant.";
RL Infect. Immun. 58:1217-1222(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=312;
RX MEDLINE=92316971; PubMed=1618782;
RA Bioerck L., Sjoerding U., Kasten W.;
RT "Structure of peptostreptococcal protein L and identification of
FT repeated immunoglobulin light chain-binding domain.";
RL J. Biol. Chem. 267:12820-12825(1992).
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN BY
AN AMIDE BOND (BY SIMILARITY).
EMBL: M86697; AAA25612.1; -
DR InterPro: IPR003147; B1.
DR InterPro: IPR004829; Csurface_antigen.
DR InterPro: IPR001899; Gram_pos_anchor.
DR InterPro: IPR006192; LPXTG.
DR Pfam: PF02246; B1; 5.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR ProDom: PD153432; Csurface_antigen; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR PROSITE: PS0847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 719 PROTEIN L.
SQ SEQUENCE 719 AA; 78983 MW; 963A8D76D5E34DD2 CRC64;

Query Match 100.0%; Score 389; DB 2; Length 719;
Best Local Similarity 100.0%; Pred. No. 3.5e-30;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEETPETDSEEVTKANLIFANGSTQTAFFKGTSEAYAYADTLKNDGEY 60
DB 98 KEETPETDSEEVTKANLIFANGSTQTAFFKGTSEAYAYADTLKNDGEY 157
QY 61 VDVAADKGYTLNKFAG 76
DB 158 VDVAADKGYTLNKFAG 173

RESULT 4
Q8ZEVE8
ID Q8ZEVE8 PRELIMINARY; PRT; 1576 AA.
AC Q8ZEVE8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative hemolysin.
GN YPO2045 OR Y2267.
OS Versinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Versinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feilwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT "Genome sequence of Versinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Zhong R.R., Plano G.V.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Blattner F.R.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Versinia pestis KIM.";

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RP SEQUENCE FROM N.A.
RC STRAIN=3316;
RX MEDLINE=95078460; PubMed=7987012;
RA Murphy J.P., Tricern A.R., Duggieby C.J.;
RT "Nucleotide sequence of the gene for peptostreptococcal protein L.";
RL DNA Seq. 4:259-265(1994).
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN BY
AN AMIDE BOND (BY SIMILARITY).
EMBL: L04466; AAA67503.1; -
DR HSP; Q51911; IGAB.
DR InterPro: IPR003147; B1.
DR InterPro: IPR002988; GA.
DR InterPro: IPR001899; Gram_pos_anchor.
DR InterPro: IPR006192; LPXTG.
DR Pfam: PF02246; B1; 4.
DR Pfam: PF01468; GA; 4.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR PROSITE: PS0847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 992 PROTEIN L.
SQ SEQUENCE 992 AA; 108700 MW; 9CFE5771578A5DCE CRC64;

Query Match 76.7%; Score 298.5; DB 2; Length 992;
Best Local Similarity 80.3%; Pred. No. 4.7e-21;
Matches 61; Conservative 4; Mismatches 6; Indels 5; Gaps 1;

QY 1 KEETPETDSEEVTKANLIFANGSTQTAFFKGTSEAYAYADTLKNDGEY 60
DB 247 EKETPE-----PEEVTIKANLIFADGSTQNAEFTFAKANSAYADALAKNDGEY 301
QY 61 VDVAADKGYTLNKFAG 76
DB 302 VDVAADKGYTLNKFAG 317

RESULT 4
Q8ZEVE8
ID Q8ZEVE8 PRELIMINARY; PRT; 1576 AA.
AC Q8ZEVE8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative hemolysin.
GN YPO2045 OR Y2267.
OS Versinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Versinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feilwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT "Genome sequence of Versinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Zhong R.R., Plano G.V.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Blattner F.R.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Versinia pestis KIM.";

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RL J. Bacteriol. 184:4601-4611(2002).
DR EMBL: AJ414151; CAC90857.1; -
DR EMBL: AE013829; AAM85827.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 1576 AA; 169976 MW; 7029EC4BA386424C CRC64;

Query Match 21.9%; Score 85; DB 16; Length 1576;
Best Local Similarity 31.2%; Pred. No. 11;
Matches 25; Conservative 11; Mismatches 26; Indels 18; Gaps 3;

QY 6 ETPETSEEVITKANLIFANGSTOTAEFGTSEAYAYADTLKKDNGEYTDV--- 62
DB 1033 ETSQGSYAEMLVGNL---NAKS-----GVSIKTTGDAIYYATNIEGGNGDITIDAGN 1083
QY 63 -----VADKGYTLNKFAG 76
DB 1084 NLYFDQVQDSORSSNIKFSG 1103

RESULT 5
Q48937
ID Q48937 PRELIMINARY; PRT; 529 AA.
AC Q48937;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Orf4 protein (Fragment).
GN ORF4.
OS Methanosarcina barkeri.
OC Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2208;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Fusaro/DSM 804;
RX MEDLINE=96184912; PubMed=8617280;
RA Vorholt J.A., Vaupel M., Thauer R.K.;
RT "A polyferredoxin with eight [4Fe-4S] clusters as a subunit of
RT molybdenum formylmethanofuran dehydrogenase from Methanosarcina
RT barkeri.";
RL Eur. J. Biochem. 236:309-317(1996).
DR EMBL: X93084; CAA63625.1; -
DR InterPro: IPR000914; SBP_bac_5.
DR Pfam: PF00496; SBP_bac_5; 1.
FT NON_TER 529 529
SQ SEQUENCE 529 AA; 58606 MW; 218001E917C0F7F4 CRC64;

Query Match 19.0%; Score 74; DB 1; Length 529;
Best Local Similarity 38.3%; Pred. No. 37;
Matches 23; Conservative 8; Mismatches 23; Indels 6; Gaps 3;

QY 15 EVTIKANLIFANGSTOTAEFGTSEAYAYADTLKKDNGEYTDVADKGYTLNIK 73
DB 119 EFKLRNNVTHDGSKMTAEVDNFTLEKVISENAKVASMLKID---SIEIVD-NYTLKIK 173

RESULT 6
Q924J9
ID Q924J9 PRELIMINARY; PRT; 451 AA.
AC Q924J9;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE S-layer protein precursor.
GN S-LAYER.
OS Lactobacillus crispatus.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=47770;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M247;
RA Ventura M., Callegari M., Morelli L.;

"Detection of a strain specific region in the S-layer sequence of
RT Lactobacillus crispatus.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ007839; CAA07708.1; -
DR InterPro: IPR004903; SLAP.
DR Pfam: PF03217; SLAP; 1.
KW S-layer; Signal.
FT SIGNAL 1 31 POTENTIAL.
FT CHAIN 32 451 S-LAYER PROTEIN.
SQ SEQUENCE 451 AA; 47012 MW; 7F79C6D0F7C458F7 CRC64;

Query Match 18.9%; Score 73.5; DB 2; Length 451;
Best Local Similarity 35.8%; Pred. No. 35;
Matches 24; Conservative 3; Mismatches 15; Indels 25; Gaps 3;

QY 26 NGSTQTAERFGTSEAYAYADTLKKDNGEYTDV-----ADKGYTL----- 70
DB 107 NGKVSADSKGT-----AVTDFSKLTNGSYTTVSGVSNFGTANKTITLGSKN 157

QY 71 -NIKFAG 76
DB 158 SNVKFAG 164

RESULT 7
Q93ZG9
ID Q93ZG9 PRELIMINARY; PRT; 477 AA.
AC Q93ZG9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE AT4925340/T30C3_20.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis cDNA clones";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P.,
RA Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y.,
RA Hsuan V.W., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
RA Nguyen M., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M.,
RA Southwick A., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.C.,
RA Yamada K., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis ORF clones";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY057543; AAL09783.1; -
DR EMBL: AY143978; AAN28917.1; -
DR InterPro: IPR001179; FKBP_PPIase.
DR Pfam: PF00254; FKBP; 1.
DR PROSITE: PS00454; FKBP_PPIASE_2; 1.
DR PROSITE: PS50059; FKBP_PPIASE_3; 1.
SQ SEQUENCE 477 AA; 52223 MW; 10C405953B17675E CRC64;

Query Match 18.5%; Score 72; DB 10; Length 477;
Best Local Similarity 26.4%; Pred. No. 52;
Matches 23; Conservative 17; Mismatches 27; Indels 20; Gaps 4;

```

QY 3 ETPETPETSSEEVITKANLIFANGSTQTAEFKGTFEKAT-----SEAYAYAD----- 50
Db 319 ESSKTPDKSAEKKTKKKK---KKPSDEAAEISGTVKEKQTPADSKSSQVRYTPNGLIVEE 375
QY 51 -TLKDNNGEYTDVADKGYTLNLFKAG 76
Db 376 LSMGKPNGRK----ADPGKTVSVRYIG 398

RESULT 8
Q9STK2 PRELIMINARY; PRT; 487 AA.
AC Q9STK2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical 53.3 kDa protein.
GN T30C3.20 OR AT4G25340.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bayan M., Rose M., Hempel S., Entian K.-D., Bancroft I., Mewes H.W.,
RA Meyer K.F.X., Lemcke K., Schueller C.;
RA Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RA Rose M., Hempel S., Entian K.-D., Mewes H.W., Lemcke K., Mayer K.F.X.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL079350; CAB45512.1; -.
DR EMBL; AL161563; CAB81345.1; -.
DR HSP; O00688; 1PBK
DR InterPro: IPR001179; FKBP_PPase.
DR Pfam; PF00254; FKBP; 1.
DR PROSITE; PS00454; FKBP_PPase_2; 1.
DR PROSITE; PS50059; FKBP_PPase_3; 1.
KW Hypothetical protein.
SQ SEQUENCE 487 AA; 53290 MW; 5B2FA21570BC0AC6 CRC64;

Query Match 18.5%; Score 72; DB 10; Length 487;
Best Local Similarity 26.4%; Pred. No. 54;
Matches 23; Conservative 17; Mismatches 27; Indels 20; Gaps 4;

QY 3 ETPETPETSSEEVITKANLIFANGSTQTAEFKGTFEKAT-----SEAYAYAD----- 50
Db 329 ESSKTPDKSAEKKTKKKK---KKPSDEAAEISGTVKEKQTPADSKSSQVRYTPNGLIVEE 385
QY 51 -TLKDNNGEYTDVADKGYTLNLFKAG 76
Db 386 LSMGKPNGRK----ADPGKTVSVRYIG 408

RESULT 9
O86487 PRELIMINARY; PRT; 947 AA.
AC O86487;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE SdrC protein.
GN "SDRC.
OS Staphylococcus aureus.

```

```

OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Newman;
RX MEDLINE=99098700; PubMed=9884231;
RA Josefsson E., McCrea K., Ni Eidhin D., O'Connell D., Cox J., Hook M.,
RA Foster T.J.;
RT "Three new members of the serine-aspartate repeat protein multigene
RT family of Staphylococcus aureus.";
RL Microbiology 144:3387-3395(1998).
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN BY
CC AN AMIDE BOND (BY SIMILARITY).
DR EMBL; AJ005645; CA006650.1; -.
DR InterPro: IPR005877; Gpos_YSIK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR InterPro: IPR006192; LPXTG
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YSIK_signal; 1.
DR TIGRFAMS; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMS; TIGR01168; YSIK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor.
SQ SEQUENCE 947 AA; 102888 MW; 3C6EFD6E35121554 CRC64;

Query Match 18.4%; Score 71.5; DB 2; Length 947;
Best Local Similarity 30.6%; Pred. No. 1.3e+02;
Matches 22; Conservative 17; Mismatches 22; Indels 11; Gaps 5;

QY 7 TPETDSEEVITKANLIFAN-GSTQTA-EFKGTFEKATSEAY-----AYADTLKKDNG-- 57
Db 407 TPETSKLDVTDQFDQVYISNDKNTATVDLMKG--QTSSNKKYIIQQVAYPDNSSTDNGKI 464

QY 58 EYTDVDVADKGYT 69
Db 465 DYTLDTDTKYS 476

RESULT 10
Q9KBX8 PRELIMINARY; PRT; 528 AA.
AC Q9KBX8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Nickel ABC transporter (Nickel-binding protein).
GN BH1796.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; AF001513; BAB05515.1; -.
DR InterPro: IPR000914; SBP_bac_5.
DR Pfam; PF00496; SBP_bac_5; 1.
KW Complete proteome.
SQ SEQUENCE 528 AA; 59381 MW; BC709550C21A66B2 CRC64;

Query Match 18.3%; Score 71; DB 16; Length 528;
Best Local Similarity 30.8%; Pred. No. 74;
Matches 20; Conservative 13; Mismatches 24; Indels 8; Gaps 3;

QY 10 TDSEEE-EVTIKANLIFANGSTQTA-EFKGTFEKATSEAYAYADTLKKDNGEYTDVADK 67
Db 106 TDGQHWTKLRDVTDFQNGKEMDAEAVKASLERALDEVAIENALKID-----EIEADG 159

```


RN	[1]	SEQUENCE	STRAIN=S
RP			
RC			

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:14:02 ; Search time 44.137 Seconds
(without alignments)
420.957 Million cell updates/sec

Title: US-08-325-278b-1_COPY_81_152

Perfect score: 371

Sequence: 1 KKTPEEPKEEVTIKANLIY.....GEYTDVADKGYTLNKFAG 72

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rviris.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	371	100.0	455	2 Q53291	Q53291 streptococ
2	371	100.0	719	2 Q51912	Q51912 peptostrept
3	308	83.0	992	2 Q51918	Q51918 peptostrept
4	98.5	26.5	216	4 Q9BPV7	Q9BPV7 homo sapien
5	98.5	26.5	398	4 Q9BPZ1	Q9BPZ1 homo sapien
6	93.5	25.2	398	11 Q9CZ02	Q9CZ02 mus musculu
7	93.5	25.2	398	11 Q91WD1	Q91WD1 mus musculu
8	89.5	24.1	1576	16 Q8ZEV8	Q8ZEV8 versinia pe
9	73	19.7	588	2 Q9S0T6	Q9S0T6 escherichia
10	70	18.9	1498	5 Q8IDP2	Q8IDP2 plasmodium
11	69.5	18.7	256	5 Q27039	Q27039 theileria p
12	69.5	18.7	256	5 Q27029	Q27029 theileria p
13	69.5	18.7	279	2 Q9ADV8	Q9ADV8 ehrlichia c
14	69.5	18.7	280	5 Q27030	Q27030 theileria p
15	69.5	18.7	451	2 Q9Z4J9	Q9Z4J9 lactobacill
16	69.5	18.7	623	2 Q9F4L0	Q9F4L0 fibrobacter

17	69.5	18.7	623	2 Q9F109	Q9F109 fibrobacter
18	69	18.6	529	1 Q48937	Q48937 methanosarc
19	68.5	18.5	243	17 Q9YF66	Q9YF66 aeropyrum p
20	68.5	18.5	280	4 Q92637	Q92637 homo sapien
21	68.5	18.5	374	4 Q92663	Q92663 homo sapien
22	68.5	18.5	375	4 Q92495	Q92495 homo sapien
23	67	18.1	492	17 Q973M8	Q973M8 sulfolobus
24	67	18.1	1433	2 Q45616	Q45616 bacillus su
25	66.5	17.9	171	6 Q95N20	Q95N20 sus scrofa
26	66.5	17.9	227	6 Q95N21	Q95N21 sus scrofa
27	66.5	17.9	256	6 Q95N22	Q95N22 sus scrofa
28	66.5	17.9	333	3 Q9UVE8	Q9UVE8 yarrowia li
29	66.5	17.9	357	6 Q8SPW5	Q8SPW5 macaca fasc
30	66	17.8	448	10 Q9SKP0	Q9SKP0 arabidopsis
31	66	17.8	585	16 Q8EJ99	Q8EJ99 shewanella
32	66	17.8	873	2 Q9Z6H6	Q9Z6H6 lactococcus
33	65.5	17.7	108	2 P72105	P72105 neisseria m
34	65.5	17.7	496	16 Q8F022	Q8F022 leptospira
35	65.5	17.7	718	16 Q98RK2	Q98RK2 mycoplasma
36	65.5	17.7	1167	17 Q8TUJ9	Q8TUJ9 methanosarc
37	65.5	17.7	4545	2 Q9X4W2	Q9X4W2 vibrio chol
38	65.5	17.7	4558	16 Q9KS12	Q9KS12 vibrio chol
39	65	17.5	359	5 Q9VBT9	Q9VBT9 drosophila
40	65	17.5	377	16 Q8CT26	Q8CT26 staphylococ
41	65	17.5	420	5 Q8T4C5	Q8T4C5 drosophila
42	65	17.5	420	5 Q8T3P4	Q8T3P4 drosophila
43	65	17.5	425	16 Q9K491	Q9K491 streptomyce
44	64.5	17.4	188	10 Q9LEH5	Q9LEH5 hordeum vul
45	64.5	17.4	383	5 Q9VTV4	Q9VTV4 drosophila

ALIGNMENTS

RESULT 1

Q53291 ID Q53291 PRELIMINARY; PRT; 455 AA.
AC Q53291;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Protein LG (Fragment).
OS Streptococcus sp.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1306;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93094283; PubMed=1460053;
RA Kihlberg B.M., Sjoerling U., Kastern W., Bjorck L.;
RT "Protein LG: a hybrid molecule with unique immunoglobulin binding properties."
RL J. Biol. Chem. 267:25583-25588(1992).
DR EMBL: S50809; AAA03280.1; -
DR HSSP: P06654; LPGA.
DR InterPro: IPR003147; B1.
DR InterPro: IPR000724; Igg_bind_B.
DR DR pfam: PF02246; B1; 4.
DR pfam: PF01378; Igg_binding_B; 2.
FT NON_TER 455
SQ SEQUENCE 455 AA; 49926 MW; 381FC235B8C8307B CRC64;

Query Match 100.0%; Score 371; DB 2; Length 455;
Best Local Similarity 100.0%; Pred. No. 4.7e-29;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKTPEEPKEEVTIKANLIYADGKQTAEFKGTFEATAEAYRYADALKKNGEYTDVA 60
|||||
Db 102 KKTPEEPKEEVTIKANLIYADGKQTAEFKGTFEATAEAYRYADALKKNGEYTDVA 161
QY 61 DKGYTLNKFAG 72
|||||
Db 162 DKGYTLNKFAG 173

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RESULT 2
Q51912 ID Q51912 PRELIMINARY; PRT; 719 AA.
AC DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Protein L precursor.
OS Peptostreptococcus magnus.
OC Bacteria; Firmicutes; Clostridia; Clostridiales;
OC Peptostreptococcaceae; Finegoldia.
OX NCBI_TaxID=1260;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=312;
RX MEDLINE=90215984; PubMed=2108927;
RA Kasten W., Holst E., Nielsen E., Sjoerding U., Bjorck L.;
RT "Protein L, a bacterial immunoglobulin-binding protein and possible
RT virulence determinant.";
RL Infect. Immun. 58:1217-1222(1990).
CC -!- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN BY
CC AN AMIDE BOND (BY SIMILARITY).
CQ EMBL; M86697; AAA25612.1; -.
DR EMBL; M86697; AAA25612.1; -.
DR InterPro; IPR003147; B1.
DR InterPro; IPR004829; Csurface_antigen.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR006192; LPXTG.
DR Pfam; PF02246; B1; 5.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR ProDom; PD153432; Csurface_antigen; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 719 PROTEIN L.
SQ SEQUENCE 719 AA; 78983 MW; 963A8D76D5E34DD2 CRC64;

Query Match 100.0%; Score 371; DB 2; Length 719;
Best Local Similarity 100.0%; Pred. No. 8.le-29;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEKTEPEKKEVTKANLIYADGKTQTAEFGTTEATAEAYRYADALKKNGEYTVDA 60
Db 174 KEKTEPEKKEVTKANLIYADGKTQTAEFGTTEATAEAYRYADALKKNGEYTVDA 233
QY 61 DKGYTLNKFAG 72
Db 234 DKGYTLNKFAG 245

RESULT 3
Q51918 ID Q51918 PRELIMINARY; PRT; 992 AA.
AC DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Protein L precursor.
OS Peptostreptococcus magnus.
OC Bacteria; Firmicutes; Clostridia; Clostridiales;
OC Peptostreptococcaceae; Finegoldia.
OX NCBI_TaxID=1260;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=312;
RX MEDLINE=90215984; PubMed=2108927;
RA Kasten W., Holst E., Nielsen E., Sjoerding U., Bjorck L.;
RT "Protein L, a bacterial immunoglobulin-binding protein and possible
RT virulence determinant.";
RL Infect. Immun. 58:1217-1222(1990).
CC -!- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN BY
CC AN AMIDE BOND (BY SIMILARITY).
CQ EMBL; M86697; AAA25612.1; -.
DR EMBL; M86697; AAA25612.1; -.
DR InterPro; IPR003147; B1.
DR InterPro; IPR004829; Csurface_antigen.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR006192; LPXTG.
DR Pfam; PF02246; B1; 5.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR ProDom; PD153432; Csurface_antigen; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 719 PROTEIN L.
SQ SEQUENCE 719 AA; 78983 MW; 963A8D76D5E34DD2 CRC64;

Query Match 100.0%; Score 371; DB 2; Length 719;
Best Local Similarity 100.0%; Pred. No. 8.le-29;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEKTEPEKKEVTKANLIYADGKTQTAEFGTTEATAEAYRYADALKKNGEYTVDA 60
Db 174 KEKTEPEKKEVTKANLIYADGKTQTAEFGTTEATAEAYRYADALKKNGEYTVDA 233
QY 61 DKGYTLNKFAG 72
Db 234 DKGYTLNKFAG 245

RESULT 4
Q9BPV7 ID Q9BPV7 PRELIMINARY; PRT; 216 AA.
AC Q9BPV7;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Similar to BNS1 (BHK21) temperature sensitivity complementing.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003039; AAH03039.1; -.
DR EMBL; BC000516; AAH00516.1; -.
SQ SEQUENCE 216 AA; 24806 MW; F29028EAECA8DB04 CRC64;

Query Match 26.5%; Score 98.5; DB 4; Length 216;
Best Local Similarity 34.6%; Pred. No. 0.04;
Matches 28; Conservative 10; Mismatches 24; Indels 19; Gaps 3;

QY 3 KTEPEKKEVTKANLIYAD-----GKTQTAETFGTTEATAEAYRYADALKK 50
Db 66 KIKEPEKEVTVKKERDRDRQREGHGRGRPEVIQSHSIFEQGPAMMK-----KK 120
QY 51 DNGEYTVDAVKG--YTLNLIK 69
Db 121 GNWDKTVDSMDGFSHIINIK 141

RESULT 5
Q9BP21 ID Q9BP21 PRELIMINARY; PRT; 992 AA.
AC DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Protein L precursor.
OS Peptostreptococcus magnus.
OC Bacteria; Firmicutes; Clostridia; Clostridiales;
OC Peptostreptococcaceae; Finegoldia.
OX NCBI_TaxID=1260;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=312;
RX MEDLINE=90215984; PubMed=2108927;
RA Kasten W., Holst E., Nielsen E., Sjoerding U., Bjorck L.;
RT "Protein L, a bacterial immunoglobulin-binding protein and possible
RT virulence determinant.";
RL Infect. Immun. 58:1217-1222(1990).
CC -!- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN BY
CC AN AMIDE BOND (BY SIMILARITY).
CQ EMBL; M86697; AAA25612.1; -.
DR EMBL; M86697; AAA25612.1; -.
DR InterPro; IPR003147; B1.
DR InterPro; IPR004829; Csurface_antigen.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR006192; LPXTG.
DR Pfam; PF02246; B1; 5.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR ProDom; PD153432; Csurface_antigen; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 719 PROTEIN L.
SQ SEQUENCE 719 AA; 78983 MW; 963A8D76D5E34DD2 CRC64;

Query Match 100.0%; Score 371; DB 2; Length 719;
Best Local Similarity 100.0%; Pred. No. 8.le-29;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEKTEPEKKEVTKANLIYADGKTQTAEFGTTEATAEAYRYADALKKNGEYTVDA 60
Db 174 KEKTEPEKKEVTKANLIYADGKTQTAEFGTTEATAEAYRYADALKKNGEYTVDA 233
QY 61 DKGYTLNKFAG 72
Db 234 DKGYTLNKFAG 245
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ID Q9BP21 PRELIMINARY; PRT; 398 AA.
AC Q9BP21; 25.2%; Score 93.5; DB 11; Length 398;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Similar to BNS1 (BHK21) temperature sensitivity complementing.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung, and Lymph;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC004484; AAH04484.1; -
DR EMBL: BC02603; AAH02603.1; -
SQ SEQUENCE 398 AA; 44396 MW; CD8AFF3257B78410 CRC64;

Query Match 26.5%; Score 98.5; DB 4; Length 398;
Best Local Similarity 34.6%; Pred. No. 0.083;
Matches 28; Conservative 10; Mismatches 24; Indels 19; Gaps 3;

QY 3 KTEPEKPEVITKANLIYAD-----GKTQTAFFKGTFFETAAYRYADALKK 50
DB 66 KIKEPKEEVYMKKREDRDRQREHGGRGPRVQSHSIFQGPAAEMMK-----KK 120
QY 51 DNGEYTVADVADKG--YTLNIK 69
DB 121 GNWKTVDVSDMGPSHIINIK 141

RESULT 6
Q9CZ02 PRELIMINARY; PRT; 398 AA.
ID Q9CZ02; 25.2%; Score 93.5; DB 11; Length 398;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE 2810426M17Rik protein.
GN 2810426M17Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fieischmann W., Gaasterland T., Glissi C., King B., Kuchiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kotsuki S.,
RA Hayashizaki Y.;
RL "Functional annotation of a full-length mouse cDNA collection";
RL Nature 409:685-690(2001).
DR EMBL: AK013165; BAB28687.1; -
DR MGD: MGI:1914315; 2810426M17Rik.
SQ SEQUENCE 398 AA; 44336 MW; B70179A124C1231B CRC64;

Query Match 25.2%; Score 93.5; DB 11; Length 398;
Best Local Similarity 33.3%; Pred. No. 0.26;
Matches 27; Conservative 11; Mismatches 24; Indels 19; Gaps 3;

QY 3 KTEPEKPEVITKANLIYAD-----GKTQTAFFKGTFFETAAYRYADALKK 50
DB 66 KIKEPKEEVYMKKREDRDRQREHGGRGPRVQSHSIFQGPAAEMMK-----KK 120
QY 51 DNGEYTVADVADKG--YTLNIK 69
DB 121 GNWKTVDVSDMGPSHIINIK 141

RESULT 7
Q91WD1 PRELIMINARY; PRT; 398 AA.
ID Q91WD1; 25.2%; Score 93.5; DB 11; Length 398;
AC Q91WD1; 33.3%; Pred. No. 0.26;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE RIKEN cDNA 2810426M17 gene.
GN 2810426M17Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary gland;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC016102; AAH16102.1; -
DR MGD: MGI:1914315; 2810426M17Rik.
SQ SEQUENCE 398 AA; 44323 MW; D509DE632C656FFD CRC64;

Query Match 25.2%; Score 93.5; DB 11; Length 398;
Best Local Similarity 33.3%; Pred. No. 0.26;
Matches 27; Conservative 11; Mismatches 24; Indels 19; Gaps 3;

QY 3 KTEPEKPEVITKANLIYAD-----GKTQTAFFKGTFFETAAYRYADALKK 50
DB 66 KIKEPKEEVYMKKREDRDRQREHGGRGPRVQSHSIFQGPAAEMMK-----KK 120
QY 51 DNGEYTVADVADKG--YTLNIK 69
DB 121 GNWKTVDVSDMGPSHIINIK 141

RESULT 8
Q8ZEV8 PRELIMINARY; PRT; 1576 AA.
ID Q8ZEV8; 25.2%; Score 93.5; DB 11; Length 398;
AC Q8ZEV8; 33.3%; Pred. No. 0.26;
DT 01-WAR-2002 (TREMBLrel. 20, Created)
DT 01-WAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-WAR-2003 (TREMBLrel. 23, Last annotation update)
DE Putative hemolysin.
GN YPO2045 OR Y2267.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebatia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltham T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrall B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague."

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RL Nature 413:523-527(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perrin N.I., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM.";
RL J. Bacteriol. 184:4601-4611(2002).
DR EMBL: AJ414151; CAC90857.1; -.
DR EMBL: AB013829; AAM85827.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 1576 AA; 169976 MW; 7029BC4BA386424C CRC64;

Query Match      24.1%; Score 89.5; DB 16; Length 1576;
Best Local Similarity 27.5%; Pred. No. 3.4;
Matches 30; Conservative 11; Mismatches 25; Indels 43; Gaps 4;

QY 1 KEKTPPEPKEEVTIKANLIYADGKTQTAEFGKTF-----EE----- 36
Db 1001 KANTTQEKGEVSLRG-----GMTATQEIKGHLGKVAETSGQDSYAEMLVGNINAKSG 1054

QY 37 ----ATAEAYRYADALKDNGEYTVD-----VADKGYTLNKFAG 72
Db 1055 VSIKTTGDYATYATNIEGGNDITTDAGNNLYFDQVQDSQRSNNIKFSG 1103

RESULT 9
Q9S0T6 PRELIMINARY; PRT; 588 AA.
AC Q9S0T6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Flagellin.
GN FLIC.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K42;
RA Ohnishi K., Ishioka K., Matsuba T., Harayama S.;
RT "Cloning of H antigen genes in E. coli serotypes and expression in
RT E. coli K-12.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB028476; BAA85085.1; -.
DR InterPro: IPR001492; Flagellin.
DR InterPro: IPR001029; Flagellin_C.
DR Pfam: PF00700; Flagellin_C; 1.
DR Pfam: PF00669; Flagellin_N; 1.
DR PRINTS: PD00207; FLAGELLIN.
DR PRODOM: PD000316; Flagellin_C; 2.
SQ SEQUENCE 588 AA; 60458 MW; 9FFFE6D819DFE55D CRC64;

Query Match      19.7%; Score 73; DB 2; Length 588;
Best Local Similarity 24.6%; Pred. No. 48;
Matches 29; Conservative 19; Mismatches 20; Indels 50; Gaps 7;

QY 5 PPEPKEEV-----TIKANLIYAD---GKTQTAEF-----KGTFEATA-EAYRY 44
Db 367 PDDASDDVLGTISYSKSKVDVLADTKATGNTTTFNSGIMTSKVSFDAGTSTDTFKD 426

QY 45 AD-----ALKKDNGEYF-----VDVADK-----GYTLNKFAG 72
Db 427 ADGAIKTKKEYTTSYAVNKDGEVTVADYAAVDSADKAVDDTKYKPTIGATVNLNSAG 484

RESULT 10
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Q8IDP2 PRELIMINARY; PRT; 1498 AA.
AC Q8IDP2;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN MAL13P1.226.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RA Harris B., Lennard N., Clark L., Line A., Barron A., Corton C.,
RA Berriman M., Pain A., Hall N., Atkin R., Chillingworth C., Doggett J.,
RA Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrell B.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL844509; CAD52577.1; -.
KW Hypothetical protein.
SQ SEQUENCE 1498 AA; 177555 MW; 10B973D7FE70F301 CRC64;

Query Match      18.9%; Score 70; DB 5; Length 1498;
Best Local Similarity 28.7%; Pred. No. 2.9e+02;
Matches 25; Conservative 14; Mismatches 28; Indels 20; Gaps 4;

QY 1 KEKTPPEPKEEVTIKANLI-----YADGKTQTA-----EFKGTFEATAEAY---RY 44
Db 1262 KEKLELEREKQLLRKKLLNCSIGNVKYSFESDSTSDSDSGDKGFKNPLYEPYNESEH 1321

QY 45 ADALKKDNGE---YTVDVADKGYTLN 67
Db 1322 TDILKKNNSPEYLYNDNVFORGECLN 1348

RESULT 11
Q27039 PRELIMINARY; PRT; 256 AA.
AC Q27039;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Merozoite surface glycoprotein precursor (Fragment).
GN TPMS1.
OS Theileria parva.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;
OC Theileria.
OX NCBI_TaxID=5875;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Muguga;
RA Shields B.R., d'Oliviera C., McKellar S., Ben-Miled L., Kawazu S.,
RA Hide G.;
RT "Selection of Diversity at Putative Glycosylation sites in the
RT immunodominant merozoite/piroplasm surface antigen of Theileria
RT parasites.";
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z48740; CAA88632.1; -.
DR InterPro: IPR003407; Merozoite_Agen.
DR Pfam: PF02488; EMA; 1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
FT NON_TER 256 256
SQ SEQUENCE 256 AA; 29528 MW; C982AEE71A45DC5B CRC64;

Query Match      18.7%; Score 69.5; DB 5; Length 256;
Best Local Similarity 31.7%; Pred. No. 40;
Matches 19; Conservative 10; Mismatches 30; Indels 1; Gaps 1;

QY 1 KEKTPPEPKEEVTIKANLIYADGKTQTAEFGKTFEATAEAYRYADALKKONGEYTVDA 60
Db 25 EEEKKKKKEDLTVDVTLSSWENVTSTPEAGGTLKAN-EGYRFKTKLVGDKTLYNVDS 83
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RESULT 12
Q27029 Q27029 PRELIMINARY; PRT; 256 AA.
AC Q27029;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Merozoite surface glycoprotein precursor (Fragment).
TPMS1.
GN Theileria parva.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;
OC Theileria.
OX NCBI_TaxID=5875;
[1]
SEQUENCE FROM N.A.
RN STRAIN=MUGUGA;
RX MEDLINE=96089836; PubMed=8538686;
RA Shields B.R., d'Oliveira C., McKellar S., Ben-Miled L., Kawazu S.,
RA Hide G.;
RT "Selection of diversity at putative glycosylation sites in the
RT immunodominant merozoite/piroplasm surface antigen of Theileria
RT parasites."
RL Mol. Biochem. Parasitol. 72:149-162(1995).
DR EMBL: U22889; AAC46910.1; -.
DR InterPro: IPR003407; Merozoite_Agen.
DR Pfam: PF02488; EMA; 1.
KW Signal.
FT SIGNAL.
FT NON_TER
SQ SEQUENCE 256 AA; 29528 MW; C982AE71A45DC5B CRC64;

Query Match 18.7%; Score 69.5; DB 5; Length 256;
Best Local Similarity 31.7%; Pred. No. 40;
Matches 19; Conservative 10; Mismatches 30; Indels 1; Gaps 1;

QY 1 KEKTEPEPKKEVTIKANLIYADGKTQTAEFGTFFETAEAYRYADALKKNGEYTVDDVA 60
   :|: | |:|:|: | : | | | | | | | | | | | | | | | | | | | | | |
DB 25 EEKKKEKKEDLTVDVTLSSWENVTSTPEAGGTLLKAN-EGYRFKTLKVGDKTYLNVDTS 83


RESULT 13
Q9ADV8 Q9ADV8 PRELIMINARY; PRT; 279 AA.
AC Q9ADV8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Major outer membrane protein P30-11.
GN Ehrlichia canis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Anaplasmataceae; Ehrlichia.
OX NCBI_TaxID=944;
[1]
SEQUENCE FROM N.A.
RN STRAIN=Oklahoma;
RX MEDLINE=98371112; PubMed=9705412;
RA Ohashi N., Unver A., Zhi N., Rikihisa Y.;
RT "Cloning and characterization of multigenes encoding the
RT immunodominant 30-kilodalton major outer membrane proteins of
RT Ehrlichia canis and application of the recombinant protein for
RT serodiagnosis."
RT J. Clin. Microbiol. 36:2671-2680(1998).
[2]
SEQUENCE FROM N.A.
RN STRAIN=Oklahoma;
RX MEDLINE=21153566; PubMed=11254561;
RA Ohashi N., Rikihisa Y., Unver A.;
RT "Analysis of transcriptionally Active Gene Clusters of Major Outer
RT Membrane Protein Multigene Family in Ehrlichia canis and E.
RT chaffeensis."
RT Infect. Immun. 69:2083-2091(2001).
DR EMBL: AF078553; AAK28690.1; -.

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RESULT 12
 Q27029 PRELIMINARY; PRT; 256 AA.
 AC Q27029;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Merzoite surface glycoprotein precursor (Fragment).
 TPMS1.
 GN Theileria parva.
 OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
 OC Theileria.
 OX NCBI_TaxID=5875;
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=Muguga;
 RC MEDLINE=96089836; PubMed=8538686;
 RA Shields B.R., d'Oliveira C., McKellar S., Ben-Miled L., Kawazu S.,
 RA Hide G.;
 RT "Selection of diversity at putative glycosylation sites in the
 RT immunodominant merzoite/piroplasm surface antigen of Theileria
 RT parasites.";
 RL Mol. Biochem. Parasitol. 72:149-162(1995).
 DR EMBL: U22889; AAC46910.1; -;
 DR InterPro: IPR003407; Merzoite_Agen.
 DR Pfam: PF02488; EMA; 1.
 GN Signal.
 FT SIGNAL 1 23 POTENTIAL.
 FT NON_TER 256 256
 SQ SEQUENCE 256 AA; 29528 MW; C982AEE71A45DC5B CRC64;
 Query Match 18.7%; Score 69.5; DB 5; Length 256;
 Best Local Similarity 31.7%; Pred. No. 40;
 Matches 19; Conservative 10; Mismatches 30; Indels 1; Gaps 1;
 QY 1 KEKTEPEKKEVTIKANLIYADGKQTQTAEFKGTFFETAEAYRYADALKKNGEYTVDDVA 60
 DB 25 EEEKKKEKEDLTVDVTLSSWENVTSTPEAGGTLKAN-EGYRFTKLVGDKTLYNVDTS 83
 RESULT 13
 Q9ADV8 PRELIMINARY; PRT; 279 AA.
 AC Q9ADV8;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE Major outer membrane protein P30-11.
 GN P30-11.
 OC Ehrlichia canis.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
 OC Anaplasmataceae; Ehrlichia.
 OX NCBI_TaxID=944;
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=Oklahoma;
 RC MEDLINE=98371112; PubMed=9705412;
 RA Ohashi N., Unver A., Zhi N., Rikihisa Y.;
 RT "Cloning and characterization of multigenes encoding the
 RT immunodominant 30-kilodalton major outer membrane proteins of
 RT Ehrlichia canis and application of the recombinant protein for
 RT serodiagnosis.";
 RL J. Clin. Microbiol. 36:2671-2680(1998).
 [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=Oklahoma;
 RC MEDLINE=21153566; PubMed=11254561;
 RA Ohashi N., Rikihisa Y., Unver A.;
 RT "Analysis of transcriptionally Active Gene Clusters of Major Outer
 RT Membrane Protein Multigene Family in Ehrlichia canis and E.
 RT chaffeensis.";
 RL Infect. Immun. 69:2083-2091(2001).
 DR EMBL: AF078553; AAK28690.1; -;
 DR InterPro: IPR003407; Merzoite_Agen.
 DR Pfam: PF02488; EMA; 1.
 GN Signal.
 FT SIGNAL 1 23 POTENTIAL.
 FT NON_TER 256 256
 SQ SEQUENCE 256 AA; 29528 MW; C982AEE71A45DC5B CRC64;
 Query Match 18.7%; Score 69.5; DB 5; Length 280;
 Best Local Similarity 31.7%; Pred. No. 44;
 Matches 19; Conservative 10; Mismatches 30; Indels 1; Gaps 1;
 QY 1 KEKTEPEKKEVTIKANLIYADGKQTQTAEFKGTFFETAEAYRYADALKKNGEYTVDDVA 60
 DB 25 EEEKKKEKEDLTVDVTLSSWENVTSTPEAGGTLKAN-EGYRFTKLVGDKTLYNVDTS 83
 RESULT 14
 Q27030 PRELIMINARY; PRT; 280 AA.
 AC Q27030;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE 32 kda surface antigen precursor (Msl protein precursor).
 GN Msl.
 OC Theileria parva.
 OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
 OC Theileria.
 OX NCBI_TaxID=5875;
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=MUGUGA;
 RC Skilton R.A., Wells C.C.W., Gobright E.E.I., Morzaria S.S.P.;
 RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
 [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=MUGUGA;
 RC Shields B.R., Fox M., McKellar S., Kinnaird J., Swan D.G.;
 RA "An upstream element of the Tamsi gene is a site of DNA - protein
 RT interactions during differentiation to the merozoite in Theileria
 RT annulata.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: L47209; AAA75252.1; -;
 DR EMBL: AJ276655; CAB93689.1; -;
 DR InterPro: IPR003407; Merzoite_Agen.
 DR Pfam: PF02488; EMA; 1.
 GN Signal.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 280 32 KDA SURFACE ANTIGEN.
 SQ SEQUENCE 280 AA; 32047 MW; 6BFF7BB6D44D589F CRC64;
 Query Match 18.7%; Score 69.5; DB 5; Length 280;
 Best Local Similarity 31.7%; Pred. No. 44;
 Matches 19; Conservative 10; Mismatches 30; Indels 1; Gaps 1;
 QY 1 KEKTEPEKKEVTIKANLIYADGKQTQTAEFKGTFFETAEAYRYADALKKNGEYTVDDVA 60
 DB 25 EEEKKKEKEDLTVDVTLSSWENVTSTPEAGGTLKAN-EGYRFTKLVGDKTLYNVDTS 83
 RESULT 15
 Q9Z4J9 PRELIMINARY; PRT; 451 AA.
 AC Q9Z4J9;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE S-layer protein precursor.
 GN S-LAYER.
 OS Lactobacillus crispatus.
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.

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OX NCBI_TaxID=47770;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M247;
RA Ventura M., Callegari M., Morelli L.;
RT "Detection of a strain specific region in the S-layer sequence of
RL Lactobacillus crispatus.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ007839; CAA07708.1;
DR InterPro; IPR004903; SLAP.
DR Pfam; PF03217; SLAP; 1.
KW S-layer; Signal.
FT SIGNAL 1 31 POTENTIAL.
FT CHAIN 32 451 S-LAYER PROTEIN.
SQ SEQUENCE 451 AA; 47012 MW; 7F79C6D0F7C458F7 CRC64;

Query Match 18.7%; Score 69.5; DB 2; Length 451;
Best Local Similarity 24.4%; Pred. No. 78;
Matches 29; Conservative 7; Mismatches 24; Indels 59; Gaps 4;

QY 4 TPEPKKEVTKANLIYA-----DGKTQTAE 29
   || : || : ||
Db 55 TPADAKYDVDPNLTATAASTVNGQTINGSITGNITASYNQSYTGTLDTKNGKVSAD 114
   || : || : ||

QY 30 FKGTPEEATAEAYRYADALKKRDNGEYTDV-----ADKGYTL-----NIKFGAG 72
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 115 SKGT-----AVTDFSKLTNGSYTIVTGVSPFNGTANANKTITIGSKNSNVKFGAG 164
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Search completed: September 3, 2003, 11:23:12
Job time : 47.137 secs